Alissa Reporter patch release history

Revision	Release Date	Comments: Enhancements, Corrections, Limitations
1.1.5	March 2023	**Correction:** • Fixed critical cybersecurity vulnerabilities. • Fixed typographical mistakes in the Custom DNA Germline application PDF report. • Fixed an issue where in case an in silico filter is used that only contains 1 of 2 (or more) overlapping genes (e.g. PRSS1 and PRSS2 on GRCh37), the impact assessment (variant annotation) sometimes would use gene(s) not included in the in silico filter
1.1.4	November 2022	**Correction:** • Fixed an issue where in rare cases samples analysed with a Custom DNA Germline application would only report a small fraction of the actually called variants (e.g. only variants on a few chromosomes instead of on all chromosomes) due to a silent internal failure of a component.
1.1.3	November 2022	**Corrections:** • Fixed an issue where sample analysis could technically fail due to NVIDIA Clara Parabricks error "uncorrectable Error Correcting Code (ECC)". The failure would result in the entire run being failed. The fix handles the failed sample properly and only fails the individual sample and not the entire run. • Fixed an issue where the CNV calling correlation heatmap (accessible via QC dashboard) expires after 2 months instead of 2 years. • Fixed an issue where QC dashboard plots are only available for internal Support users (and not available for external users) due to a permission issue.
1.1.2	September 2022	**Corrections:** • Fixed an issue where the download of PDF reports could fail in case certain browser plugins were installed. • The underlying Django framework is updated from version 3.2.13 to 3.2.145 to fix an open Common Vulnerabilities and Exposure (CVE). • Additional data has been procured allowing the "problematic regions" to be updated for the Human All Exon V8 Germline application (XT chemistry). This will make the "problematic regions" more accurate whilst not impacting the actual data analysis. • Fixed an issue where the action log export in rare cases could result in "broken records" when an individual action log entry contains a "new line" character, effectively creating a new line in the exported file, rather than keeping the single record on a single line.

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		• Improved the explanation on how certain QC metrics are calculated for the Custom DNA Germline application. • Fixed an issue where designs in SureDesign that have missing mandatory values (e.g., DesignID field missing) crash the API resulting in designs not being importable. Now, missing values will always be properly handled and no longer crash the API. • Fixed an issue where automated data imports from AWS can get stuck (not complete, but also not fail properly) in case the triggered error message contains invalid characters. Proper sanitization of error messages is added preventing imports from getting stuck. • Fixed an issue where designs in SureDesign that have missing mandatory values (e.g., DesignID field missing) crash the API resulting in designs not being importable. Now, missing values will aways be properly handled and no longer crash the API in SureDesign API call. • Fixed an issue where analyses could get stuck or fail due to AWS provisioning faulty GPU machines or GPU machines with 0 GPU processors.
1.1.1	July 2022	**Corrections:** • 'Duplicate file error' and frozen 'in progress' status during upload. These situations were triggered when the entire run failed due to upload of last chunk of the last file of a set of files being uploaded twice. • In rare cases, ExomeDepth did not calculate the log2 ratio for a single bin (missing value). In that case, the CNV viewer throwed an error when opening the CNV viewer from that CNV or another CNV on the same chromosome. Other chromosomes or CNV on other chromosomes were not affected. Eventually, the CNV viewer was non-functional for the affected chromosome. • 'Version 4 chemistry' (available for "Illumina HiSeq 2000/2500" and "Illumina HiSeq 2000/2500 Merge Lanes") was not properly displayed in the "sequencing kit" field on the detailed run view page (it used to show "<NA>") • Action log could be susceptible to cross-side scripting (XSS) in certain cases • In rare cases, the "Read length distribution" plot (accessible via the QC dashboard) was plotted in the wrong order. This could result in a discrepancy between the "average read length" QC metric and the data shown in the "Read length distribution" plot. • Variants in the "Tabular CNV file" were only sorted on chromosome instead of on chromosome and position • Multiple instances of the same "A subset of the used in silico filter was defined on a different genome build compared to the genome build user for analysis and therefore ignored"

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		warning was shown in case an in silico filter contains more than one ignored entry. After the issue fix, the warning is shown once at a maximum now. • Samples analyzed with small custom designs and that have a uniform coverage (and no inaccessible regions) failed with technical failure due to a missing inaccessible regions file. • Import of custom designs from SureDesign into Alissa Reporter failed due to a perceived wrong format of the targets.txt file for custom designs that were designed using either cytobands or only positional coordinates (e.g., chromosome/start/stop). The implemented fix will always import and just skip the targets.txt file if it has an unexpected format • FASTQ files with .fq or .fq.gz extensions can be uploaded but were rejected by the analysis pipeline (eventually resulting in a failed analysis). Now, .fq and .fq.gz files are properly processed by the analysis pipeline • Implemented a short-term mitigation for an observed issue with provisioning of GPU worker machines in certain AWS availability zones (e.g., observed on APAC deployment). It has been observed that GPU worker machines (required for analysis with NVIDIA Clara Parabricks) are sometimes provisioned without actual GPUs, resulting in technical failure of the sample (and consequently the entire run). The short-term mitigation consists of properly failing the single sample affected by the faulty worker machine and properly continuing the analysis for the other samples. A more robust solution (i.e., rejecting the faulty GPU worker machine and spinning up a new GPU worker machine) will be implemented with a next release • In rare cases, ASW would provision GPU worker machines with insufficient resources to execute NVIDIA Clara Parabricks (e.g., g5.2xlarge). These types of AWS GPU worker machines are removed from the list of machines that can be provisioned by AWS **Enhancements:** • Implemented different improvements to increase the performance stability of on-the-fly retrieval of variant annotation from Alissa Interpret for large volumes of variants • Implemented different improvements to increase the performance stability of automated support notifications
1.1	June 2022	See Release Notes on Alissa Reporter product page