Illumina TruSight™ Software Suite Release Notes

v1.5.0

June 2020

Introduction

TruSight™ Software Suite (TSS) is designed for translating genomic sequencing data in meaningful, interpretable results in rare disease cases. Highlights include:

Comprehensive, ultra-rapid variant calling

Use DRAGEN™ secondary analysis to call small variants, structural variants, mitochondrial variants, repeat expansions, runs of homozygosity, and SMN1/SMN2 variants.

Simplified, customizable case management

Manage cases from sample acquisition to report, assign cases to users, configure pipeline settings, and set quality control (QC) thresholds.

Intuitive, high-powered interpretation and reporting

Filter variants via gene lists, inheritance modes, custom annotations, and complex logic; flag, sort, and prioritize important variants; use customizable reporting templates.

Secure, compliant environment

TruSight Software Suite has been independently audited and certified for HIPAA compliance, ISO27001, and ISO13485. It is built to enable data privacy and compliance with the principles of GDPR.

These Release Notes detail the key features and changes to software components for the for the commercial release of TruSight Software Suite v.1.5.0. The software has been through a beta testing program (v.1.1) and an early access program (v.1.3.0).

For information on how to use the system, see the TruSight Software Suite Online Help. TruSight Software Suite is a comprehensive solution for alignment, variant calling, variant annotation, filtering, interpretation, curation, and reporting, including features such as:

- Automatic secondary analysis with DRAGEN™ and annotation of:
    - Small Variants, CNVs, SVs, Mitochondrial variants, ROH, STRs, SMA
- Case Dashboard and Test Management
- IGV Visualization
- Complex custom filters
- Custom flagging of variants
- Custom annotation
- SpliceAI & PrimateAI
- Gene lists from phenotypes
- Storage of variant curation
- Visualization of aggregate data for genes or variants
- Customized report generation
- Audit logging

- Command-line interface for uploading FASTQs
- API documentation

NEW FEATURES

- Test Management
  - Custom repeat expansion unit thresholds
- Case Management
  - AOH block calculation in QC metrics
  - Modify indications after case is 'Ready for Interpretation'
- Variant Grid / Filters
  - Multi-level sorting on the columns in the variant grid
  - Zygosity comparator columns
  - Display summary of critical transcript-level data across all transcripts
  - Virtual Panel Option (gene list management) enhancements
  - Update the Phenotype Overlap column when indications have been modified
- Variant Details
  - Updated CNV/SV workflow
  - Case-specific/independent variant comments
  - Comment link-outs to previous cases
  - Multiple flags per variant
- Curation
  - ACMG criteria-based curation workflow for SNV variants
  - Large variant classification updated from variant details
  - Updates to canonical transcript designation
- Reporting
  - Additional fields for clinical JSON and PDF enhancement
  - Update variants associations from the report tab
  - Variant table editable in the report page
- Admin
  - Ability to manage active and inactive cases
  - Workgroup Administration Console (WAC) improvements
  - Add –config option to CLI uploader tool
  - Track sample usage and storage per domain for billing
  - Enabling terms and conditions functionality

- Release versions
    - TruSight Software Suite v.1.5.0 runs DRAGEN v.3.5.7 for secondary analysis
    - TSS v.1.5.0 uses Nirvana v.3.10 for annotation
    - TSS v.1.5.0 uses KNS-API v.0.8.0 beta.13149 and KNS-UI v.0.10.0-beta.484 for curation

RESOLVED ISSUES

- Defect repairs (bug fixes) from v1.3 release.

Issue Key	***Description***
OLYM-11326	Certain BAM and VCF fields are not correctly displayed in IGV pop out for that variant.
OLYM-11333	ZFIN linkout for SMN1 returns an error.
OLYM-11313	100x single sample FASTQ takes >6 hours to process.
OLYM-9913	New curation association date is stored and displayed in UTC time, making some associations dated in the future.
OLYM-11367	Case manager can't make interpretation comments or notes when manager's name is >50 chars.
OLYM-11382	Variant headers for ROH variants have formatting issues in the PDF report.
OLYM-11407	Error messaging for disabled variant associations is incorrect.
OLYM-11363	When genomic files are not sorted by position, BED file uploads result in an error.
OLYM-11429	Non-proband family member can be selected on interpretation page.
OLYM-11371	Some CNV variants have "feature elongation" annotations, but the user cannot filter for that in CNV consequence filter.
OLYM-11370	When the report is completed and approved, the user can still add gene associations to report.
OLYM-11220	When applying the gene filter, some checkbox selections do not persist.
OLYM-11405	Adding a case to CaseLog remains in pending state, without ingesting the case. The workaround is manual bulk upload of cases into CaseLog.

