



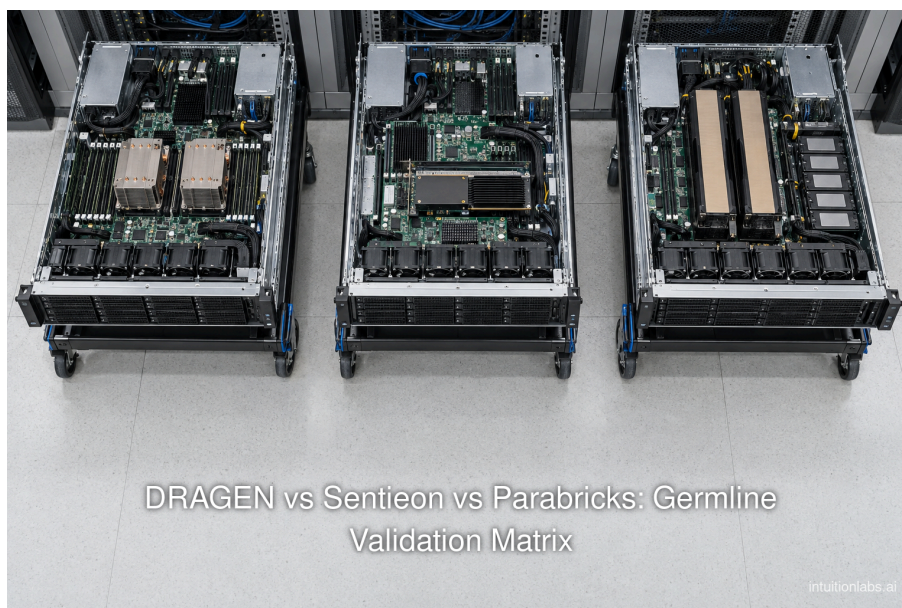
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DRAGEN vs Sentieon vs Parabricks: Germline Validation Matrix

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Executive Summary

DRAGEN vs Sentieon vs Parabricks is a choice among versioned analysis workflows, reference representations, deployment modes, and support arrangements. A product name alone does not identify the caller being validated. **Illumina DRAGEN** lists server release **4.6.2**, posted September 30, 2026 (support.illumina.com); its **Software Mode** became available October 8, expanding deployment beyond field-programmable gate arrays (FPGAs) (developer.illumina.com). **Sentieon DNaseq** targets Genome Analysis Toolkit (GATK) small-variant equivalence, while **DNAscope** offers a different calling approach and broader documented variant scope (www.sentieon.com) (www.sentieon.com). **NVIDIA Parabricks** lists container **4.8.0-1**, updated October 13, 2026 (catalog.ngc.nvidia.com), with distinct GATK, DeepVariant, and pangenome workflows (docs.nvidia.com) (docs.nvidia.com).

The independent **2025** Google Cloud Platform (GCP) study compared **five exomes and five genomes**, using older DNaseq and Parabricks releases, without DRAGEN (ascpt.onlinelibrary.wiley.com). Its reported genome costs overlapped: **\$8.02 to \$10.67** for Sentieon and **\$8.13 to \$10.63** for Parabricks (ascpt.onlinelibrary.wiley.com), excluding Sentieon licensing (ascpt.onlinelibrary.wiley.com). These observations cannot rank current DNAscope, DRAGEN Software Mode, and modern Parabricks configurations. The evidence discussed below informs pilot design; it does not establish a current three-way accuracy or price winner.

The validation baseline also needs updating. The National Institute of Standards and Technology (NIST) now lists Genome in a Bottle (GIAB) **HG002 v5.0q** for small and structural variants (www.nist.gov), explicitly marking HG002 **v4.2.1** as deprecated (www.nist.gov). Historical truth sets remain useful for reproducing published comparisons, but their identity, benchmark regions, and intended scope must be recorded. The Global Alliance for Genomics and Health (GA4GH) recommends stratification by variant type and genomic context (www.ga4gh.org).

