

NGS Data Analysis Made Easy

Key Benefits

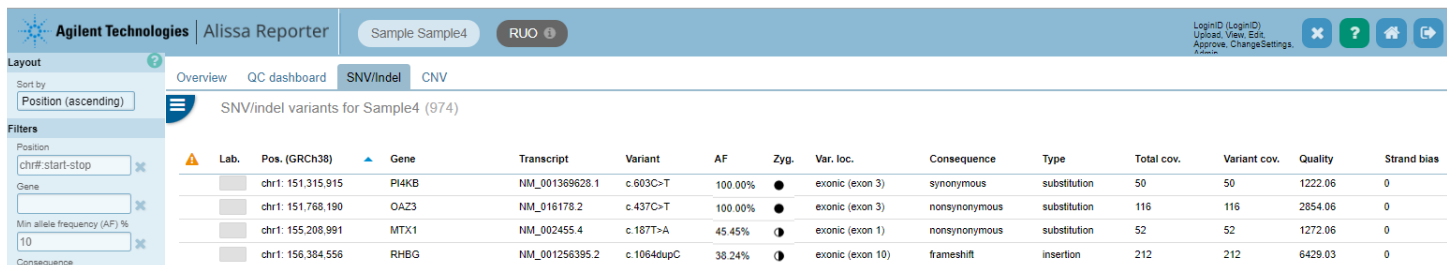
- Variant detection from DNA
- Built-in quality control dashboard
- Fully integrated genome browser
- Intuitive and automated software
- Seamless connection to Alissa Interpret

Streamlined NGS data analysis for the modern lab

The Agilent Alissa Reporter platform is an intuitive and streamlined cloud-based NGS secondary analysis software-as-a-service (SaaS) solution that delivers high performance variant detection with integrated genome browsing, a built-in quality control (QC) dashboard, and seamless connectivity to Agilent Alissa Interpret software. Alissa Reporter completely automates data upload, analysis, and export, including direct export from your Amazon Web Services account.

High-performance variant detection

From a single genomic sample, researchers can get more valuable information than ever before. Alissa Reporter supports parallel variant detection from DNA specimens. With Alissa Reporter's secondary analysis capabilities, you can detect single-nucleotide variants (SNVs), insertions and deletions (indels), and copy number variants (CNVs). As a fully transparent solution, Alissa Reporter includes confidence scores next to CNV calls.



Lab.	Pos. (GRCh38)	Gene	Transcript	Variant	AF	Zyg.	Var. loc.	Consequence	Type	Total cov.	Variant cov.	Quality	Strand bias
	chr1: 151,315,915	PI4KB	NM_001369628.1	c.603C>T	100.00%	●	exonic (exon 3)	synonymous	substitution	50	50	1222.06	0
	chr1: 151,768,190	OA23	NM_016178.2	c.437C>T	100.00%	●	exonic (exon 3)	nonsynonymous	substitution	116	116	2854.06	0
	chr1: 155,208,991	MTX1	NM_002455.4	c.187T>A	45.45%	●	exonic (exon 1)	nonsynonymous	substitution	52	52	1272.06	0
	chr1: 156,384,556	RHBG	NM_001256395.2	c.1064dupC	38.24%	●	exonic (exon 10)	frameshift	insertion	212	212	6429.03	0

Figure 1. Alissa Reporter detects variants from DNA giving users high confidence in their results. SNVs and indels are reported in the SNV/indel module. The CNV detection module identifies both amplifications and deletions.

Integrated genome browser

Users can easily look further into the raw read pileups for a given SNV/indel variant by navigating to the genome browser clicking **Show pileup** while hovering over a variant.

The screenshot shows the Alissa Reporter interface with a table of SNV/indel variants for Sample 1 (25153). The table columns include Lab, Pos. (GRC...), Gene, Transcript, Variant, AF, Var. loc., Consequence, Type, Total cov., Variant cov., and Quality. A tooltip is displayed over the variant at position chr20:609,898 (GRCh38), showing details like ALT frequency (99.50%), REF/ALT states (CG/GC), and REF/ALT lengths (2/2). The tooltip also includes an 'Open in view' button and a 'Show pileup' button.

