

NGS Data Analysis Made Easy

Key Benefits

- Optimized Agilent SureSelect pipelines, now including support for SureSelect Cancer CPG panels
- Built-in quality control dashboard
- Fully integrated genome browser
- Intuitive and automated software
- Increased data analysis speed

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 and a built-in quality control (QC) dashboard. Alissa Reporter completely automates data upload, analysis, and export, including direct export from your Amazon Web Services account.

High-performance variant detection for germline and somatic samples

From a single genomic sample, quickly get more valuable information than ever before using Alissa Reporter. Analyze a germline exome sample in less than 60 minutes and a somatic exome sample in less than 120 minutes. Alissa Reporter supports parallel variant detection from DNA specimens improving analysis efficiencies. With Alissa Reporter's secondary analysis capabilities, detect single nucleotide variants (SNVs), insertions and deletions (indels), copy number variants (CNVs), and translocations (TLs). Using Agilent SureSelect Cancer CGP assay, Alissa Reporter also identifies RNA gene fusions. Obtain information about cancer research biomarkers such as tumor mutational burden (TMB), microsatellite instability (MSI), and internal tandem duplication (IDT) mutations for more precise and comprehensive data.

Agilent Technolo	nologies Alissa Reporter Sample Sample 1 RUO 0	
🕋 Start page	Overview QC dashboard SNV/Indel CNV Translocation TMB MSI	
List of Runs	Method: Tumor-only Agilent Technologies Alissa Reporter	Sample Sample1 RUO ()
⊥ Sample Sample1	Number of raw SNVs and indels: 61,842 Number of SNVs and indels filtered by germline/somatic databases: 51,585 A Start page Overview QC dashboard	SNV/Indel CNV Translocation TMB MSI
	Number of SNVs and indels filtered by other sources: 8,928	
	Number of low-impact SNVs and indels: 1,118 Runs Number of low-impact SNVs and indels: Number of high-impact SNVs and indels: 211 Number of valid sites: 269	lly
	TMB score (Mutations/Mb): 120.72 Sample Sample 1 Number of somatic sites: 220	
	MSI score (%): 81.78	

Figure 1. Alissa Reporter detects variants from DNA giving users high confidence in their results. SNVs and indels and IDTs (i.e. FLT3) are reported in the SNV/indel module, CNV detection module identifies both amplifications and deletions, translocations are listed in the Translocation module and biomarker results for TMB and MSI can be viewed in their respective modules.

Integrated genome browser

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

Agilent Technolo	gies A	Alissa	Reporter	Sample	Sample1	RUO 🚯				admin (ir Upload, View Approve, Adn	Edit,	× ?	
🕋 Start page	Overv	iew C	QC dashboard	RNA fusion	Exon skipping								
List of Runs	₽	RNA	fusion variants	for Sampl	e1 (16)								
Sample Sample1	A	Lab.	Name 🔺	Junc. reads	Span. reads	A Tot. sup. r	Splice type	Left break 🔺	Left gene	Right bre 🔺	Right gene	FFPM	 Splice pattern
			CCDC6RET	5	0	5	Ref	chr10: 59,906,	CCDC6	chr10: 43,116,5	RET	31.1997	GT-AG
			CD74ROS1	7	0	7	Ref	chr5: 150,404,	CD74	chr6: 117,324,4	ROS1	43.6796	GT-AG
			EGFRAC069	2	1	3	Ref	chr7: 55,200,4	EGFR	chr11: 121,426 -	AC069287.1	18.7198	GT-AG
			EML4ALK	20	0	20	Ref	chr2: 42,295,5	EML4	chr2: 29,223,5	ALK	124.7988	GT-AG
		Flyer	ETV6NTRK3	21	0	21	Ref	chr12: 11,869,9	ETV6	chr15: 87,940,	NTRK3	131.0387	GT-AG
			FGFR3BAIAP	26	v8 Flyer 🗙	Ø		^{CO} chr4: 1,806,934 +	FGFR3	chr7: 98,362,4	BAIAP2L1	162.2384	GT-AG
			FGFR3TACC3	45	Name:	ETV6NTRK3		chr4: 1,806,934 +	FGFR3	chr4: 1,739,702 +	TACC3	280.7972	GT-AG
			KIF5BRET	53	Left breakpoint:	chr12: 11,869,969 -	GRCh38)	chr10: 32,017,	KIF5B	chr10: 43,114,4	RET	330.7167	GT-AG
			LMNANTRK1	21	Right breakpoint:	chr15: 87,940,753	(GRCh38)	chr1: 156,130,	LMNA	chr1: 156,874,	NTRK1	131.0387	GT-AG
			NCOA4RET	5				chr10: 46,012,	NCOA4	chr10: 43,116,5	RET	31.1997	GT-AG
			PAX8PPARG	9	Open in view	w Show	fusion	chr2: 113,235,3	PAX8	chr3: 12,379,7	PPARG	56.1594	GT-AG
			SLC34A2ROS1	5		Viewer		chr4: 25,664,3	SLC34A2	chr6: 117,324,4	ROS1	37.4396	GT-AG
			SLC45A3BRAF	18	-			chr1: 205,680,	SLC45A3	chr7: 140,794,	BRAF	112.3189	GT-AG
			TFGNTRK1	15	0	15	Ref	chr3: 100,732,	TFG	chr1: 156,874,	NTRK1	93.5991	GT-AG
			TMPRSS2ERG	10	0	10	Ref	chr21: 41,508,	TMPRSS2	chr21: 38,584,	ERG	62.3994	GT-AG
			TPM3NTRK1	16	0	16	Ref	chr1: 154,170,	TPM3	chr1: 156,874,	NTRK1	99.8390	GT-AG



