

1. Whole Genome Sequencing (WGS), low coverage depth:
 - a. Perform WGS in DNA extracted from FFPE samples with a validated, documented (SOP) methodology.
 - b. Perform WGS in DNA extracted from fresh Frozen samples with a validated, documented (SOP) methodology.
 - c. Perform WGS with minimal DNA quantities from samples of limiting size, such as core needle biopsies with a validated, documented (SOP) methodology.
 - d. Produce WGS for both frozen and FFPE cases with the following requirements:
 - i. Quality control metrics:
 1. Average coverage of bases will be 10X or greater.
 2. >85% of bases in genome will have >5X coverage
 3. At least 30 Gb sequence per sample
 - ii. Production time frame: 4 months
 - iii. Minimum case capacity: 100 cases/month; 1200 cases/year
2. Whole Genome Sequencing (WGS), high coverage depth:
 - a. Perform WGS in DNA extracted from FFPE samples with a validated, documented (SOP) methodology.
 - b. Perform WGS in DNA extracted from fresh Frozen samples with a validated, documented (SOP) methodology.
 - c. Perform WGS with minimal DNA quantities from samples of limiting size, such as core needle biopsies with a validated, documented (SOP) methodology.
 - d. Produce WGS for both frozen and FFPE cases with the following requirements:
 - i. Quality control metrics:
 1. Average coverage of bases will be 30X or greater for non-tumor and 80X or greater for tumor.
 2. >85% of bases in genome will have >15X coverage for non-tumor and >40x for tumor.
 3. At least 220 Gb sequence per sample
 - ii. Production time frame: 4 months
 - iii. Minimum case capacity: 100 cases/month; 1200 cases/year
3. Exome Sequencing (WES):
 - a. Perform WES in DNA extracted from FFPE samples with a validated, documented (SOP) methodology.
 - b. Perform WES in DNA extracted from fresh Frozen samples with a validated, documented (SOP) methodology.
 - c. Perform WES with minimal DNA quantities from samples of limiting size, such as core needle biopsies with a validated, documented (SOP) methodology.
 - d. Develop methods and SOP for WES using different capture methods as required by the Program Office
 - e. Produce WES for both frozen and FFPE cases with the following requirements:
 - i. Quality control metrics:
 1. Average coverage of bases within the targeted exome will be 150X or greater.
 2. >75% of reads will be on-target
 3. >85% of reads will be on-target +/- 100 bp
 4. >85% of bases in target exome will have >40X coverage
 5. >75% of bases in target exome will have >80X coverage
 6. At least 8 Gb sequence per sample

- ii. Production time frame: 3 months
- iii. Minimum case capacity: 100 cases/month; 1200 cases/year

4. Total RNA sequencing (RNAseq)

- a. Perform RNAseq in total RNA extracted from FFPE samples with a validated, documented (SOP) methodology.
- b. Perform RNAseq in total RNA extracted from fresh Frozen samples with a validated, documented (SOP) methodology.
- c. Perform RNAseq with minimal total RNA quantities from samples of limiting size, such as core needle biopsies with a validated, documented (SOP) methodology.
- d. Develop methods and SOP for RNAseq using different capture methods as required by the Program Office
- e. Produce RNAseq for both frozen and FFPE cases with the following requirements:
 - i. Quality Control Metrics:
 - 1. % rRNA reads - typically this is <2%
 - 2. Number of Mapped reads - >150 Million reads
 - 3. Read 1/Read 2 Ratio: 1:1 with a maximum 20% deviation
 - 4. % Mapped Reads: > 85%
 - 5. % Properly Paired reads - >80%
 - 6. Maximum Number of genes not detected: 4000
 - ii. Production time frame: 3 months
 - iii. Minimum case capacity: 100 cases/month; 1200 cases/year

5. Transcriptome Sequencing (mRNASeq):

- a. Perform mRNAseq in RNA extracted from FFPE samples with a validated, documented (SOP) methodology.
- b. Perform mRNAseq in RNA extracted from fresh Frozen samples with a validated, documented (SOP) methodology.
- c. Perform mRNAseq with minimal RNA quantities from samples of limiting size, such as core needle biopsies with a validated, documented (SOP) methodology.
- d. Develop methods and SOP for mRNASeq using different capture methods as required by the Program Office
- e. Produce mRNAseq for both frozen and FFPE cases with the following requirements:
 - i. Quality Control Metrics:
 - a. Number of Mapped reads: >150 Million reads
 - b. % Mapped Reads: > 85%
 - c. % rRNA reads: <2%
 - d. Read 1/Read 2 Ratio: 1:1 with a maximum 20% deviation
 - e. % Properly Paired reads - >80%
 - f. Maximum Number of genes not detected: 4000
 - ii. Production time frame: 3 months
 - iii. Minimum case capacity: 100 cases/month; 1200 cases/year

6. microRNA Sequencing (miRNASeq):