Lab	Pos. (GRC...)	Gene	Transcript	Variant	AF	Var. loc.	Consequence	Type	Total cov.	Variant cov.	Quality
	chr20: 326,089	SOX12	NM_006943.3	c.165G>A	17.70%	exonic (exon 1)	synonymous	substitution	195	33	75.19
	chr20: 382,549	TRIB3	NM_001301201.1	c.4G>A	5.80%	exonic (exon 2)	nonsynonymous	substitution	115	6	10.64
	chr20: 391,328	TRIB3	NM_021158.4	c.333T>C	49.10%	exonic (exon 3)	synonymous	substitution	110	52	160.12
	chr20: 396,582	TRIB3	NM_021158.4	c.969C>T	31.80%	exonic (exon 4)	synonymous	substitution	167	51	134.44
	chr20: 410,526	RBCK1	NM_001323960.1	c.282C>T	68.30%	exonic (exon 3)	synonymous	substitution	112	75	233.42
	chr20: 487,542	CSNK2A1	NM_177559.3	c.858C>T	24.30%	exonic (exon 12)	synonymous	substitution	128	29	74.12
	chr20: 609,812	TCF15	NM_004609.3	c.426T>C	59.90%	exonic (exon 1)	synonymous	substitution	141	84	257.62
	chr20: 609,898	TCF15	NM_004609.3	c.339_340delC...	99.50%	exonic (exon 1)	inframe	delins	224	224	946.28
	chr20: 675,537	SCRT2				exonic (exon 1)	nonsynonymous	substitution	198	60	151.09
	chr20: 761,203	SLC52A3				exonic (exon 6)	synonymous	substitution	105	71	238.52
	chr20: 763,806	SLC52A3				exonic (exon 4)	synonymous	substitution	146	119	376.63
	chr20: 763,926	SLC52A3				exonic (exon 4)	synonymous	substitution	171	17	39.06
	chr20: 765,454	SLC52A3				exonic (exon 3)	synonymous	substitution	187	37	98.53

Figure 2. While hovering over a variant, click **Show pileup** to jump to the integrated genome browser.

Alissa Reporter automatically links users to the genome browser for manual inspection of raw reads.

The screenshot shows the integrated genome browser view for a variant at position chr20:609,898 (GRCh38). The view includes tracks for Variants, Transcripts, Regions, Coverage, Runner up frequency, Reference genome, and Cytoband. A tooltip is visible over the variant, showing details like ALT frequency (99.50%), REF/ALT states (CG/GC), and REF/ALT lengths (2/2). The tooltip also includes an 'Open in view' button.

Figure 3. View raw read pileups directly from Alissa Reporter's integrated genome browser.

Users can also visualize CNVs with Alissa Reporter's **CNV Viewer** function.

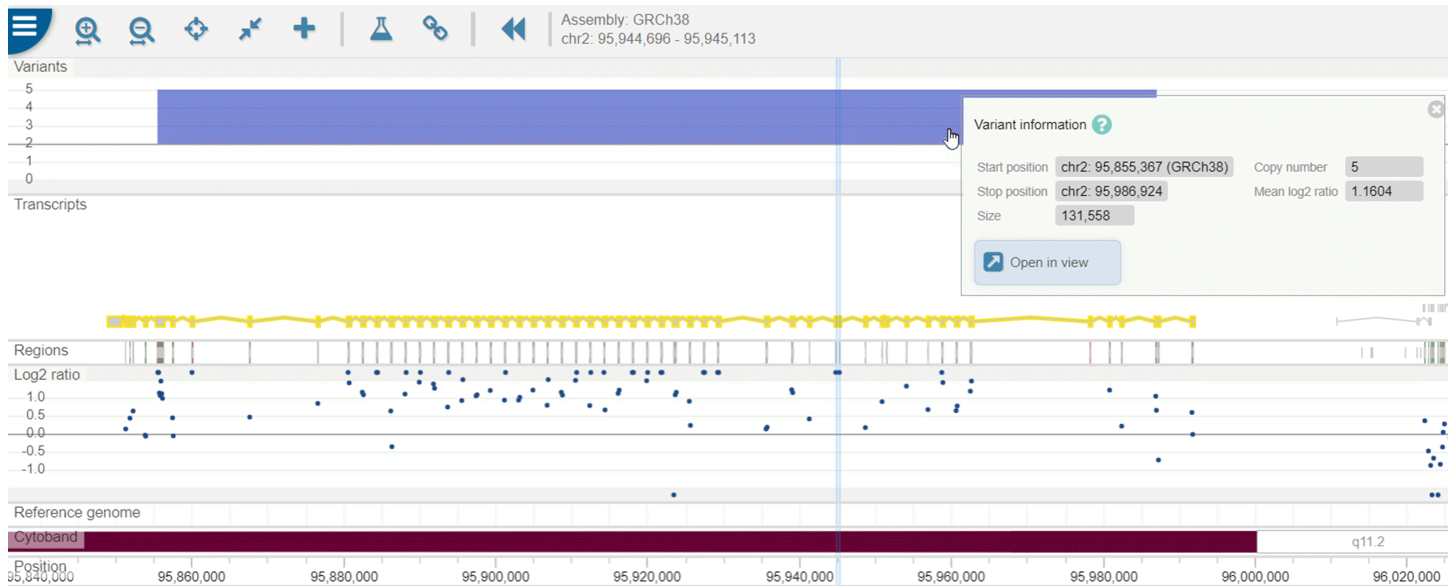


Figure 4. View raw read pileups directly from Alissa Reporter's integrated genome browser.

