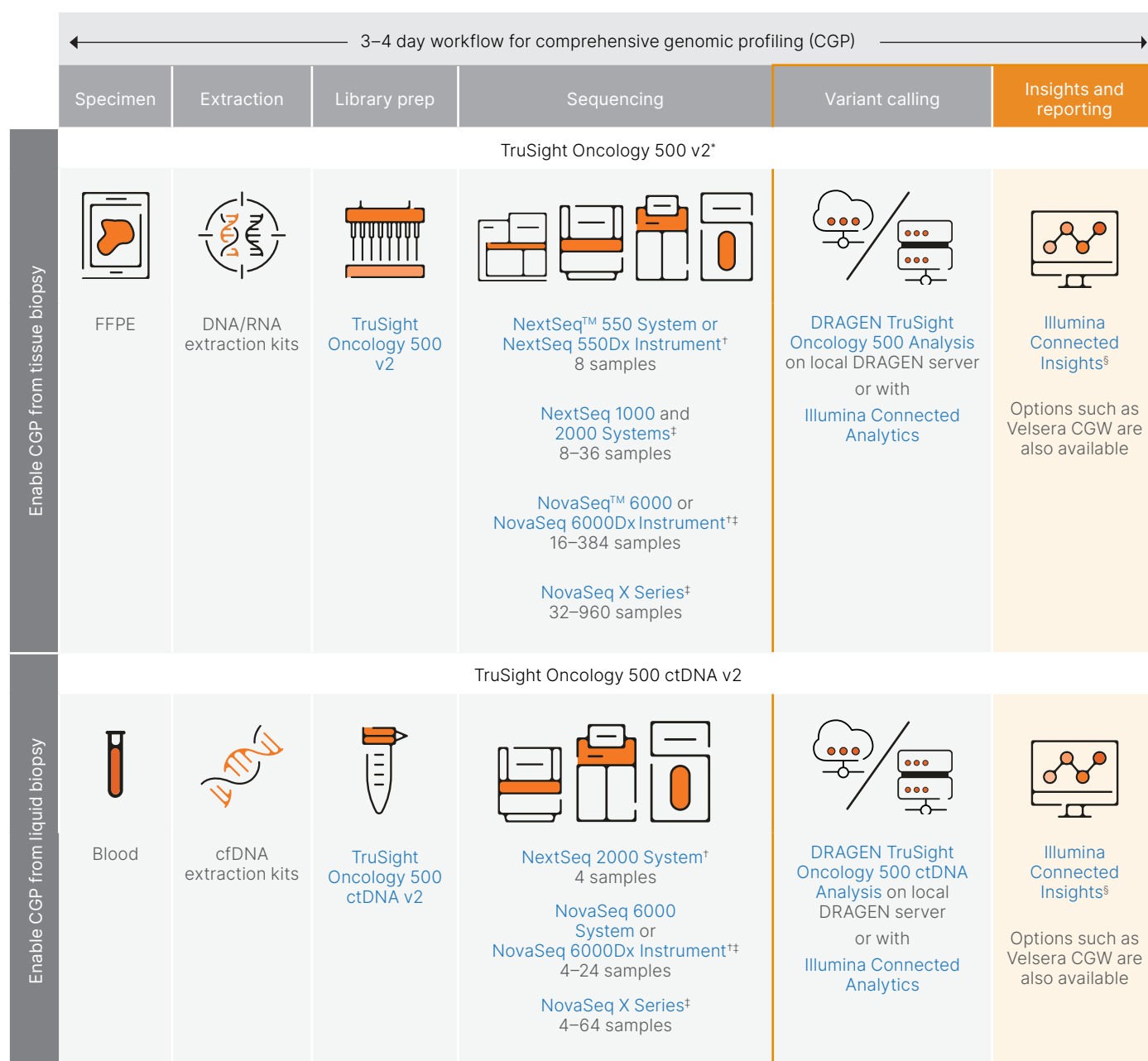# illumina®

Data analysis and reporting for the TruSight™ Oncology 500 portfolio

Integrated bioinformatics provide sample-to-insight workflows to enable solid tumor CGP

DRAGEN™ secondary analysis for the TruSight Oncology 500 portfolio reduces analysis time by 2–10×. DRAGEN TruSight Oncology 500 and DRAGEN TruSight Oncology 500 ctDNA Analysis Software, provided with each kit, can be run locally with an on-premises DRAGEN server or in the cloud via Illumina Connected Analytics (ICA). Options for customized reporting and insights include Illumina Connected Insights and Velsera Clinical Genomics Workspace (CGW).