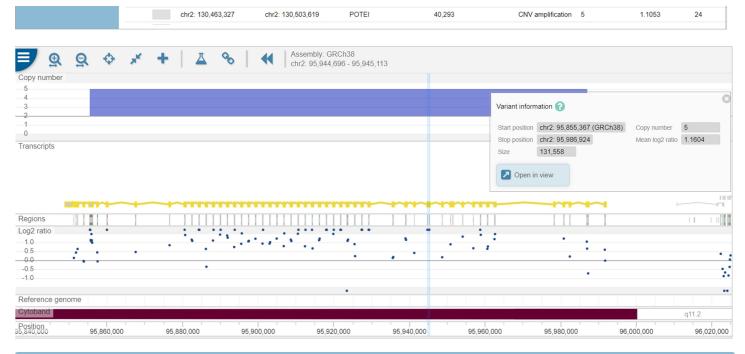
Figure 2. All called DNA and RNA variants can be visualized in Alissa Reporter's genome browser. While hovering over an RNA gene fusion, click Show pileup to jump to the integrated genome browser.

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

	× + @		E ♣ ✔ I ▲ % I ← Assembly: GRCh38 chr20:609,898	
Read pileup				
			Variant information ?	
		- F	Position chr20: 609,898 (GRCh38) ALT frequency 99.50%	
1 1 1			Type delins REF/ALT states CG/GC	
			Total coverage 224 REF/ALT lengths 2/2 Variant quality 946 946	
Variants			Open in view	
Transcripts				
Regions				
Coverage				
Runner up frequency			. 11	
Reference genome				
Cytoband			p13	

Figure 3. Inspect read pileups, coverage and variant information in the pileup view.

Users can also visualize CNVs and TLs with Alissa Reporter's CNV and Translocation Viewer function.



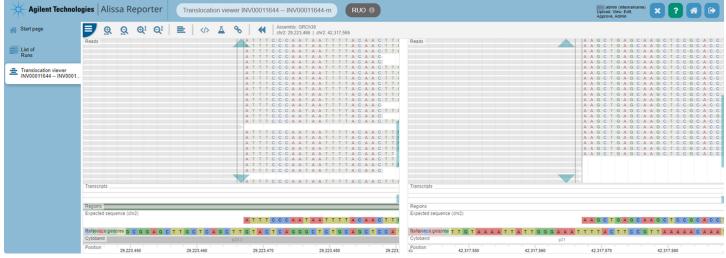


Figure 4. Visualize CNV calls and their log2 ratios in Alissa Reporter's CNV viewer (upper pic) and view read pileups of DNA translocation in the translocation viewer.

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 expected 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.

