Data Sheet
Genomics

Agilent
Trusted Answers

# Exome Enrichment Using the Agilent SureSelect Human All Exon V8 Panel for Tumor Profiling and Agilent Alissa Reporter

**Key benefits**

- Powerful performance with SureSelect exome enrichment for germline and somatic samples
- SureSelect Human All Exon V8 panel provides excellent uniformity of coverage for CNV detection
- Alissa Reporter is an integrated and optimized software for somatic exome data analysis

## Integrated Whole-Exome Sequencing Solutions

Whole-exome sequencing (WES) is increasingly being adopted in oncology testing and research to comprehensively profile tumor samples. WES is the benchmark for determining tumor mutation burden (TMB), which is used to guide treatment selection as TMB is an emerging predictive biomarker for response to immune checkpoint inhibitors. In the field of recurrence monitoring, WES is used to identify mutations in tumor samples to create individualized next-generation sequencing (NGS) assays for monitoring minimal residual disease (MRD). WES is also used to identify neo-antigens in tumor immunotherapy research.

Agilent now provides a WES solution for cancer research labs that includes exome enrichment reagents and software for variant analysis and interpretation. This sequencing solution enables simultaneous detection of somatic single nucleotide variants (SNVs), insertions/deletions (indels), copy number variations (CNVs), and internal tandem repeats (ITDs), delivering a streamlined workflow with increased sensitivity to detect disease-causing mutations.

The Agilent SureSelect Human All Exon V8 panel provides comprehensive coverage of protein coding regions from RefSeq, CCDS, and GENCODE, as well as the TERT promoter region. The exome panel, powered by machine learning-based probe design and a new production process, delivers excellent enrichment performance, as well as efficient and cost-effective exome sequencing. The exome panel can be easily augmented to include customized content for specific applications. The exome enrichment workflow is natively automated on the Agilent Magnis NGS prep and Bravo automated liquid handling systems for enhanced productivity in the laboratory.

Users can readily examine sequencing data using the Agilent Alissa Reporter software, a FASTQ-to-report exome sequencing solution for seamless and efficient variant analysis. Raw data can be analyzed with the Agilent Alissa Reporter software, an intuitive and streamlined cloud-based NGS software-as-a-service (SaaS) solution that simultaneously detects SNVs, indels, CNVs, and ITDs. Users can easily navigate data with integrated genome browsing, a built-in quality control (QC) dashboard.

