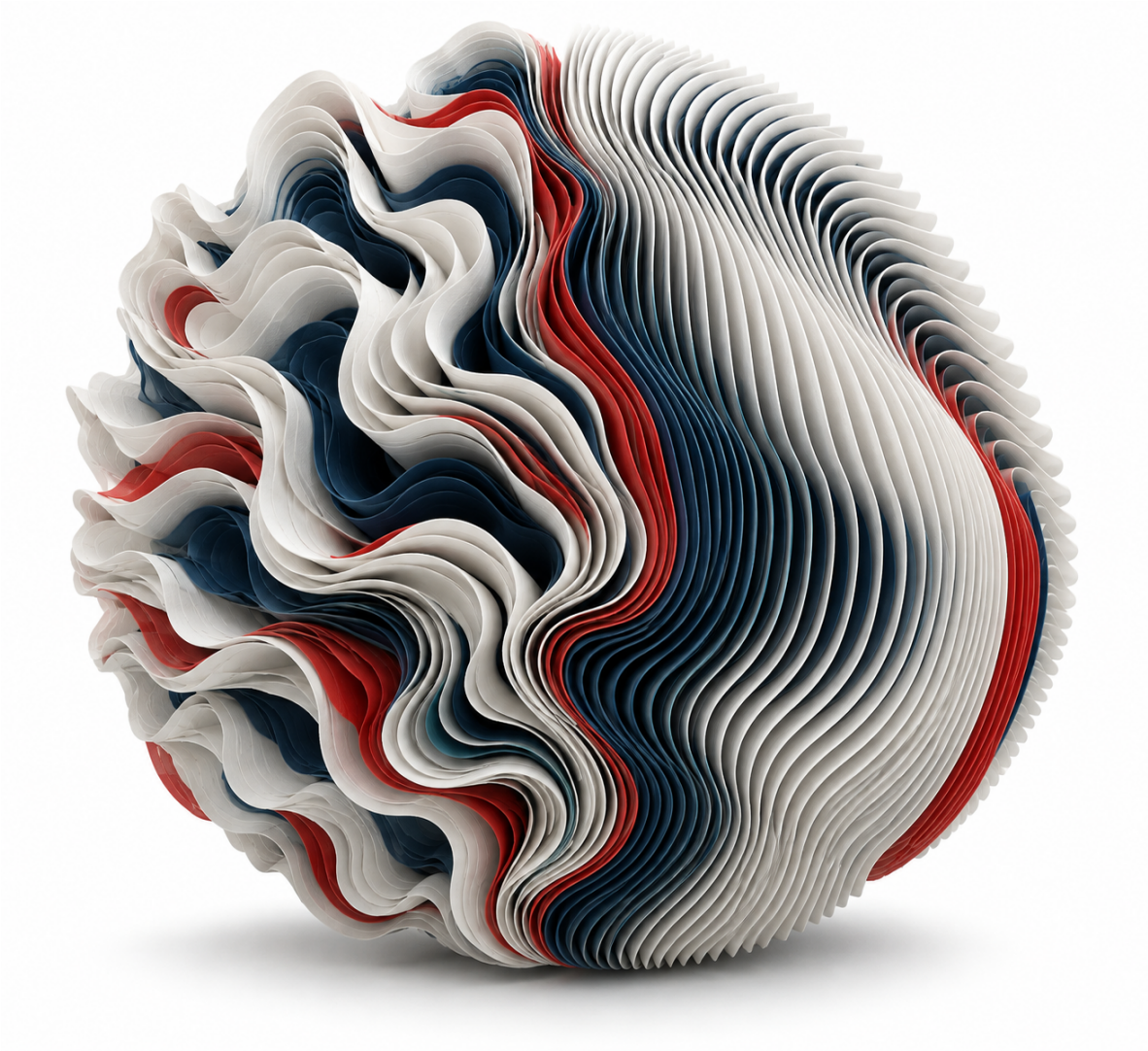
Gennext

SOMATIC

FOR MOLECULAR PATHOLOGY

See the whole picture in somatic variant analysis.

