

DRAGEN v3.10.9

Software Release Notes

Introduction

These release notes detail the key changes to software components for the Illumina® DRAGEN™ Bio-IT Platform v3.10.9.

Changes are relative to DRAGEN™ v3.10.8. If you are upgrading from a version prior to DRAGEN™ v3.10.8, please review the release notes for a list of features and bug fixes introduced in subsequent versions.

DRAGEN™ Installers, User Guide and Release Notes are available here:

https://support.illumina.com/sequencing/sequencing_software/dragen-bio-it-platform.html

The 3.10.9 software package includes installers for the on-site server:

- DRAGEN™ SW Intel Centos 7 - dragen-3.10.9-8.el7.x86_64.run
- DRAGEN™ SW Intel Oracle 8 - dragen-3.10.9-8.1.el8.x86_64.run

The following configurations are also available on request:

- Amazon Machine Image (AMI)
- Microsoft Azure Image (VM)
- RPM packages for Centos 7 for Amazon Web Services (AWS)

Deprecated platforms:

- Support for DRAGEN Server v1 FPGA cards has been deprecated since DRAGEN™ v3.10
- Support for Ubuntu has been deprecated since DRAGEN™ v3.9
- Support for Intel CentOS 6 has been deprecated since DRAGEN™ v3.8

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Overview

Below is a summary of the changes included in this DRAGEN™ v3.10.9 patch release. This is a minor update.

Issues Resolved

Issues resolved on DRAGEN™ v3.10.9, compared to v3.10.8

Component/s	Defect ID	Description
Gvcf Genotyper	DRAGEN-17321	Fix for core dump in VCF preload when input files stream from S3, due to incorrect paths
Gvcf Genotyper	DRAGEN-17644	Fix a confusing error message when variant-list file does not exist
Gvcf Genotyper	DRAGEN-17500	Fix a segfault and bug in vcf normalization exposed by a unique variant in a customer sample
CNV	DRAGEN-17615	Fix for missing chromosome in CNV output, due to incorrect early exit caused when prior chromosome has no events
AWS Marketplace	DRAGEN-17466	Fix for AWS marketplace license failure
SNV VC	DRAGEN-17729 A500-17851	Fix a bug with MNV+GVCF mode. Some variant sites that were present in the VCF were not present in the GVCF, due to filtering out of decomposed MNVs in the GVCF.
Joint Caller	DRAGEN-17210 SET-2904	Fix to add missing sdID from dbSNP to output VCF during Joint Calling
Installer	DRAGEN-22634	Fix for DKMS systemd unit change breaking networking

Known Issues

Known issues of the DRAGEN™ v3.10.9 release:

New issues found since v3.10.8 release

Component/s	Defect ID	Issue Description	Remedy / Workaround
QC Metrics	SET-2665 DRAGEN-16385	DRAGEN can generate abnormal (extremely large) coverage metrics on some samples	Issue affects DRAGEN v3.8, v3.9, v3.10 on market releases. There is no workaround for this issue. The issue was discovered after this patch was finalized. Future patch release(s) will have a fix

Component/s	Defect ID	Issue Description	Remedy / Workaround
scRNA	SET-2792 DRAGEN-16360	Out of memory on NextSeq2K instrument when with Single Cell RNA analysis, for very large sample	Issue affects scRNA for DRAGEN on-sequencer on NextSeq2K. There is no workaround for this issue. The issue was discovered after this patch was finalized. Future patch release(s) will have a fix. User can reduce the coverage of sequencing for the scRNA sample.
DRAGEN BCL	DRAGEN-18618	DRAGEN BCL using FPGA HW acceleration for ZIP, encounters error loading FPGA bitstream, when downgrading from DRAGEN v4.0 to v3.x	Issue can be resolved by issuing "dragen_reset -r" after downgrading from DRAGEN v4.0 to v3.x The issue was discovered after this patch was finalized. Future patch release(s) will have a fix.
Gvcf Genotyper	DRAGEN-16614	Exception thrown when indexing is enabled and concatenation is disabled	Disable vcf indexing when output file concatenation is disabled, for GvcfGenotyper runs
Ora compression, UMI	DRAGEN-17533	Exception when using Ora inputs for map/align and Ora input for "---umi-source".	The "umi-source" option does not support Ora input. The workaround is to supply FASTQ file as "umi-source"
Downsampling, UMI	DRAGEN-17082	When downsampling is used with UMIs via "enable-down-sampler=true", the BAM does not contain SA tags	No workaround. Issue is specific to the use case combination of UMI collapsing and use of down sampler.