The recommended decision is conditional: shortlist workflows that support the required samples, outputs, references, and infrastructure, then run a matched raw-read-to-variant pilot with predefined acceptance thresholds. Separate whole-genome sequencing (WGS) from whole-exome sequencing (WES), and single-nucleotide variants (SNVs) from insertions and deletions (indels). Include queueing, retries, licensing, storage,

and export in cost. For molecular diagnostics, validate the complete intended test: the US Food and Drug Administration (FDA) guidance places third-party software in that end-to-end context (www.fda.gov). This report provides a buyer protocol, not diagnostic certification.

Introduction and Background

Accelerated secondary analysis converts sequencing reads into aligned evidence and variant calls. The purchasing question is therefore more specific than which platform is fastest: which **workflow configuration** produces an acceptable result, on the laboratory's samples, within its turnaround and operating constraints? DRAGEN integrates germline analysis from raw reads through variant calling (help.dragen.illumina.com), whereas Parabricks exposes multiple caller-specific workflows (docs.nvidia.com) (docs.nvidia.com). Treating either name as a single interchangeable algorithm obscures choices that the pilot must make explicit.

The comparison covers short-read germline WGS and WES for biotech genomics teams, clinical research groups, and molecular-diagnostics validation teams. Its publication baseline is October 13, 2026; sources were retrieved October 15. Where a source does not establish historical availability, the report identifies an observed documentation baseline rather than claiming a release existed on publication day. This distinction matters for Sentieon's currently labeled **202503.04** documentation, whose calendar release date was not established (support.sentieon.com).

Define the deliverable before procuring infrastructure. A Variant Call Format (VCF) file is a tab-delimited representation of variation (www.ebi.ac.uk); its existence does not establish that the desired variants were callable. Compressed Reference-oriented Alignment Map (CRAM) uses reference-based compression (www.ebi.ac.uk), so reference retention belongs in the handover plan. A genomic VCF (gVCF) intermediate supports workflows that retain per-sample information for subsequent joint genotyping (gatk.broadinstitute.org). Those are different acceptance boundaries.

Research use and diagnostic use also require separate decisions. FDA's germline next-generation sequencing (NGS) guidance concerns tests intended to aid diagnosis of suspected germline diseases (www.fda.gov). A research comparison can measure analytical performance without establishing clinical validity or suitability for a particular diagnostic service.

IntuitionLabs' relevant perspective is that of an adjacent implementation advisor: its published services include data engineering and business intelligence (intuitionlabs.ai). Accordingly, this report emphasizes reproducible data handling, evidence capture, and operating ownership. The products remain the three vendors' analysis offerings.

Illumina DRAGEN

Capabilities

The version boundary changes the deployment comparison. Illumina's downloads page lists **DRAGEN 4.6.2** server installers and distinguishes them from sequencing-platform-specific installations (support.illumina.com) (support.illumina.com). The new **central processing unit (CPU)** path runs on supported **x86-64** infrastructure

without requiring an FPGA (help.dragen.illumina.com). It would therefore be inaccurate to classify every DRAGEN option as an FPGA appliance.

The documented germline application includes SNVs, indels, copy-number variants (CNVs), structural variants (SVs), repeat expansions, and quality metrics (help.dragen.illumina.com). Buyers should nevertheless request an output inventory for their exact mode and enabled analyses. A broad application description does not mean that every feature runs in every deployment.

Illumina's earlier **4.5** announcement described expanded pangenome representation and personalization (www.illumina.com). Its reference builder produces a proprietary DRAGEN reference (help.dragen.illumina.com). A reproducible comparison must retain that resource alongside the original reference assembly, rather than recording only an assembly nickname.

Adoption

DRAGEN's integration with sequencing environments makes **installation ownership** a practical adoption question. The server reference resources are explicitly distinguished from sequencing-platform resources (support.illumina.com). A laboratory should establish who owns reference provisioning, installer approval, output transfer, and rollback when analysis moves between those environments.

Software Mode adds an operational dependency: the analysis node needs outbound Hypertext Transfer Protocol Secure (HTTPS) access for licensing (help.dragen.illumina.com). The procurement review should therefore include a real connectivity test from the intended compute network. Approval of a cloud architecture diagram alone does not demonstrate that a batch node can authenticate during a run.

Strengths and Limitations

Illumina describes Software Mode results as **bit-exact** against FPGA Mode (www.illumina.com). That is a vendor equivalence claim within its specified configuration, useful as a pilot hypothesis rather than a substitute for laboratory evidence.