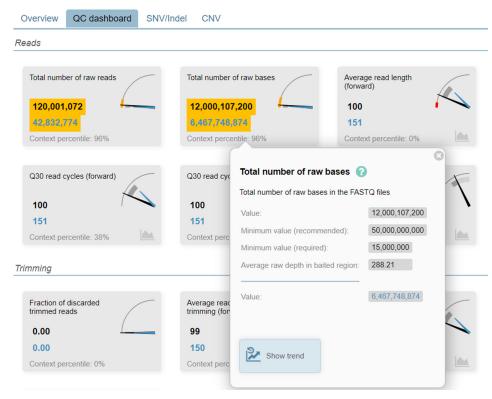


Figure 5. Alissa Reporter's QC dashboard helps you quickly find the metrics that matter most.

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 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.

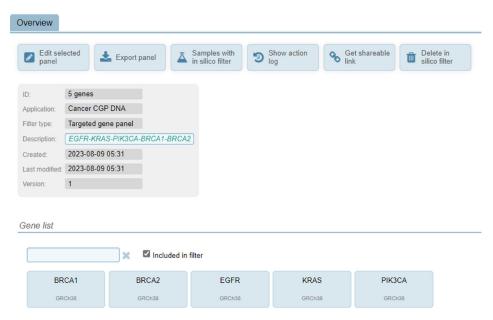


Figure 6. Filter based on your genes and/or regions of interest.

Predefined analysis pipelines

Through optimized analysis pipelines for Agilent SureSelect Human All Exon V7 and V8, SureSelect Cancer CGP DNA and RNA assays, and SureSelect custom panels, users can assess their results with confidence.

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

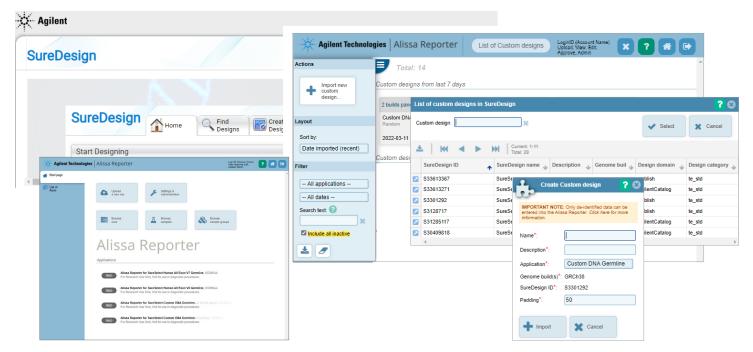


Figure 7. Use optimized analysis pipelines to run your SureSelect Human All Exon V7, V8, SureSelect Cancer CGP DNA and RNA assays, and custom panels. Import your SureSelect custom design into Alissa Reporter.

A FASTQ-to-result, fully automated NGS software workflow

Alissa Reporter turns raw NGS FASTQ files into variant call format (VCF) files for SureSelect Human All Exon V7 and V8 germline, SureSelect Cancer CGP, and custom germline and somatic applications.

Alissa Reporter Workflow

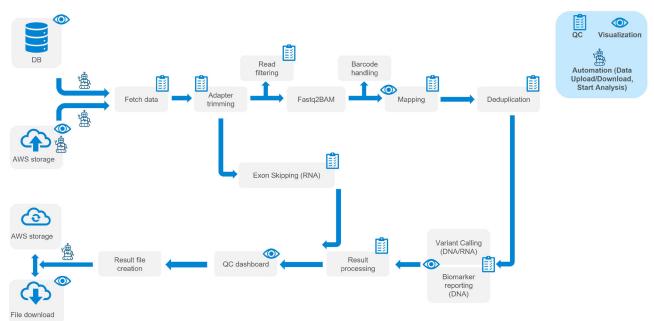


Figure 8. Germline and somatic workflow using Alissa Reporter.

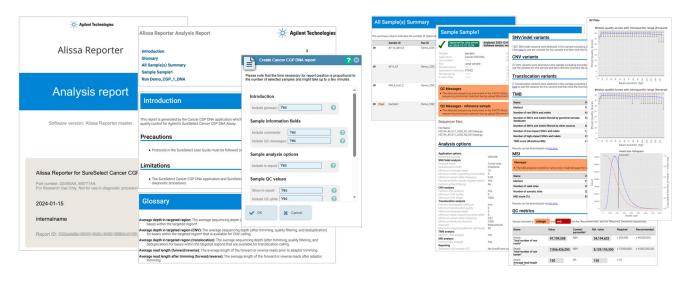


Figure 9. Download a PDF report of the secondary analysis results from Alissa Reporter.

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