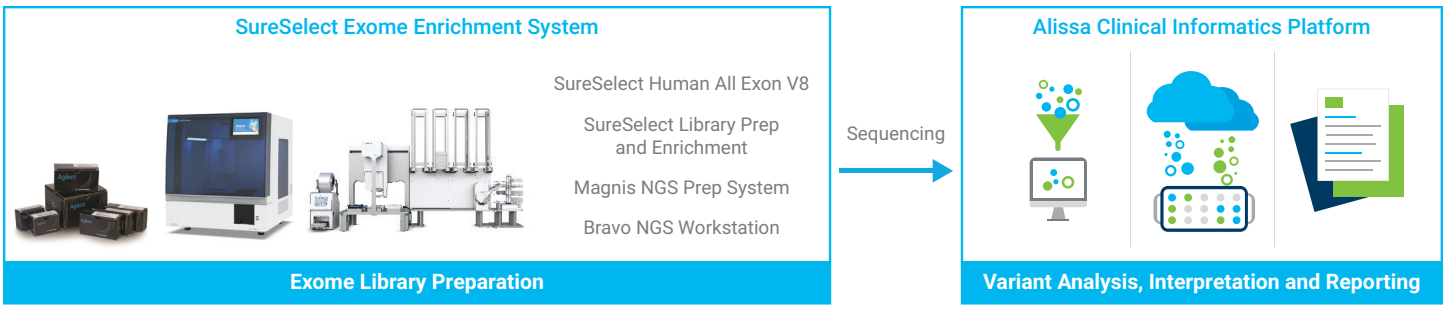



**Figure 1. Agilent whole-exome sequencing solutions.** The Agilent SureSelect Human All Exon V8 panel can be paired with the Agilent Bravo NGS workstation, Agilent Magnis NGS prep system, and Agilent Alissa Reporter software to achieve operational efficiency. The exome is readily automated on the Bravo NGS workstation for high-throughput applications. The Agilent Magnis Human All Exon V8 kit is pre-aliquoted for use on the Magnis NGS prep system, which requires only 10 minutes of initial setup time and delivers eight exome-enriched libraries in less than nine hours without further operator intervention.

## Alissa Reporter for 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 somatic DNA specimens, and with the software's secondary analysis capabilities, SNVs, indels, CNVs, and ITDs can easily be determined (Figure 2). As a fully transparent solution, Alissa Reporter includes confidence scores next to CNV calls.