- a. Perform miRNAseq in RNA extracted from FFPE samples with a validated, documented (SOP) methodology.
- b. Perform miRNAseq in RNA extracted from fresh Frozen samples with a validated, documented (SOP) methodology.
- c. Perform miRNAseq with minimal RNA quantities from samples of limiting size, such as core needle biopsies with a validated, documented (SOP) methodology.
- d. Develop methods and SOP for miRNASeq using different capture methods as required by the Program Office

- e. Produce miRNAseq for both frozen and FFPE cases with the following requirements:
 - i. Quality Control Metrics:
 - 1. Number of Mapped reads: >5 Million reads
 - 2. % Mapped Reads: > 85%
 - 3. Percentage of miRNA detected: >85%
 - ii. Production time frame: 2 months
 - iii. Minimum case capacity: 100 cases/month; 1200 cases/year

7. Small RNA Sequencing (smallRNASeq)

- a. Perform smallRNASeq in RNA extracted from FFPE samples with a validated, documented (SOP) methodology.
- b. Perform smallRNASeq in RNA extracted from fresh Frozen samples with a validated, documented (SOP) methodology.
- c. Perform smallRNASeq with minimal RNA quantities from samples of limiting size, such as core needle biopsies with a validated, documented (SOP) methodology.
- d. Develop methods and SOP for miRNASeq using different capture methods as required by the Program Office
- e. Produce smallRNASeq for both frozen and FFPE cases with the following requirements:
 - i. Quality Control Metrics:
 - 1. Number of Mapped reads: >5 Million reads
 - 2. % Mapped Reads: > 85%
 - 3. Percentage of miRNA detected: >85%
 - ii. Production time frame: 2 months
 - iii. Minimum case capacity: 100 cases/month; 1200 cases/year

8. Whole Genome Methylation Sequencing (WGMetSeq):

- a. Perform WGMetSeq in DNA extracted from FFPE samples with a validated, documented (SOP) methodology.
- b. Perform WGMetSeq in DNA extracted from fresh Frozen samples with a validated, documented (SOP) methodology.
- c. Perform WGMetSeq with minimal DNA quantities from samples of limiting size, such as core needle biopsies with a validated, documented (SOP) methodology.
- d. Develop methods and SOP for WGMetSeq using different capture methods as required by the Program Office
- e. Produce WGMetSeq for both frozen and FFPE cases with the following requirements:
 - i. Quality Control Metrics:
 - 1. Average Depth of Coverage >15x
 - 2. >75% of reads will be on-target
 - 3. At least 20 Gb sequence per sample
 - ii. Production time frame: 3 months
 - iii. Minimum case capacity: 100 cases/month; 1200 cases/year

9. Methylation Array (MetArray):

- a. Perform MetArray in DNA extracted from FFPE samples with a validated, documented (SOP) methodology.
- b. Perform MetArray in DNA extracted from fresh Frozen samples with a validated, documented (SOP) methodology.
- c. Perform MetArray with minimal DNA quantities from samples of limiting size, such as core needle biopsies with a validated, documented (SOP) methodology.

- d. Produce MetArray for both frozen and FFPE cases with the following requirements:
 - i. Number of CpG sites interrogated >400K
 - ii. Production time frame: 1 month
 - iii. Minimum case capacity: 100 cases/month; 1200 cases/year

10. SNP6 Array (SNP6):

- a. Perform SNP6 in DNA extracted from fresh Frozen samples with a validated, documented (SOP) methodology.
- b. Perform SNP6 with minimal DNA quantities from samples of limiting size, such as core needle biopsies with a validated, documented (SOP) methodology.
- c. Produce SNP6 for frozen cases with the following requirements:
 - i. Percentage SNP call: >90%
 - ii. Production time frame: 1 month
 - iii. Minimum case capacity: 100 cases/month; 1200 cases/year

11. Deep Sequence Targeted Validation (Validation):

- a. Perform Validation in DNA extracted from FFPE samples with a validated, documented (SOP) methodology.
- b. Perform Validation in DNA extracted from fresh Frozen samples with a validated, documented (SOP) methodology.
- c. Perform Validation with minimal DNA quantities from samples of limiting size, such as core needle biopsies with a validated, documented (SOP) methodology.
- d. Produce Validation for both frozen and FFPE cases with the following requirements:
 - i. Quality Control Metrics:
 - 1. Average Depth of Coverage for targets >400x
 - 2. Minimal coverage per target: 100x
 - 3. Minimal number of targets assayed: 100
 - ii. Production time frame: 1 month
 - iii. Minimum case capacity: 100 cases/month; 1200 cases/year

12. Reverse Phase Protein Arrays (RPPA):

- a. Perform RPPA in DNA extracted from fresh Frozen samples with a validated, documented (SOP) methodology.
- b. Perform RPPA with minimal DNA quantities from samples of limiting size, such as core needle biopsies with a validated, documented (SOP) methodology.
- c. Produce RPPA for frozen cases with the following requirements:
 - i. Minimum number of antibodies: 200
 - ii. Production time frame: 1 month
 - iii. Minimum case capacity: 100 cases/month; 1200 cases/year