An integrated analysis experience, from DNA and RNA findings to evidence review and reporting.



DNA + RNA

Integrated review

Accelerated processing

≈30 minutes / sample

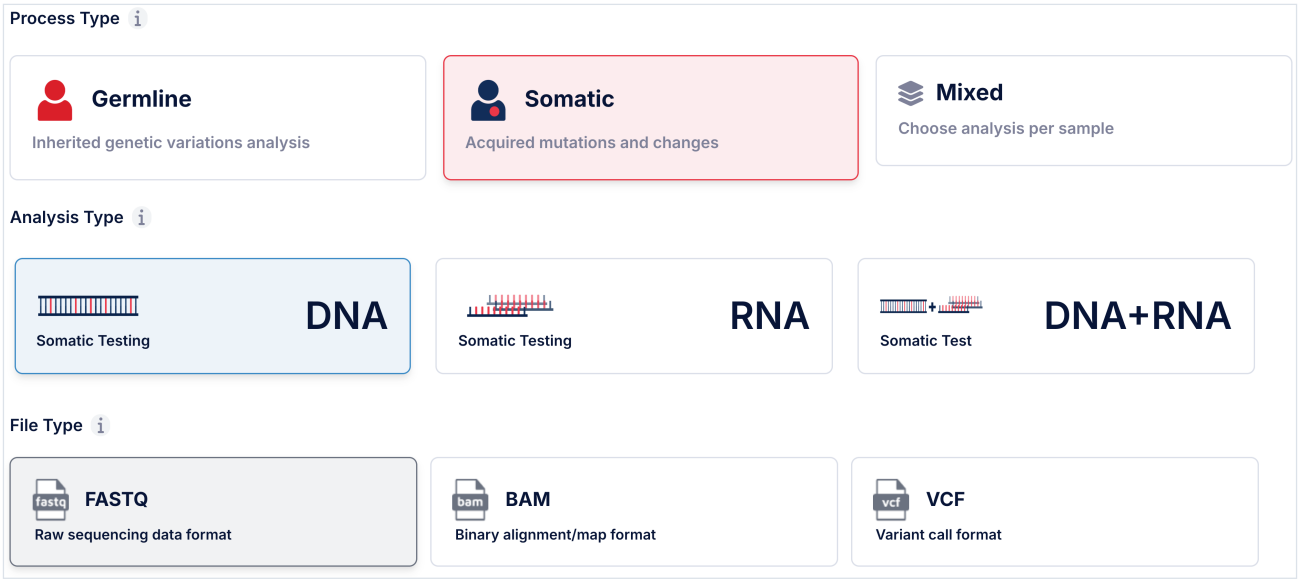
Data at your institution

Federated architecture

One workflow, from file to analysis.

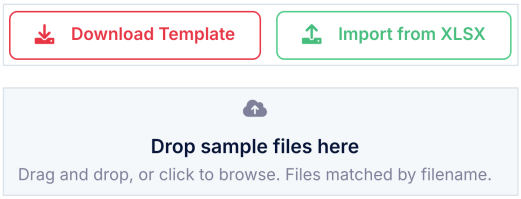
Choose DNA, RNA or DNA+RNA analysis.
Add your files, start processing and review sample quality.

01 / ANALYSIS AND FILE TYPE



Gennext also supports germline variant analysis.