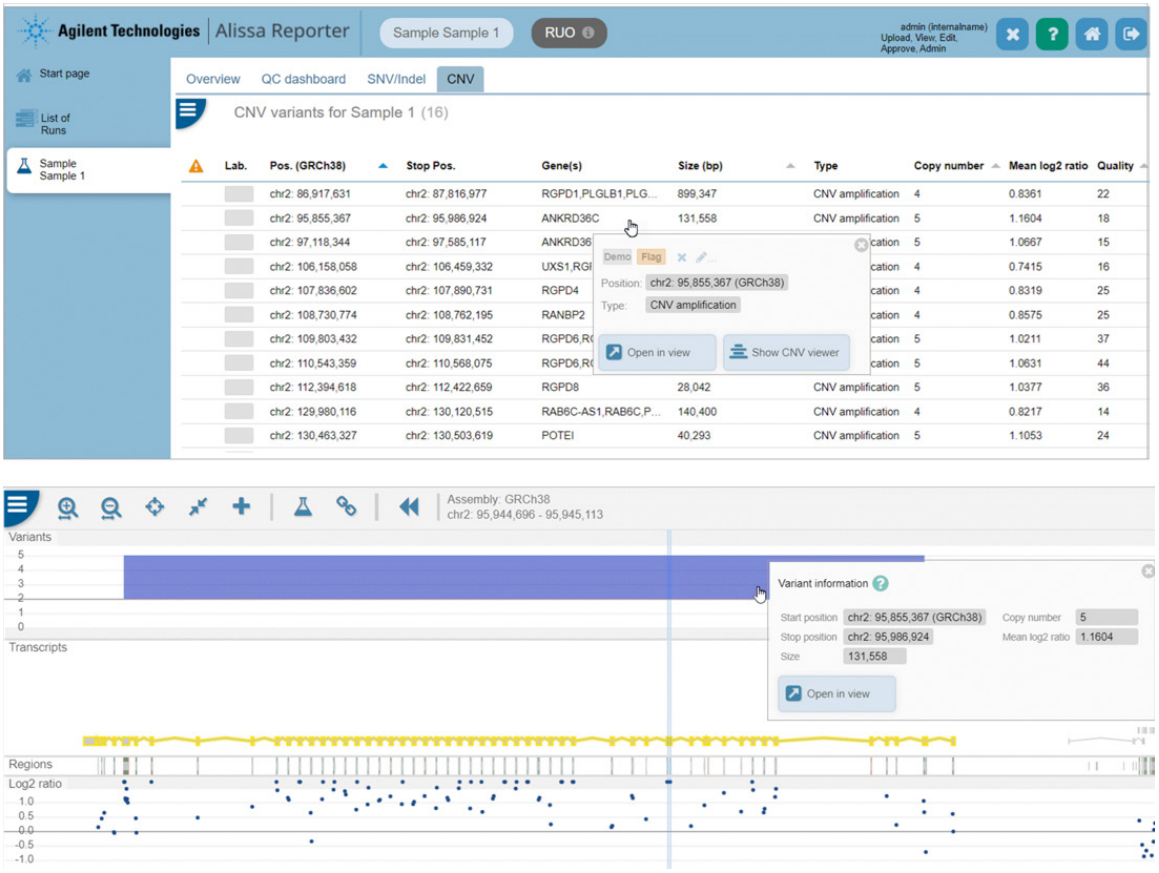



**Figure 2. Agilent Alissa Reporter detects SNVs, indels, CNVs, and ITD variants from exome sequencing.** The Alissa Reporter CNV detection module detects both CNV amplifications and deletions, down to the gene level. CNVs are visualized in a sortable and filterable table. A link to the detailed view is available from within the overview table, in which CNVs can visually be inspected using an integrated genome browser (CNV viewer). A CNV amplification in gene ANKRD36C is shown.

## 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 (Figure 3), users can immediately assess whether key QC metrics of individual samples (or the entire run) are within the anticipated range. The software 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 identify trends and deviations from expected performance parameters over time.

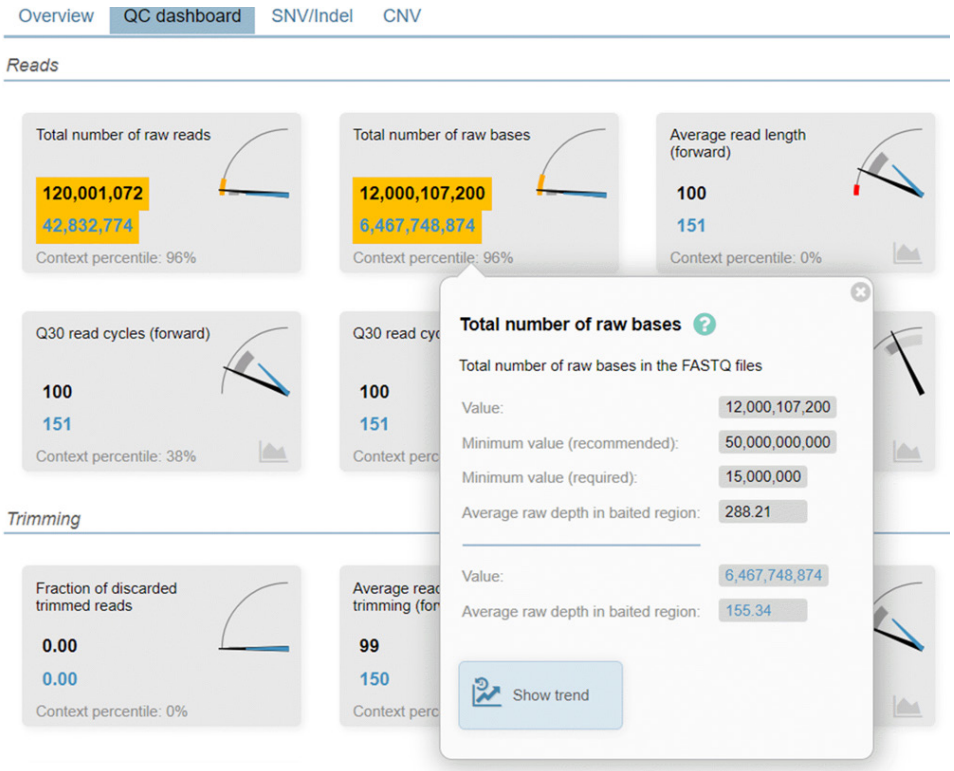



**Figure 3.** The Agilent Alissa Reporter QC dashboard helps you quickly find the metrics that matter most.

## Virtual Gene and/or Regions Panels

If users are only interested in analyzing a subset of genes or regions, the Alissa Reporter in silico filter (Figure 4) enables the creation of virtual gene panels. Create targeted gene panels in advance based on your subpanels of interest or edit your selected panel when needed. 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 the software will automatically filter the dataset based on this selection.

