MCCRD-SOP0063: Detection of Consensus Molecular Subtype (CMS) Classification of Colorectal

Cancer from RNASeq Data

Laboratory: Molecular Characterization and Clinical Assay Development Laboratory

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# MCCRD-SOP0063: Detection of Consensus Molecular Subtype (CMS) Classification of Colorectal Cancer from RNASeq Data

Effective Date: 2/3/2023

## Please check for revision status of the SOP at

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

## PDMR NCI Patient-Derived Models Repository An NCI Precision Oncology Initiative Resource

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## **APPROVALS**

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## **VERSION INFORMATION**

## 1. Change History

Revision	Description
	Internal SOP used by MOCHA Laboratory
2/3/2023	Standardize SOP for posting to PDMR internal site for use by designated NCI intramural laboratories

## 2. Related SOPs

MCCRD\_SOP0012: RNASeq Transciptome Data Analysis Pipeline and Specifications

## 3. Reference Documentation

Number	Title/Link
[1]	Eide PW, Bruun J, Lothe RA, Sveen A. CMScaller: an R package for consensus molecular subtyping of colorectal cancer pre-clinical models. Sci Rep. 2017
[2]	https://github.com/peterawe/CMScaller

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## 1.0 PURPOSE/SCOPE

This Standing Operating Procedure (SOP) describes procedures for detection of Consensus Molecular Subtype (CMS) classification of colorectal cancer models using RNASeq 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 research purposes only and no clinical samples will be processed using this SOP.

## 2.0 DESCRIPTION OF CMS CLASSIFICATION

- Normalized count data for colorectal cancer PDX samples are generated following the RNASeq data analysis pipeline in the SOP MCCRD\_SOP0012.
- 2.2 CMS classification of PDX sample is determined using CMScaller<sup>[1,2]</sup> in R package.

#### 3.0 CODE DESCRIPTION

- 3.1 CMS classification of PDX sample is determined by running the following command in R:
  - res <- CMScaller(dataset, RNAseq=TRUE, doPlot=TRUE)
- 3.2 Consensus CMS class at model level is determined by majority voting across all PDX specimens within the model. In models which don't have any PDX specimes, CMS class is determined by the prediction results on PDC or PDOrg specimens.
- 3.3 CMS classification "Admixture" is reported if no majority can be called.