# Detection of Consensus Molecular Subtype (CMS) Classification of Colorectal Cancer from RNASeq Data

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# **SIGNATURE APPROVALS:**

| Laboratory Director:   |                        | Signature / Date: |
|--|------------------------|-------------------|
| Must be signed by a minimum of one of those listed at the right: | Biswajit Das, Ph.D.    |                   |
|  | Chris Karlovich, Ph.D. |                   |
|  | Mickey Williams, Ph.D. |                   |
| Author/Owner:  | Lily Chen, Ph.D.       | Signature / Date: |
|  |                        |                   |

### **REVISION HISTORY:**

| Document No.  | Version | Description of Revision | Effective Date |
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| MCCRD-SOP0063 | 1.0     | Original Release        | 02/03/2023     |

# 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 REFERENCE DOCUMENTATION

| Number | Title/Link  |
|--------|---|
|        | 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   |

## 3.0 RELATED SOPS

Available on the PDMR website: <a href="https://pdmr.cancer.gov/sops">https://pdmr.cancer.gov/sops</a>

| Document Number | Title   |
|-----------------|---|
| MCCRD-SOP0012   | RNASeq Transciptome Data Analysis Pipeline and Specifications |

| Detection of Consensus Molecular Subtype       |
|--|
| (CMS) Classification of Colorectal Cancer from |
| RNASeq Data                                    |

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### 4.0 DESCRIPTION OF CMS CLASSIFICATION

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

## 5.0 CODE DESCRIPTION

- 5.1 CMS classification of PDX sample is determined by running the following command in R: res <- CMScaller(dataset, RNAseq=TRUE, doPlot=TRUE)
- 5.2 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.
- 5.3 CMS classification "Admixture" is reported if no majority can be called.