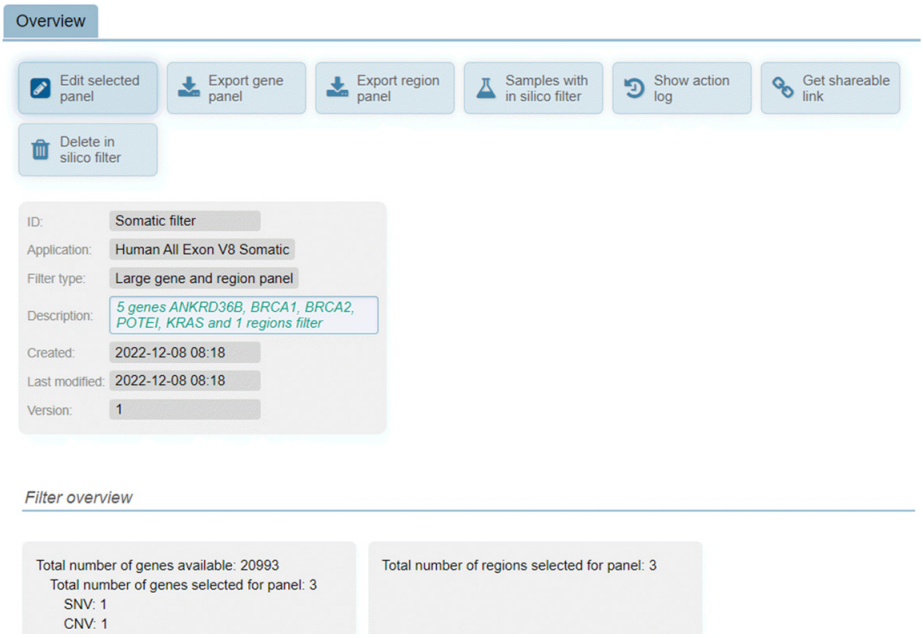
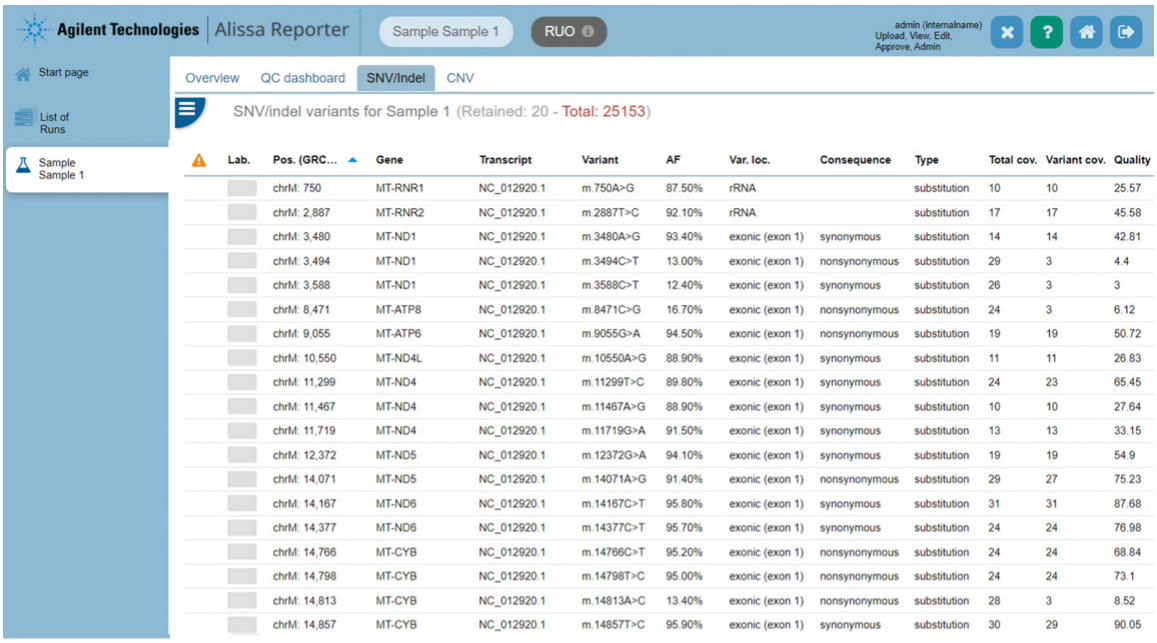