02 / BULK FILE UPLOAD



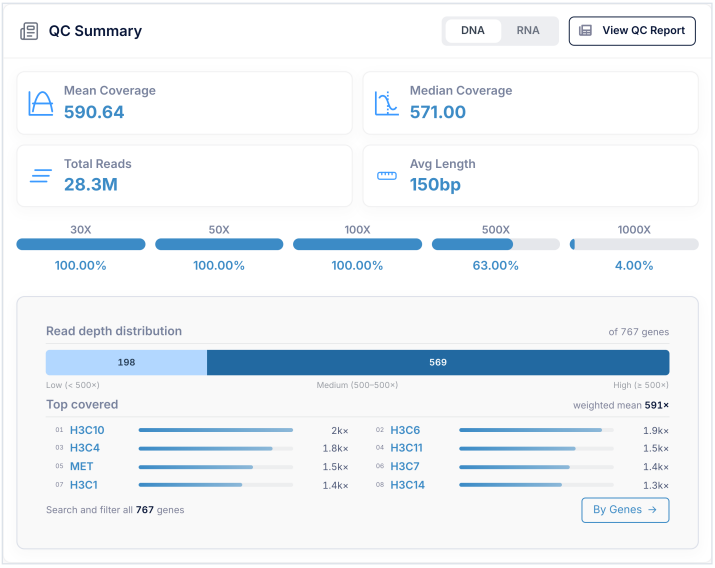
Import sample details from Excel, then upload the associated files together.

≈30

minutes / sample

DNA + RNA together

03 / REVIEW QUALITY



QC Summary: read metrics, coverage thresholds and gene distribution.

Prioritize by tumor type.

Variants associated with the tumor type selected during upload are highlighted.
Refine your review with clinical and functional filters.

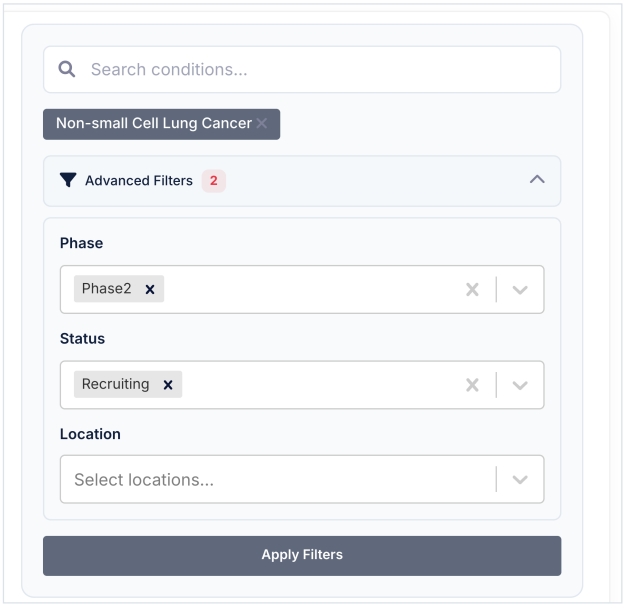
SELECTED GENE AND VARIANT / MET



NSCLC example · MET p.D963_R974del · Likely Oncogenic

Filter clinical trials, step by step

01 / SELECT CRITERIA



Select condition, phase and status.
Add a location if needed.

02 / REVIEW RESULTS



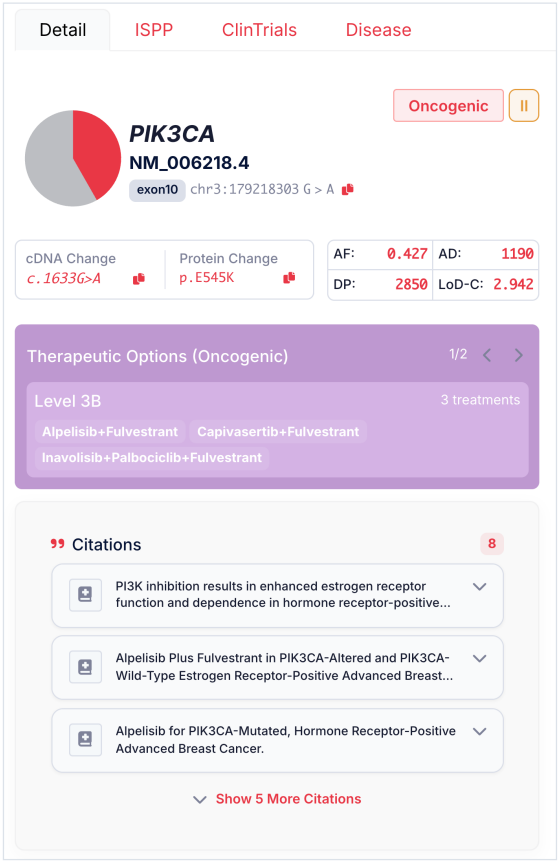
Use **Apply Filters** to narrow the list, then open a matching study to review its details.