Known issues at the time of v3.10.8 release

Component/s	Defect ID	Issue Description	Remedy / Workaround
BCL	DRAGEN-16555	Minimum Adapter Overlap setting not working	Whether it's set to a valid or invalid value, an error message is displayed. No workaround
Infrastructure	DRAGEN-16498	AWS f1.4x LICENSE_MSG Challenge get token error: Get instance ID failed (Unable to retrieve AWS identity signature)	Timeout while retrieving AWS instance ID has been observed. The rate of occurrence has been too low to measure. This leads to failure in the licensing and dragen job exits, run fails. Re-run would pass

Component/s	Defect ID	Issue Description	Remedy / Workaround
DNA Alignment	DRAGEN-16468	Bam generated from file conversion CRAM-> BAM with hg19_alt_masked_v2 reference has invalid header	Reproducible issue that has been shown to have existed since v3.7 or earlier. When converting from CRAM to BAM using dragen "file-conversion" method, the BAM has an invalid header due to a bug in the CRAM reader. No workaround. Re-header the file
DNA Alignment	DRAGEN-16467	Germline workflow is slower with graph hash table	Dragen run time is roughly 6.3% slower with graph aligner and graph reference is used, compared to non-graph. The increased run time is in both mapper and variant caller phases. No workaround
Dedup/UMI	DRAGEN-16412	Probabilistic UMI output is different from run to run	There is a run-run variation in the UMI probabilistic model. Non-prob model (non-random UMI) does not have run-to-run variation. The variation leads to ~2 reads being missing from output. This impact shall be a very small fraction.
DupMarking	DRAGEN-16399	Assertion `pos < m_num_bits' failed, in Dupmark:: DupmarkTable:: getDuplicates()	Crash in duplicate marking when there are more than 4G read pairs, which can happen when reads of multiple replicates are combined into one read group through manual BAM file editing. The system has a physical limit. Not a regression from prior releases
Cloud / Azure	DRAGEN-16335	popen exception on azure cloud suites	A very long running workflow such as TSO500 ctDNA crashes on Azure due to eventual failure in popen() calls. The issue is reproducible. No workaround
Somatic	DRAGEN-16319	Elevated SNP and INDEL FP on ICGC datasets	The impact of the issue is an elevated number of FPs for ICGC datasets in 3.10 compared to 3.9: a 5-6% increase in the SNP FPs and a 25%-30% increase in the INDEL FPs.
DNA Alignment	DRAGEN-16308	read trimmer adapter trimming sigabort during RecomputeTags:: computeTags	Reproducible when running different read trimmers back-back. Workaround to run dragen_reset

Component/s	Defect ID	Issue Description	Remedy / Workaround
Amplicon Gene Fusion	DRAGEN-16254	Excessive RNA Amplicon runtime on large samples	RNA Amplicon run time is very long when the coverage is significantly higher than expected for typical Amplicon samples
SNV VC Somatic	DRAGEN-16149	Germline MNV - phased calls with same PS and GT and within distance threshold are not getting combined into MNVs	Some phased calls are not getting combined into MNVs to MNV output. Full support for germline MNV is planned for a subsequent release
Metrics scRNA	DRAGEN-15950	A run-run variation in scRNA output	Some datasets have run-to-run variations in the mapping metrics Q30 metrics field. The issue affects only the metrics output and not the caller output
BCL	DRAGEN-15944	DRAGEN BCL logs insufficient warning when corrupt files supplied	In the rare event of a corrupt aggregated bcl.bgzf input file, the customer will correctly receive an error message of the lane and the cycle that is corrupted, but not the specific file name.
Methyl-Seq	DRAGEN-15796	md5sum discordance b/w cloud and local runs	Impacts multi-pass mode and specific dataset. Single pass mode has been the recommended mode and does not have the issue. Multi-pass will be deprecated in future.
DNA Alignment EH	DRAGEN-15151	Large run to run variation of mapper run time for EH	Up to 20% run time variation seen for mapper phase
HW GRAPH RNA VC	DRAGEN-13717	RNA VC hits ERROR: Invalid node flags	Issue is a HW graph error and rare (happens once every 6-9 months in routine VC testing). The assertion check / trap will remain in place so that invalid results will not be produced for end user. If seen in field, recommendation is to re-run sample as it is expected to pass.
Compression	DRAGEN-10783	BAM input to DNA mapper: Deflate engine error: 0x9080 on stream 1	Extremely low repeatability. A re-run will pass

SW Installation Procedure

- Download the desired installer from the Illumina support website and unzip the package
- The archive integrity can be checked using: `./<DRAGEN 3.10.9 .run file> --check`

- Install the appropriate release based on your Linux OS with the command: `sudo sh <DRAGEN 3.10.9 .run file>`
- Please follow the installer instructions. Server power cycle may be required after installation, depending on the currently installed version. If an updated FPGA shell image needs to load from flash, this is only achieved with power cycle.
 - A power cycle is required when upgrading from v3.3.7 or older
 - A power cycle is required when downgrading to v3.3.7 or older
 - A power cycle is not required when upgrading from a release after v3.3.7
- Procedure to downgrade to v3.3.7 or older:
 - Requires the following three steps. The prior .mcs file needs to be flashed manually:
 - Install the prior release: `sudo sh <DRAGEN 3.3.7 .run file>`
 - `program_flash /opt/edico/bitstream/07*/*.mcs`
 - Power cycle

Release History

Revision	Release Reference	Originator	Description of Change
00	CN 1069786	Cobus De Beer	Initial release
01	CN 1085211	Cobus De Beer	Updated e18 installer version Added DRAGEN-22634 to fixed issues Updated to latest template