**OHSU Research Cores and Shared Resources**

**Massively Parallel Sequencing**

A unit of the Integrated Genomics Laboratory

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**The MPSSR provides genomic scale sequencing services to the OHSU community.**

**Introduction**

The MPSSR uses the Illumina HiSeq 2500 and NextSeq 500 to generate genomic scale sequencing data for a variety of applications. Each lane of the HiSeq 2500 high throughput eight lane flow cell can sequence approximately 280 million unique templates and generate as many as 56 billion bases. One run on the single lane NextSeq 500 flow cell can sequence approximately 400 million unique templates and generate as many as 120 billion bases.

**Services**

The MPSSR provides library preparation services for the following applications:

1. Standard RNAseq
2. Sequence capture DNAseq
3. Whole genome DNAseq
4. Metagenomics
5. ChIPseq
6. RNAseq stranded
7. RNAseq low input

Investigators may submit their own libraries as well.

Sequencing data is assembled by the MPSSR into fastq files using the Illumina Bcl2Fastq package. Fastq format is the standard for high throughput sequencing data and the files can be used for a variety of analyses - including, but not limited to, alignment to a reference genome, examination of differential expression, identification of genomic variants, and determination of enrichment levels from protocols such as chromatin immunoprecipitation (ChIP).

**Equipment**

- Illumina HiSeq 2500
- Illumina NextSeq 500
- Illumina cBot
- Covaris S2 Sonicator
- Agilent Bioanalyzer
- Agilent TapeStation
- ABI StepOne and StepOnePlus Real Time PCR Systems
- 10x Genomics Single Cell System

**Information**

Please visit our website for information:

[www.ohsu.edu/mpssr](http://www.ohsu.edu/mpssr)

Drop-ins for consultation are welcome. Come by to ask questions about designing experiments and working with the data or just to learn about the technology.

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**Director**
Robert Searles, Ph.D.

**Staff**
Amy Carlos
Rachel Henson

**Informatics**
Chenwei Lin

**Location**
Laboratory Room 5390
Office Room 5327A
Richard Jones Hall
3181 SW Sam Jackson Park Road,
Portland OR 97239

**Email**
searlesr@ohsu.edu
carlosa@ohsu.edu

**Phone**
Director
503.418.2736
Lab Staff Office
503.418.9378

**Web**
[www.ohsu.edu/mpssr](http://www.ohsu.edu/mpssr)