In this example: NSCLC, Phase2 and Recruiting. Two matching study records are shown.

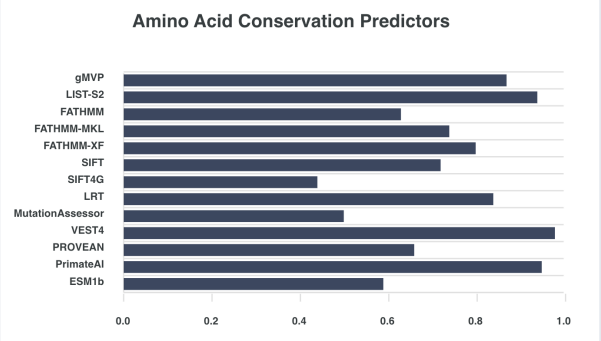
Explore the variant and its evidence.

Review classification, allele fraction and therapeutic options.
Access current literature through the variant's citation records.

PIK3CA p.E545K / DETAIL PANEL



ISPP / SAME VARIANT



Compare functional-effect predictions for the same variant.

LoD-C: read support

The same 5% AF may represent 5/100, 50/1,000 or 500/10,000 reads. LoD-C uses read counts to assess statistical support for a true variant signal.

LoD-C > 2.5: significant statistical support

Clinical relevance is assessed separately.

IGV / SEPARATE READ-REVIEW EXAMPLE



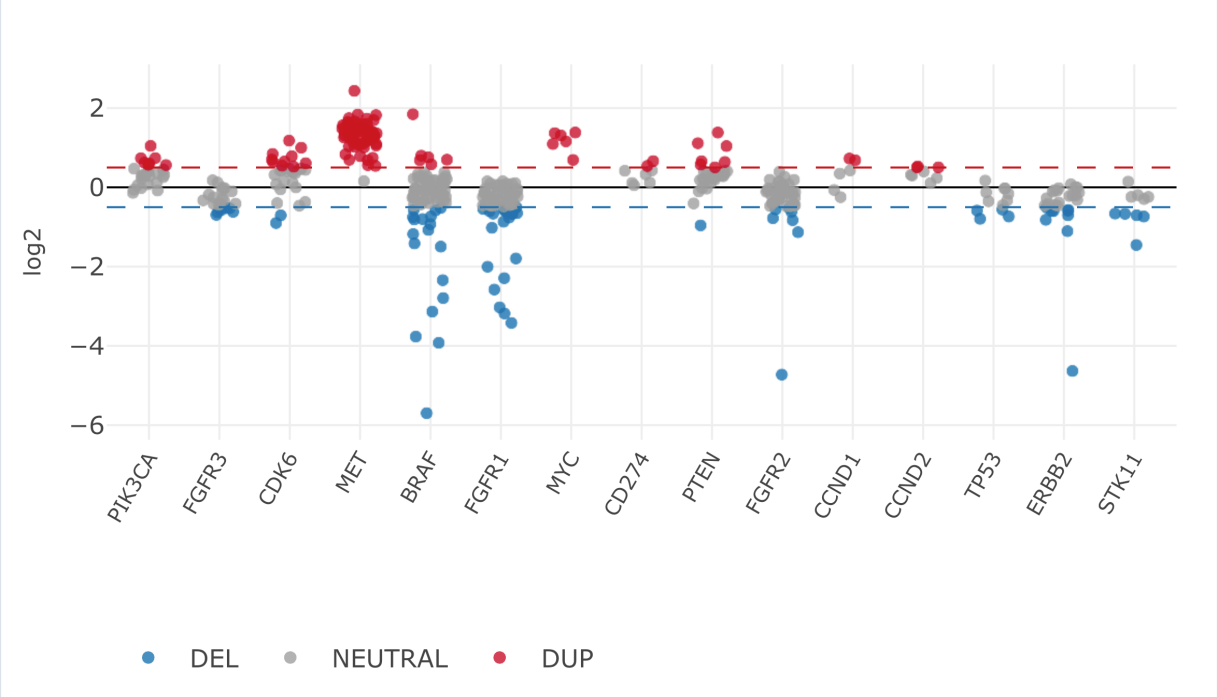
MET rs38852 · Alternative A: 236 (+), 230 (-) reads

