

EPIGENOMICS

| Application | Sample Requirements | Read Length ^{&} | Average Output ^{&} | Platform | Sample Minimum* | Deliverables |
|-------------------------------------|---|--------------------------------------|---------------------------------|----------|-----------------|---|
| ATAC-Seq | Cells: 5,000-50,000 from fresh or cryopreserved cells Viability: > 90% Other: 1.5 ml tube | Nucleosome positioning: 2 x 75 bp | 2 x 40M reads | NextSeq | 8 | Excel peak calling table, QC report, FASTQ files |
| | | TF profiling: 2 x 50 bp | 2 x 120M reads | NovaSeq | 6 | |
| ChIP-Seq (H3K27ac) | Amount: 1x10 ⁷ cells | 1 x 75 bp | 25M reads | NextSeq | 12 | |
| ChIP-Seq (library preparation only) | Amount: ≥ 50 ng Volume: ≥ 15 ml Other: ≥ 5-fold increase over negative control; input control | 1 x 75 bp | TF profiling: 25M reads | NextSeq | 12 | |
| | | | Histone profiling: 50M reads | NextSeq | 12 | |
| Whole Genome Bisulfite Sequencing | Integrity: ≥ 12 kb Amount: ≥ 1 μg [#] Volume: ≥ 20 μl | 2 x 150 bp | 30X coverage | NovaSeq | 4 | Bedgraph with CpG sites, bedgraph with all C, summary QC table, MultiQC report, FASTQ files |

* Turnaround time of 12-15 business days for library preparation and sequencing if sample minimum is met. If sample minimum is not met, please allow for extra lead time. Alternatively, samples may be processed sooner for an additional cost. Contact genomics@cshs.org for more information.

[#] As measured with a fluorescent dye, such as Qubit or QUANT-iT PicoGreen.

[§] For alternate read lengths or outputs, please contact genomics@cshs.org.