Built-in QC dashboard for operational excellence

Alissa Reporter helps users quickly verify that an NGS assay is performing as planned. With the built-in QC dashboard, users can immediately assess whether key quality control metrics of individual samples (or the entire run) are within the anticipated range. Alissa Reporter flags problematic samples and shows users where the QC metric has deviated from recommended values.

Alissa Reporter can track and display QC metrics longitudinally. By analyzing quality control data across runs, users can easily spot trends and deviations from expected performance parameters over time.

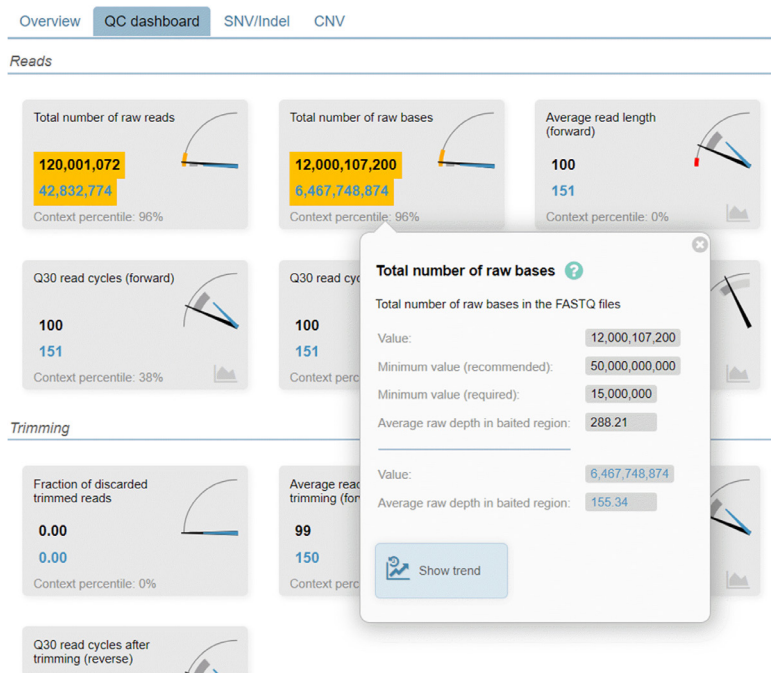


Figure 5. Alissa Reporter's QC dashboard helps you quickly find the metrics that matter most.

Virtual gene and/or regions panels

If users are only interested in analyzing a subset of genes or regions, Alissa Reporter's in silico filter enables the creation of virtual gene panels.

Create targeted gene panels in advance based on your subpanels of interest, or edit your selected panel on the fly. It is easy to manage in silico filters with Alissa Reporter's intuitive filtering functions. Simply select or upload the gene(s) and/or region(s) to be included, and Alissa Reporter will automatically filter the dataset based on this selection.

Overview

Edit selected panel | Export gene panel | Export region panel | Samples with in silico filter | Show action log | Get shareable link | Delete in silico filter

ID: Somatic filter
Application: Human All Exon V8 Somatic
Filter type: Large gene and region panel
Description: 5 genes ANKRD36B, BRCA1, BRCA2, POTE1, KRAS and 1 regions filter
Created: 2022-12-08 08:18
Last modified: 2022-12-08 08:18
Version: 1

Filter overview

Total number of genes available: 20993
Total number of genes selected for panel: 3
SNV: 1
CNV: 1
SNV + CNV: 1
Total number of genes not selected: 20990

Total number of regions selected for panel: 3

Figure 6. Filter based on your genes and/or regions of interest.

Predefined analysis pipelines

Through optimized analysis pipelines for SureSelect Human All Exon V7 and V8 and for SureSelect custom panels, users can assess their results with confidence.

The SureDesign import module in Alissa Reporter enables users to easily access their SureSelect custom panels.

Figure 7. Use optimized analysis pipelines to run your SureSelect Human All Exon V7, V8 and custom panels. Import your SureSelect custom design into Alissa Reporter.

An end-to-end automated NGS software workflow

Alissa Reporter turns raw NGS FASTQ files into Variant Call Format (VCF) files for key files for Agilent SureSelect Human All Exon V7 and V8 germline and for custom germline applications. As part of the Agilent Alissa Clinical Informatics platform, Alissa Reporter seamlessly transfers data to the Alissa Interpret tertiary analysis solution for a fully integrated end-to-end NGS software workflow.