Pink: forward (+) · Purple: reverse (-)
Reads sorted by base at the variant position.

From copy number to fusions.

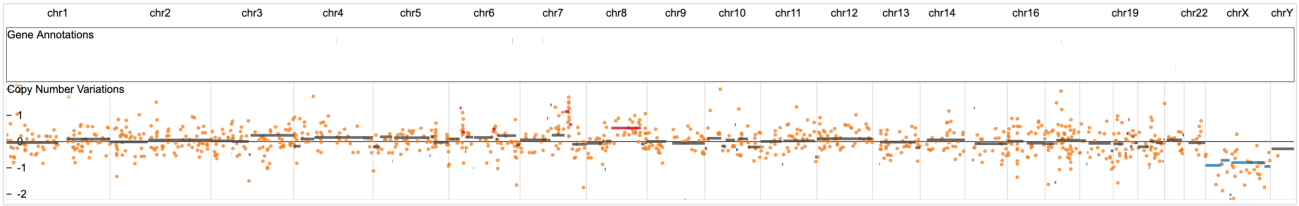
Review copy-number changes by gene and genomic position.
Add RNA findings to the molecular profile.

CNV / GENE-LEVEL REVIEW



Review copy-number changes across oncogenes such as MET and MYC. In this example, the gain in the MET region is visible in the gene-level plot.

GENOME-WIDE COPY-NUMBER CONTEXT



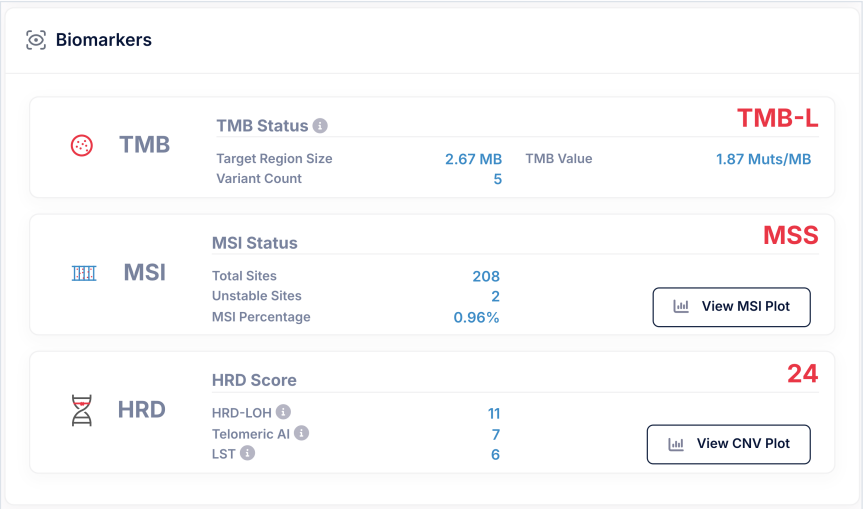
Review RNA fusions with their evidence.

Assess fusion partners, breakpoints and supporting reads together. Arriba and STAR-Fusion results support the review.

Review biomarkers together.

Move from TMB, MSI and HRD results to the measurements behind them.

