MCCRD-SOP0057: Detection of Microsatellite Instability (MSI) Status from Whole Exome

Sequencing Data

Laboratory: Molecular Characterization and Clinical Assay Development Laboratory
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Effective Date: 7/3/2020

#### Please check for revision status of the SOP at

https://pdmr.cancer.gov/sops/

PDMR NCI Patient-Derived Models Repository
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#### **VERSION INFORMATION**

## 1. Change History

Revision	Description
	Internal SOP used by MOCHA Laboratory
7/3/2020	Standardize SOP for posting to PDMR internal site for use by designated NCI intramural laboratories

### 2. Related SOPs

MCCRD\_SOP0011: Whole Exome Sequencing Data Analysis Pipeline and Specifications

#### 3. References

- [1] Beifang Niu\*, Kai Ye\*, Qunyuan Zhang, Charles Lu, Mingchao Xie, Michael D. McLellan, Michael C. Wendl and Li Ding#.MSIsensor: microsatellite instability detection using paired tu-mor-normal sequence data. Bioinformatics 30, 1015–1016 (2014).
- [2] https://github.com/niu-lab/msisensor2

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#### 1.0 PURPOSE/SCOPE

This Standing Operating Procedure (SOP) describes procedures for detection of microsatellite instability (MSI) status using whole exome sequencing (WES) data for reporting in the NCI Patient-Derived Models database as performed by the Molecular Characterization Laboratory (MoCha) at the Frederick National Laboratory for Cancer Research. This SOP is for researchuse purposes only; do not use for clinical sample analysis.

## 2.0 DESCRIPTION OF MSI DETECTION

- b. The processed bam files are generated using whole exome sequence (WES) data following the WES data analysis pipeline in the SOP MCCRD SOP0011.
- c. MSI status is estimated using MSIsensor2 package<sup>[1,2]</sup>.

## 3.0 CODE DESCRIPTION

- d. MSIsensor2 is used to detect MSI score for tumor sample
  - o msisensor2 msi -M msisensor2/models hg19 -t \${file}.bam -o \${file}
- e. MSI status is determined based on the recommended msi score cutoff value 20%
  - MSI-H: msi score  $\geq$  20%
- f. Otherwise, MSI-Stable