MCCRD-SOP0059: PDMR NextGen Sequence Versioning Structure

Effective Date: 3/15/2023

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

PDMR NCI Patient-Derived Models Repository
An NCI Precision Oncology Initiative[SM] Resource

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APPROVALS

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VERSION INFORMATION

1. Change History

Revision	Description
3/19/2021	Standardize SOP for posting to PDMR internal site for use by designated NCI intramural laboratories

1.0   PURPOSE/SCOPE

This Standard Operating Procedure (SOP) describes the steps necessary to set up NGS file names beginning with NextGen sequencing (NGS) pipeline SOPs version 2.0. After that point, the NGS filenames will use the following structure to define the pipeline used for analysis. **This SOP is for research purposes only and no clinical samples will have file names determined using this SOP.**

2.0   REAGENTS & EQUIPMENT

2.1   Equipment

Description	Model #	Vendor
HiSeq	HiSeq 2500	Illumina
NovaSeq	NovaSeq 6000	Illumina

3.0   PDM NGS DATA FILE NOMENCLATURE AND VERSIONING

3.1   The structure of the version used in filenames is va.b.c.d.e. Table 1 lists all version definitions currently in use.

3.1.1   "v" simply indicates version

3.1.2   Numbers in the "a" location indicate the major pipeline version

3.1.3   Numbers in the "b" location indicate the minor pipeline version

3.1.4   Numbers in the "c" location indicate the sequence platform

3.1.5   Numbers in the "d" location indicate the laboratory assay used

3.1.6   Numbers in the "e" location indicate the how the data were merged

3.2   Below is example of an NGS filename. Tildes are used in the filename to allow automated linking of files in the PDMR database.

3.2.1   114551~080-T~M667M228~v2.0.1.51.0~WES.vcf

3.3   Note that earlier NGS pipelines (e.g., v1.2 and 1.3) only tracked the pipeline version in the filename, not the analysis information.

TABLE 1: Definitions of version annotation beginning with v2.0 of the NGS pipeline

Version	Description: Assay, Material, Input (where relevant)
2	Pipeline version (major revision)
2.0	Pipeline version (minor revision)
2.0.1	HiSeq
2.0.2	NovaSeq 6000 v1.0 Sequencing reagents used
2.0.3	NovaSeq 6000 v1.5 Sequencing reagents used
2.0.1.X.1	FASTQ files from multiple batches/runs were merged
2.0.1.X.0	No data were merged at FASTQ level
2.0.1.X.2	Merged FASTQ file was generated using different DNA inputs in the same assay
2.0.1.50.X	SureSelect v5 Exome, Flash Frozen, 600ng
2.0.1.51.X	SureSelect v5 Exome, Flash Frozen, 50ng
2.0.1.52.X	SureSelect v5 Exome, FFPE, 50ng
2.0.1.53.X	SureSelect v5 Exome, FFPE, 600ng
2.0.1.60.X	SureSelect v6 Exome, Flash Frozen, 600ng
2.0.1.61.X	SureSelect v6 Exome, Flash Frozen, 50ng
2.0.1.62.X	SureSelect v6 Exome, FFPE, 50ng
2.0.1.63.X	SureSelect v6 Exome, FFPE, 600ng
2.0.1.4.X	TruSeq RNA Exome, Flash Frozen, 10 ng (DV200 >70)
2.0.1.5.X	TruSeq RNA Exome, FFPE, 20 ng (DV200 >70)
2.0.1.6.X	TruSeq RNA Exome, Flash Frozen, 4X40ng (DV200 <70) or re-runs of failed 10 or 20 ng
2.0.1.7.X	TruSeq RNA Exome FFPE, 4X40ng (DV200 <70)
2.0.1.8.X	Ultra-Low input WES (Input DNA <50 ng)
2.0.1.9.X	Fibroblast material used as germline surrogate
2.0.1.10.X	PBMC used as germline (prioritized as germline specimen)

Version	Description: Assay, Material, Input (where relevant)
2.0.1.11.X	TruSeq RNA Exome, Flash Frozen, 1x40ng (DV200 <70)
2.0.1.12.X	TruSeq RNA Exome, FFPE, 1x40ng (DV200 <70)
2.0.1.13.X	TruSeq RNA Exome – Library input and DV200 uncategorized
2.0.1.14.X	TruSeq RNA Exome - 10 ng (DV200 >70) FFPE, RNA Access
2.0.1.15.X	TruSeq RNA Exome, FFPE, 1x40ng (DV200 >70)
2.0.1.16.X	TruSeq RNA Exome, Flash Frozen, 1x40ng (DV200>70)
2.0.1.17.X	TruSeq RNA Exome, Flash Frozen, 1x70ng (DV200 between 50 and 70)
2.0.1.18.X	TruSeq RNA Exome, Flash Frozen, 1x100ng (DV200 <50)
2.0.1.19.X	TruSeq RNA Exome, FFPE, 1x70ng (DV200 between 50 and 70)
2.0.1.20.X	TruSeq RNA Exome, FFPE, 1x100ng (DV200 <50)
2.0.1.21.X	TruSeq RNA Exome, Flash Frozen, 1x100ng
2.0.1.22.X	TruSeq RNA Exome, FFPE, 1x100ng