After the variant of interest has been identified in Alissa Interpret, users can easily link back to Alissa Reporter to visualize read pileups in Alissa Reporter's highly responsive, integrated genome browser.



Agilent Technologies Alissa Interpret

Files | Patients | Analyses | Gene Profiles | MVL | Configuration | Search | Help

Patient: P_Sample1_S1 > Analysis: A_Sample1_S1

General | Variant triage | Variant review | Quality | Reports

Triage & Classify

Molecular variants | CNVs

Variant List: 33,173 variants (total)

Gene	Position	Ref	Alt	Read Depth	VAF (%)	CNV	Type	Transcript	cDNA	Location	Exon	Effect	Protein	External Databases	Simil.	Info
RBCK1	20:410,526	C	T	112	68.3		snp	NM_001323960.1	c.282C>T	exonic	3	synonymous	p.Tyr94=	Q		
CSNK2A1	20:487,542	G	A	128	24.3		snp	NM_177559.3	c.858C>T	exonic	12	synonymous	p.His286=	Q		
TCF15	20:609,812	A	G	141	59.9		snp	NM_004609.3	c.426T>C	exonic	1	synonymous	p.Arg142=	Q		
TCF15	20:609,898-609,899	C	G	224	99.5		substitution	NM_004609.3	c.339_340delCGinsGC	exonic	1	inframe	p.Thr113_Leu114=	Q		
SCRT2	20:675,537	G	A	198	30.7		snp	NM_033129.4	c.65C>T	exonic	1	nonsynonymy	p.Ala22Val	Q		
SLC52A3	20:761,203	A	G	105	68.0		snp	NM_001370086.1	c.1233T>C	exonic	6	synonymous	p.Ser411=	Q		

Figure 8. Send data directly from Alissa Reporter to Alissa Interpret for a streamlined NGS data analysis experience. Link back to Alissa Reporter to view read pileups for variants of interest.

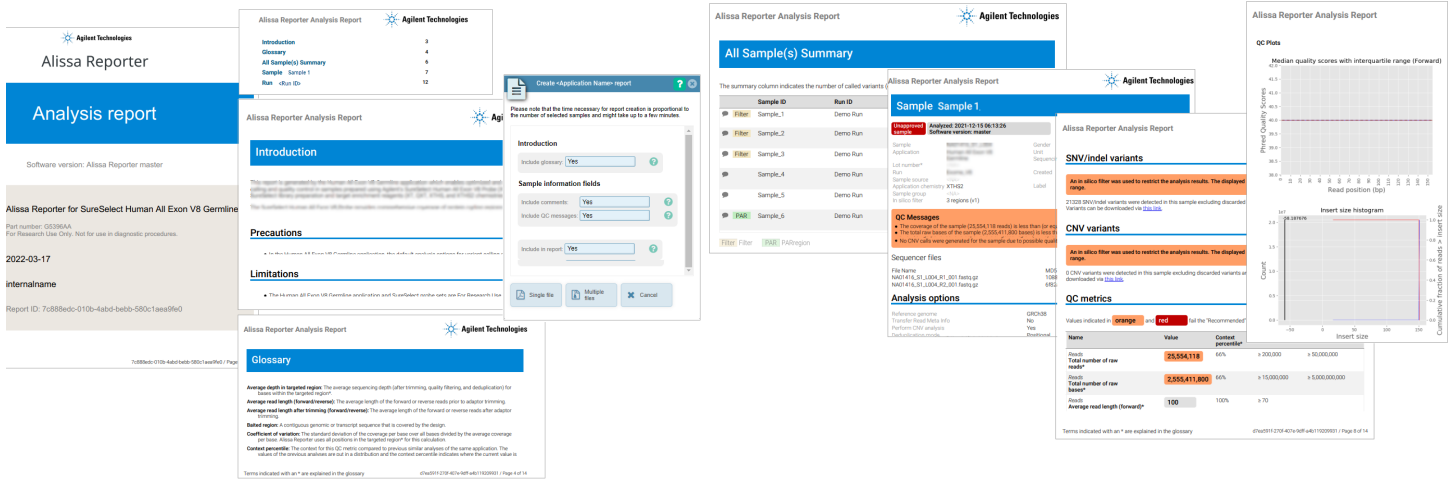


Figure 9. Download a PDF report of the secondary analysis results from Alissa Reporter. For further information regarding tertiary analysis in Alissa Interpret please visit our [product page](#).

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For Research Use Only. Not for use in diagnostic procedures.

Alissa Interpret is a USA Class I Exempt Medical Device, Europe CE IVD, Canada and Australia Class I IVD Device PR7000-3107

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