KNOWN ISSUES

Issue Key	Description
OLYM-12034	Custom columns include the text "CUSTOM COLUMN" as the column name.
OLYM-12002	When 20 flags are used, the Interpretation header fails to load correctly.
OLYM-11967	Any case ingested prior to v.1.5 will have all variants marked as "unreviewed" by showing a blue dot under "Status" column.
OLYM-12098	Links to previous cases shown under Caselog summary are working correctly. Workaround is to manually search for cases using the case ID.
OLYM-9211	Details about the OTHER variant are seen before those of the SIBLING variant in variant details.
OLYM-10103	When a locked filter tab with indications applied is duplicated, default phenotype genes are seen in the additional genes section. Workaround is to delete the genes seen in additional genes box or create a new tab without duplicating the locked tab.
OLYM-10375	Pop outs appear cut off at different points depending on the size of the user's screen.
OLYM-10382	For variants spanning many genes, the transcripts tab does not load correctly.
OLYM-10555	When filtering with OMIM, gnomAD and ClinGen filters, the "exclude consequences" filter does not return correct results.
OLYM-11328	Variant headers for ROH variants have formatting issues in the PDF report.
OLYM-11337	When a user with API Access role accesses interpretation page directly, user is redirected to a broken page. Workaround is to manually update the URL.
OLYM-11406	If a variant spans multiple genes and one of the genes has information associated with it, the user is unable to add information to other genes. A workaround exists by using the Edit button to manually enter gene information.
OLYM-11801	When the user creates a virtual variant, the variant is successfully created but there is no green success banner message.
OLYM-11880	When a variant has only one transcript, the popup window shows other transcripts with the same information repeated.

OLYM-12058	When a variant association has two versions in the KNS (one enabled and one in draft state), the user sees an error message.
OLYM-12070	Selecting a gene list in test management will close the entire Gene List modal, not just the gene list dropdown menu.
OLYM-12077	If a gene list name contains (_) underscore in it, the gene list autocomplete is unable to find it. Workaround is to create gene lists without (_).
OLYM-12079	When uploading an STR customer annotation file from Excel, a whitespace error is introduced and the genome build information cannot be read. Workaround is to manually remove any whitespaces after the reference genome in the TSV file.
OLYM-12082	WalkMe functionality is not set up in the UI.
OLYM-12116	If a case has been open for >1 hour, IGV URLs can expire and gene tracks will not load. Workaround is to reload the case.
OLYM-12136	For ROH variants, the partial overlap symbol does not work correctly, and is applied to all ROH variants regardless of overlap.
OLYM-12147	When adding InDels to a report, the variant ID may get cutoff in the report modal instead of wrapping around.
OLYM-12181	In certain SVs, false positive de novo calls are seen. This issue has been fixed in a subsequent DRAGEN release.
OLYM-12239	Gene lists uploaded with this valid gene (GS1-24F4.2) do not load correctly.
OLYM-12244	If a variant spans >2400 genes, the transcript tab fails to upload correctly.
OLYM-12243	The DRAGEN QC BED file requires the "chr" prefix for GRCh38 builds. Workaround is to ensure files have the "chr" prefix.
OLYM-12277	When user has multiple tabs open and logs out of one tab, other tabs will be inactive but may show data last viewed. Workaround is to manually log out of each open TSS tab.
OLYM-12285	When cases are deleted, there is a delay before they are deleted from CaseLog.
OLYM-12219	CaseLog summary does not update with alternate allele frequency even after the addition of related cases.
OLYM-12231	Only the most recent variant association shows in the variant details tab when "get new associations" is clicked. All associations show correctly in the variant grid.

OLYM-12268	It may take up to 24 hours to ingest cases into CaseLog.
OLYM-12270	If an analysis fails with a WES error, downloading logs for the case does not work.
OLYM-12271	When cases are added to CaseLog, there is a delay before they are seen in the CaseLog summary.
OLYM-12290	In certain rare cases, phenotype overlap ingestion fails and the case cannot be interpreted. User must contact tech support to manually clear the error and reupload the sample.