Release Notes

Agilent Alissa Align & Call v1.0

Product Name and Version Number

Alissa Align & Call v1.0.0.74

Product Part Number

G5357AA

Overview

Alissa Align & Call is a collaborative, multi-user, web-based platform for analysis of Next Generation Sequencing (NGS) data from samples enriched with Agilent's SureSelect, HaloPlex, or OneSeq target enrichment libraries and reagents. The software provides the following functionality:

- Trimming of raw sequencing reads (Illumina platform only) to trim low-quality bases from the ends, remove 3' adaptor sequences, and mask reference-biased bases and enzyme footprints. The program can also synchronize the mate pair files and keep only reads which have a mate in both files for paired end runs.
- Alignment of reads to genomic locations using the Burrows-Wheeler aligners (BWA or BWA-MEM).
- Identification of variants – i.e., single nucleotide polymorphisms (SNPs) and small insertions/deletions (indels) – in a single sample, and, for OneSeq analyses, identification of copy number variants (CNVs) and copy-neutral loss of heterozygosity (cnLOH).
- Visualization of variants in a genome viewer interface that supports display of custom and default tracks.
- Annotation of variants and exclusion of variants in the analysis results.
- Generation of QC assessment files that give the user confidence in the assay results.
- Direct export of analysis results from Alissa Align and Call to Alissa Interpret, when a licensed Alissa Interpret account is available.
- Seamless navigation between Alissa Align and Call and Alissa Interpret.
- Shared access to all sample files and results for all users within the same workgroup.
- Assignment of user-specific roles, managed by a workgroup administrator, that define the permitted user privileges for each account in the workgroup.

Single Sample analysis

Run a single sample analysis when you want to find variants in individual samples. SNPPET, an in-house algorithm developed specifically for the detection of low allele frequency variants, is used to identify variants. For samples that were target-enriched using Agilent's HaloPlex^{HS} or SureSelect$^{XT\ HS}$, duplicate reads will be flagged and merged based on the incorporated molecular, allowing for an even more accurate detection of alleles at low frequencies.

OneSeq analysis

Run a OneSeq analysis when your DNA sample was enriched using Agilent's OneSeq target enrichment libraries and reagents. A OneSeq analysis simultaneously finds CNVs, copy-neutral loss of heterozygosity (cnLOH), SNPs, and indels in a single sample. Copy number changes are detected by comparing an experimental sample to a known reference sample. The in-house developed SNP calling algorithm SNPPET is used to call point mutations and indels. The high-frequency, minor allele SNPs covered by the OneSeq backbone design are used to determine copy-neutral LOH.

Supported Browsers

Chrome Version 36.0 +

Known issues for Align and Call that may impact end users

1. Sometimes when login session times out and user attempts to log in again, the application fails to display the Alissa portal page. (TT#279201)
2. When multiple analyses access the same input file simultaneously, the analysis job may fail. (TT#279824)
3. In cases of samples with very high read depth, loading the display of reads in the genome viewer is slow due to slow response from server. (TT#280738, TT#280849)
4. In some cases, when user tries to log out of the system, it may take longer for the system to response. (TT#279591)
5. In particular cases, when user aborts an analysis job, the job status does not properly update. (TT#280949)
6. Sometimes when a new job is submitted, it stays in Queued state for a long time until another job is submitted. (TT#281673)

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