3–4 day workflow for comprehensive genomic profiling (CGP)					
Specimen	Extraction	Library prep	Sequencing	Variant calling	Insights and reporting

TruSight Oncology 500 v2*

Enable CGP from tissue biopsy

| FFPE | DNA/RNA extraction kits | TruSight Oncology 500 v2 | NextSeq™ 550 System or NextSeq 550Dx Instrument† 8 samples

NextSeq 1000 and 2000 Systems‡ 8–36 samples

NovaSeq™ 6000 or NovaSeq 6000Dx Instrument†‡ 16–384 samples

NovaSeq X Series‡ 32–960 samples | DRAGEN TruSight Oncology 500 Analysis on local DRAGEN server
or with
Illumina Connected Analytics | Illumina Connected Insights§

Options such as Velsera CGW are also available |

TruSight Oncology 500 ctDNA v2

Enable CGP from liquid biopsy

| Blood | cfDNA extraction kits | TruSight Oncology 500 ctDNA v2 | NextSeq 2000 System† 4 samples

NovaSeq 6000 System or NovaSeq 6000Dx Instrument†‡ 4–24 samples

NovaSeq X Series‡ 4–64 samples | DRAGEN TruSight Oncology 500 ctDNA Analysis on local DRAGEN server
or with
Illumina Connected Analytics | Illumina Connected Insights§

Options such as Velsera CGW are also available |

* Not available for sale in Japan. † NextSeq 550Dx or NovaSeq 6000Dx Instruments in research mode only. ‡ Requires separate, standalone DRAGEN server if local secondary analysis is desired. § Illumina Connected Insights supports user-defined tertiary analysis through API calls to third-party knowledge sources.

Better variant calling with DRAGEN analysis

Accurate

- DRAGEN secondary analysis brings award-winning accuracy to TruSight Oncology 500 v2
- 99.83% accuracy score with the precisionFDA Truth Challenge V2[1,2]

Comprehensive

- Comprehensive coverage of all variant classes: SNVs, indels, CNVs, MNVs, SVs; immuno-oncology and other gene signatures: TMB, MSI, and HRD (GIS)*
- Beta features[†] available with TruSight Oncology 500 v2 enable reporting of absolute copy numbers and gene-level LOH

Fast

- DRAGEN secondary analysis completes 2–10× faster than other pipelines

Assay	No. of samples[b]	Third-party server[a]	DRAGEN Server v4	DRAGEN analysis on ICA[b]
		Analysis time[c]		
TruSight Oncology 500 v2	8 tissue biopsy	5.5 hr	2.2 hr	3 hr
	16 tissue biopsy	12 hr	4.5 hr	3.5 hr
	32 tissue biopsy	18 hr	9 hr	3 hr
	72 tissue biopsy	24 hr	20.5 hr	4 hr
TruSight Oncology 500 ctDNA v2	24 liquid biopsy	216 hr (9 days)	20 hr (< 1 day)	2.5 hr (< 1 day)

a. Third-party server: c5.9×large instance (36 vCPU, 72 GiB memory).
b. Time presented includes 0.5 hr queing time, however queue times may vary.
c. Approximate analysis times are based on actual runs, analysis times will vary.

ICA, Illumina Connected Analytics.

Flexible

- Local and cloud-based analysis allow labs to choose an option that best suits their needs
- User interface designed for general users as well as bioinformatics professionals

Easy to use

- User-friendly interface to set up and configure analysis
- No manual touchpoints available with automated data transfer and analysis kickoff
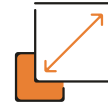
Scalable

- Cloud-based analysis enables scaling without additional hardware investment
- Reducing manual touchpoints with automation allows scalability without adding headcount

Drive more genomic insights with the TruSight Oncology 500 portfolio and DRAGEN analysis:

- ✓ TruSight Oncology 500 with DRAGEN analysis
- ✓ DRAGEN secondary analysis

* HRD (GIS) is for tissue workflows only (not available with TruSight Oncology 500 ctDNA).
† Beta features have not been verified by Illumina. See customer release notes for v2.6 for more details.

SNV, single nucleotide variant; indels, insertions and deletions; CNV, copy number variant; MNV, multinucleotide variant; SV, structural variant; TMB, tumor mutational burden; MSI, microsatellite instability; HRD, homologous recombination deficiency; GIS, genomic instability; LOH, loss of heterozygosity.

References

1. Food and Drug Administration. Truth Challenge V2: Calling Variants from Short and Long Reads in Difficult-to-Map Regions. precision.fda.gov/challenges/10. Published 2020. Accessed March 14, 2022.
2. Illumina. DRAGEN Sets New Standard for Data Accuracy in PrecisionFDA Benchmark Data. Optimizing Variant Calling Performance with Illumina Machine Learning and DRAGEN Graph. illumina.com/science/genomics-research/articles/dragen-shines-again-precisionfda-truth-challenge-v2.html. Published January 12, 2022. Accessed March 14, 2022.

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