TMB · MSI · HRD

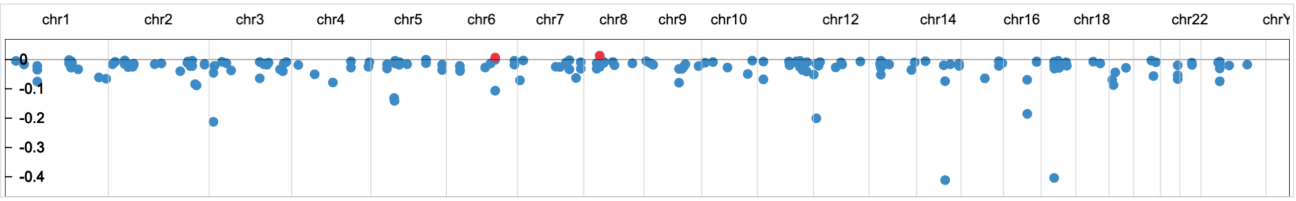


From result to detail.

Review biomarkers in one panel. Open the MSI and HRD plots to examine the underlying measurements.

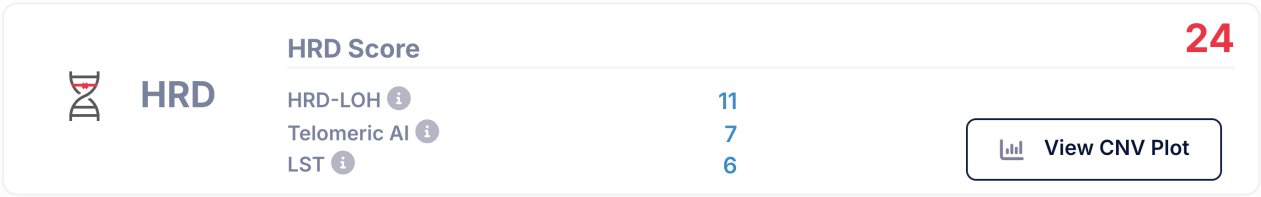
Gennext biomarker panel · actual application view.

MSI / ACROSS CHROMOSOMES



The plot shows microsatellite sites across chromosomes in the “Difference” view. Red points indicate sites classified as unstable; blue points indicate stable sites. In this example, 2 of 208 sites are unstable (0.96%), and the result is MSS.

