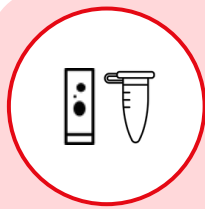


## Signomax™ Epigenomics As A Service

Auristone offers Epigenomics-as-a-Service to help propel your discoveries. We aim to provide you with the support you need to accelerate your research endeavours. Signomax™ offers both RNA Sequencing (RNA-Seq) and/or Nano Chromatin Immunoprecipitation Sequencing (ChIP-Seq) as a service.

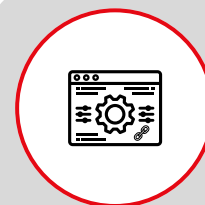
### Signomax™ Service



Multiple sample types



High Pass Rate



Customisable Analysis



Publication ready data



End-to-End Support



Post Completion:  
Signomax™ Report



### RNA-Seq

RNA-Seq is a technique that uses Next-Generation Sequencing (NGS) to provide active transcriptome profiling, which includes identifying and quantifying gene expression. We provide end-to-end workflow for Whole Transcriptome Sequencing (WTS) for Formalin-Fixed Paraffin-Embedded (FFPE) samples. Signomax™ accommodates low sample input and has no limits on DV200.

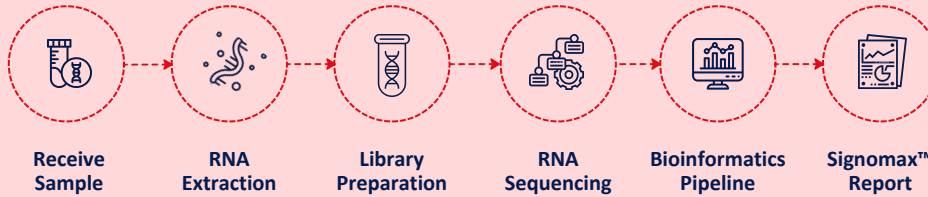
	Auristone	Vendor A	Vendor B	Vendor C
Input amount	300 ng	500 ng	500 ng	1 µg
DV200	No limit	No limit	50%	Not specified

### Sample Requirement

Sample Type	Dimensions	Minimum Amount
FFPE slides	Thickness: 5 µm thick/slide	10 slides + 1 H&E stained slide
FFPE blocks	Tissue surface area: min 2.5 cm <sup>2</sup> /section	1 block + 1 H&E stained slide*
Extracted RNA	-	400 ng

\*where applicable

### Workflow



As part of the service, we provide raw read files (FASTQ), aligned reads files (BAM), gene-level counts, transcript-level counts and genomic distribution of aligned reads. For in-depth, customised bioinformatics analysis or more information on our services, please contact us.

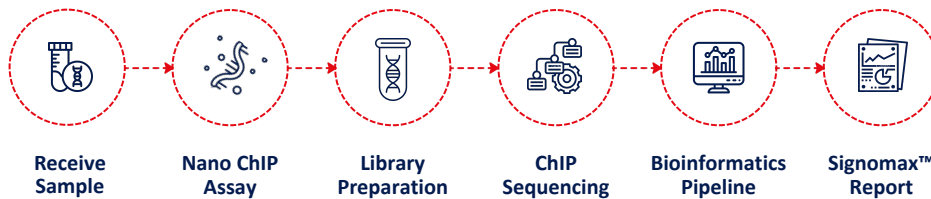
### Nano ChIP-Seq

ChIP-Seq is the most commonly employed method for examining interactions between proteins and DNA, and for detecting localization of histone modifications across the genome. Histone marks that are used in Signomax™ include H3K4me3 and H3K27ac. We provide end-to-end workflow for fresh frozen/FFPE samples with low input.

### Sample Requirement

Sample Type	Minimum Amount
Fresh frozen (cell line)	2 million cells per mark
Fresh frozen (tissue)	10 mg tissue per mark
FFPE	15 slides per mark

### Workflow



We provide raw read files (FASTQ), aligned reads files (BAM), read coverage (bigWig), localization and visualization of reads on genome as well as regions identified from peak calling. For more information on our services, please do not hesitate to contact us.

Order RNA-Seq or ChIP-Seq alone, or combine them both to obtain a comprehensive epigenomic profile of gene expression patterns and histone modification localizations.

For more information on Signomax™ as a service, contact us at:

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