**Figure 4.** The virtual gene panel option enables users to filter based on genes and/or regions of interest.

## Somatic Variant Detection on the Mitochondrial Genome

The mitochondrial genome poses several challenges to the identification and understanding of somatic variants. Alissa Reporter's optimized SureSelect Human All Exon V8 and SureSelect custom panel pipelines come with a dedicated mitochondrial DNA analysis option (Figure 5). The workflow enables labs to explore the state of mitochondria by enabling the detection of mitochondrial variants (that is, SNVs) to identify heteroplasmy. Alissa Reporter delivers mitochondrial variant detection with high sensitivity, helping labs to confidently identify biomarkers in metabolic disease research.




| Lab. | Pos. (GRC... | Gene | Transcript | Variant | AF | Var. loc. | Consequence | Type | Total cov. | Variant cov. | Quality |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | chrM: 750 | MT-RNR1 | NC_012920.1 | m.750A>G | 87.50% | rRNA | | substitution | 10 | 10 | 25.57 |
| | chrM: 2,887 | MT-RNR2 | NC_012920.1 | m.2887T>C | 92.10% | rRNA | | substitution | 17 | 17 | 45.58 |
| | chrM: 3,480 | MT-ND1 | NC_012920.1 | m.3480A>G | 93.40% | exonic (exon 1) | synonymous | substitution | 14 | 14 | 42.81 |
| | chrM: 3,494 | MT-ND1 | NC_012920.1 | m.3494C>T | 13.00% | exonic (exon 1) | nonsynonymous | substitution | 29 | 3 | 4.4 |
| | chrM: 3,588 | MT-ND1 | NC_012920.1 | m.3588C>T | 12.40% | exonic (exon 1) | synonymous | substitution | 26 | 3 | 3 |
| | chrM: 8,471 | MT-ATP8 | NC_012920.1 | m.8471C>G | 16.70% | exonic (exon 1) | nonsynonymous | substitution | 24 | 3 | 6.12 |
| | chrM: 9,055 | MT-ATP6 | NC_012920.1 | m.9055G>A | 94.50% | exonic (exon 1) | nonsynonymous | substitution | 19 | 19 | 50.72 |
| | chrM: 10,550 | MT-ND4L | NC_012920.1 | m.10550A>G | 88.90% | exonic (exon 1) | synonymous | substitution | 11 | 11 | 26.83 |
| | chrM: 11,299 | MT-ND4 | NC_012920.1 | m.11299T>C | 89.80% | exonic (exon 1) | synonymous | substitution | 24 | 23 | 65.45 |
| | chrM: 11,467 | MT-ND4 | NC_012920.1 | m.11467A>G | 88.90% | exonic (exon 1) | synonymous | substitution | 10 | 10 | 27.64 |
| | chrM: 11,719 | MT-ND4 | NC_012920.1 | m.11719G>A | 91.50% | exonic (exon 1) | synonymous | substitution | 13 | 13 | 33.15 |
| | chrM: 12,372 | MT-ND5 | NC_012920.1 | m.12372G>A | 94.10% | exonic (exon 1) | synonymous | substitution | 19 | 19 | 54.9 |
| | chrM: 14,071 | MT-ND5 | NC_012920.1 | m.14071A>G | 91.40% | exonic (exon 1) | nonsynonymous | substitution | 29 | 27 | 75.23 |
| | chrM: 14,167 | MT-ND6 | NC_012920.1 | m.14167C>T | 95.80% | exonic (exon 1) | synonymous | substitution | 31 | 31 | 87.68 |
| | chrM: 14,377 | MT-ND6 | NC_012920.1 | m.14377C>T | 95.70% | exonic (exon 1) | synonymous | substitution | 24 | 24 | 76.98 |
| | chrM: 14,766 | MT-CYB | NC_012920.1 | m.14766C>T | 95.20% | exonic (exon 1) | nonsynonymous | substitution | 24 | 24 | 68.84 |
| | chrM: 14,798 | MT-CYB | NC_012920.1 | m.14798T>C | 95.00% | exonic (exon 1) | nonsynonymous | substitution | 24 | 24 | 73.1 |
| | chrM: 14,813 | MT-CYB | NC_012920.1 | m.14813A>C | 13.40% | exonic (exon 1) | nonsynonymous | substitution | 28 | 3 | 8.52 |
| | chrM: 14,857 | MT-CYB | NC_012920.1 | m.14857T>C | 95.90% | exonic (exon 1) | synonymous | substitution | 30 | 29 | 90.05 |