HRD / SCORE AND COMPONENTS

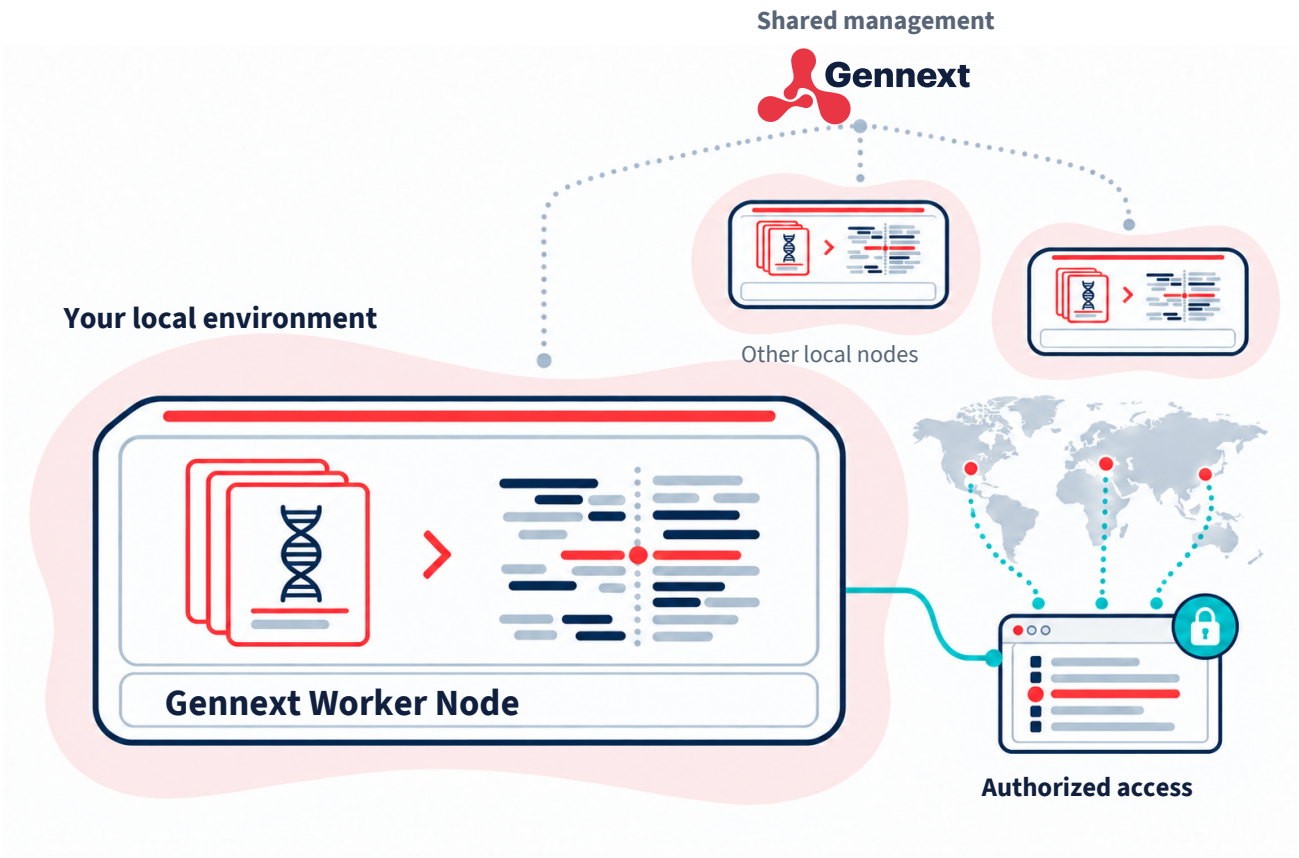


Review the components behind the score.

Inspect HRD-LOH, telomeric allelic imbalance and LST values. Select “View CNV Plot” to explore copy ratio and allelic distribution.

Your data is processed and stored at your institution.

Gennext Worker Node processes and stores genomic data at your institution. Manage the workflow through Gennext.



Authorized access from anywhere.

Share access to your analyses according to user permissions.

Only you

Analysis team

Authorized institutional users

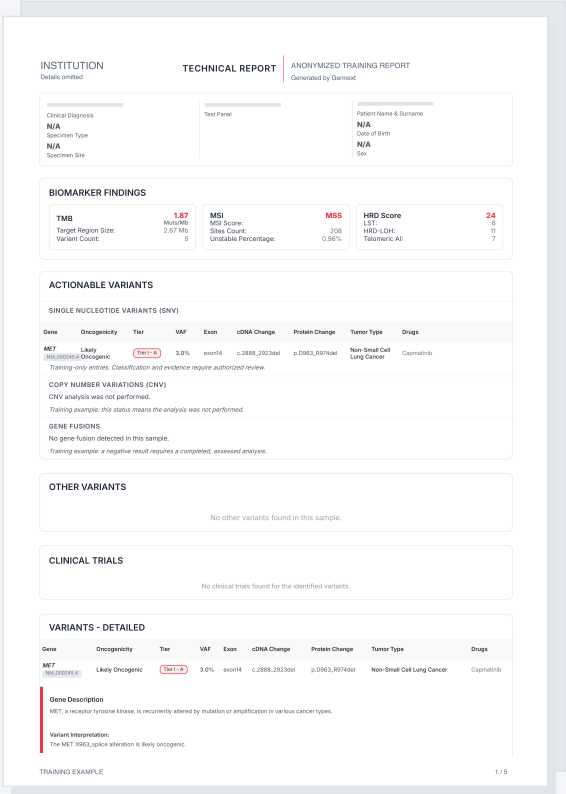
Supports workflows aligned with KVKK and GDPR requirements.

