**Sequencing Terminology List**

**Sequencing**- Determining composition of nucleic acids

**NGS**- Next-generation sequencing; sequencing in a high-throughput, parallel manner

**Sample-** Nucleic acid from a single biological source.

**Library**- A nucleic acid sample prepared for NGS, includes indexes and adaptors

**Library prep**- Molecular techniques to generate libraries for sequencing, including adding indexes and adaptors

**Index**- Unique nucleic acid sequence added to individual library to distinguish between samples. Allows for multiplexing.

**Adaptors**- Specific nucleic acid (or protein for Nanopore) added to samples needed to sequence.

**Metagenomics**- Sequencing approach that identifies ALL nucleic acid in a sample.

**Amplicon-** Sequencing approach that amplifies SPECIFIC nucleic acid. PCR based.

**Enrichment**- Any technique that increases the ratio of target nucleic acid

**Depletion-** Any technique that decreases the ratio of non-target nucleic acid

**Multiplexing-** Sequencing more than 1 sample on a flow cell

**Flow cell**- Matrix where sequencing physically occurs.

**Illumina**- Short reads, sequencing by synthesis.

**MinION**- Long-reads, single molecule sequencing.

**Base Calling-** Converting molecule data to sequence data

**Read**- Sequence of a single molecule.

**.FastQ-** Text based format of nucleotide data (or amino acid) that includes quality scores

**.Fasta-** Text based format of nucleotide data (or amino acid) that does not include quality scores

**Contig**- Contiguous sequence. Assembled reads.

**Q score**- Quality score.

**Contamination**- Sequences from sources other than target.