**Figure 5.** Comprehensive analysis results of the mitochondrial genome displayed in the SNV/indel table and read pileup view available in Agilent Alissa Reporter.

# Ordering Information

### Compatible with Fast Hybridization

| Product Description | 16 Rxns | 96 Rxns | 96 Rxns Auto |
|---|---|---|---|
| SureSelect XT HS Human All Exon V8 | 5191-6873 | 5191-6874 | 5191-6875 |
| SureSelect XT HS Human All Exon V8+UTR | 5191-7401 | 5191-7402 | 5191-7403 |
| SureSelect XT HS Human All Exon V8+NCV | 5191-7407 | 5191-7408 | 5191-7409 |
| **Product Description** | **2 Hybs** | **12 Hybs** | **12 Hybs Auto** |
| SureSelect XT HS PreCap Human All Exon V8 | 5191-6876 | 5191-6877 | 5191-6878 |
| SureSelect XT HS PreCap Human All Exon V8+UTR | 5191-7404 | 5191-7405 | 5191-7406 |
| SureSelect XT HS PreCap Human All Exon V8+NCV | 5191-7410 | 5191-7411 | 5191-7412 |

### Compatible with Overnight Hybridization

| Product Description | 16 Rxns | 96 Rxns | 96 Rxns Auto |
|---|---|---|---|
| SureSelect XT Human All Exon V8 | 5191-6879 | 5191-6891 | 5191-6892 |
| SureSelect XT Human All Exon V8+UTR | | Contact Sales | |
| SureSelect XT Human All Exon V8+NCV | | Contact Sales | |
| **Product Description** | **2 Hybs** | **12 Hybs** | **12 Hybs Auto** |
| SureSelect XT PreCap Human All Exon V8 | 5280-0032 | 5280-0033 | 5280-0034 |
| SureSelect XT PreCap Human All Exon V8+UTR | | Contact Sales | |
| SureSelect XT PreCap Human All Exon V8+NCV | | Contact Sales | |

### Compatible with Magnis NGS Prep System

| Product Description | 32 Rxns | 96 Rxns |
|---|---|---|
| Magnis SSEL XT HS Human All Exon V8, Rev B | G9772C | G9772D |
| Magnis SSEL XT HS2 Human All Exon V8, Rev B | G9774A | G9774B |
| Magnis SSEL XT HS2 Human All Exon V8+UTR | G9779A | G9779B |
| Magnis SSEL XT HS2 Human All Exon V8+NCV | G9778A | G9778B |

### Other Configurations

| Product Description | |
|---|---|
| SureSelect Human All Exon V8+Pan-Cancer | Contact Sales |
| SureSelect Human All Exon V8+Mitochondrial Genome | Contact Sales |
| SureSelect Human All Exon V8+OneSeq CNV Backbone | Contact Sales |

### Automation and Software

| Product Description | |
|---|---|
| Magnis NGS Prep System | Contact Sales |
| Bravo NGS (Option A) | Contact Sales |
| Bravo NGS Workstation (Option B) | Contact Sales |
| Alissa Reporter | Contact Sales |

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