The local Worker Node deployment and access locations are illustrative.

From raw data to reporting. In your institution's format.

Your institution's report format is configured in Gennext.
Selected findings and clinical interpretations are reported in that format.

Example report · Page 1



INSTITUTION
Details omitted

TECHNICAL REPORT | ANONYMIZED TRAINING REPORT
Generated by Gennext

Clinical Diagnosis: N/A
Specimen Type: N/A
Specimen Site:
Test Panel:
Patient Name & Surname: N/A
Date of Birth: N/A
Sex:

BIOMARKER FINDINGS

TMB	1.87 Muts/Mb	MSI	MSS	HRD Score	24
Target Region Size:	2.67 Mb	MSI Score:		LST:	6
Variant Count:	5	Sites Count:	208	HRD-LOH:	11
		Unstable Percentage:	0.96%	Telomeric AI:	7

ACTIONABLE VARIANTS

SINGLE NUCLEOTIDE VARIANTS (SNV)

Gene	Oncogenicity	Tier	VAF	Exon	cDNA Change	Protein Change	Tumor Type	Drugs
MET NM_000245.4	Likely Oncogenic	Tier I - A	3.0%	exon14	c.2888_2923del	p.D963_R974del	Non-Small Cell Lung Cancer	Capmatinib

Training-only entries. Classification and evidence require authorized review.

COPY NUMBER VARIATIONS (CNV)
CNV analysis was not performed.
Training example: this status means the analysis was not performed.

GENE FUSIONS
No gene fusion detected in this sample.
Training example: a negative result requires a completed, assessed analysis.

OTHER VARIANTS
No other variants found in this sample.

CLINICAL TRIALS
No clinical trials found for the identified variants.

VARIANTS - DETAILED

Gene	Oncogenicity	Tier	VAF	Exon	cDNA Change	Protein Change	Tumor Type	Drugs
MET NM_000245.4	Likely Oncogenic	Tier I - A	3.0%	exon14	c.2888_2923del	p.D963_R974del	Non-Small Cell Lung Cancer	Capmatinib

Gene Description
MET, a receptor tyrosine kinase, is recurrently altered by mutation or amplification in various cancer types.

Variant Interpretation:
The MET X963_splice alteration is likely oncogenic.

TRAINING EXAMPLE 1 / 5

MORE FROM THE REPORT

Gene panel content

Report · Page 3 / excerpt

CYLD	*CYP17A1*	*DAXX*	*DCUN1D1*	*DDR1*
DHX15	*DHX9*	*DICER1*	*DIS3*	*DIS3L2*
DOT1L	*DPYD*	*E2F3*	*EED*	*EGFL7*
ELF3	*EML4*	*EP300*	*EPCAM*	*EPHA2*
EPHB4	*ERBB2*	*ERBB3*	*ERBB4*	*ERCC1*
ERRFI1	*ESR1*	*ESR2*	*ETS1*	*ETV1*
EZR	*FAM175A*	*FAM46C*	*FANCA*	*FANCC*
FANCL	*FANCM*	*FAS*	*FAT1*	*FBXO11*

Coverage details

Report · Page 4 / excerpt

REGIONS BELOW 50X COVERAGE

GENE	MEAN DEPTH	MIN DEPTH
HLA-A	5x	0x
HLA-C	0x	0x
PPP4R2	534x	2x
HLA-B	71x	16x
RB1	608x	17x
NF1	696x	18x
RANBP2	615x	24x
MAGEC3	156x	33x
ANKRD26	567x	50x

Examples from pages 1, 3 and 4 of a Gennext training report. Institution and identifying details omitted.

Learn to use Gennext step by step with Gennext Community.
Scan the QR code to explore our somatic analysis tutorials.

Gennext

gennext.bio

Video Tutorials

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info@gennext.bio · +90 (216) 500 44 71

Discover Gennext.

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