- **Integrated scope:** Evaluate the combined small-variant, SV, CNV, and repeat outputs where the application supports them (help.dragen.illumina.com).
- **Mode selection:** Compare supported CPU deployment with the proposed FPGA deployment as separate operating configurations (help.dragen.illumina.com).
- **Reference portability:** Preserve the built reference, source assembly, and generation settings (help.dragen.illumina.com).
- **License accounting:** Record the analysis tier and applicable charging system; human-sample licensing is described on a per-sample basis (help.dragen.illumina.com).
- **Infrastructure cost:** Budget compute and storage separately because published DRAGEN analysis pricing excludes them (www.illumina.com).

Illumina's launch material carries a **Research Use Only** restriction (developer.illumina.com). A diagnostic team must obtain the exact intended-use statement for the proposed product and deployment and evaluate it within its own test-validation process. The general DRAGEN brand does not establish diagnostic suitability.

Sentieon DNaseq and DNAscope

Capabilities

DNaseq and DNAscope must occupy different rows in the laboratory's experiment plan. Sentieon describes DNaseq as matching GATK SNP and indel results, and DNAscope as additionally offering SV, CNV, and segmental-duplication analysis (www.sentieon.com). A single-nucleotide polymorphism (SNP) is a single-base variant considered in population context; pilot scorecards should state whether their SNP category includes all evaluated SNVs.

Linear DNAscope accepts aligned and unaligned input formats and supports whole-genome or targeted hybrid-capture preparations (support.sentieon.com). Its pangenome workflow creates a personalized reference and lifts realigned reads back to the standard reference (support.sentieon.com). That architecture differs from treating a graph aligner and a deep-learning caller as interchangeable steps.

The **model bundle** is part of the analytical configuration. Sentieon requires a pipeline-specific, sequencing-platform-specific pangenome bundle and a matching population VCF (support.sentieon.com). The reference, model, population resource, and chemistry should therefore be versioned together.

Adoption

Sentieon's support page describes deployment on x86 or ARM servers and cloud instances without requiring graphics processing units (GPUs) or FPGAs (www.sentieon.com). The pilot should determine workload-specific sizing and concurrency.

The dated Q2 update's linear benchmark explicitly used **202503.03** (www.sentieon.com). This report distinguishes the observed documentation version from that dated benchmark configuration.

Commercial licensing is described as an **annual flat fee** based on estimated usage (www.sentieon.com). The standard cluster arrangement involves license-server connectivity, while compute clients need not themselves access the internet (support.sentieon.com). These details can affect an isolated research environment's deployment design.

Strengths and Limitations

Sentieon's documentation enables a buyer to frame distinct equivalence, model-based, and pangenome experiments rather than one undifferentiated Sentieon test.

- **Existing CPU capacity:** Include available CPU nodes in the pilot, with measured concurrency and memory headroom (www.sentieon.com).
- **Chemistry matching:** Require the applicable model bundle; the vendor documents an Ultima model retrained for **Solaris 2.0** chemistry (www.sentieon.com).
- **WES boundaries:** Freeze target intervals; the pangenome tutorial recommends a Browser Extensible Data (BED) target file for exomes (support.sentieon.com).
- **Feature status:** Confirm whether the requested pangenome SV/CNV features remain beta in the selected release (support.sentieon.com).

- **Input encoding:** Verify the required Sanger Phred+33 quality-score encoding for DNaseq FASTQ inputs (support.sentieon.com).

No diagnostic intended-use authorization for the proposed Sentieon configuration was established in this research. The buyer should request the contractual and labeling evidence that applies to its own intended workflow.

NVIDIA Parabricks

Capabilities

The verification fetch identifies **Parabricks 4.8.0-1** as the latest catalog tag, updated October 13, 2026 (catalog.ngc.nvidia.com). The functional discussion uses retrieved **4.7.1** documentation (docs.nvidia.com); a 4.8 deployment requires its own release and configuration review. Artifact availability and reviewed documentation are different baselines. The catalog also provides signed images and architecture-specific digests (catalog.ngc.nvidia.com). Procurement records should retain the immutable image identity, beyond the human-readable tag.

Parabricks' linear germline workflow takes paired FASTQ reads, a Burrows-Wheeler Aligner (BWA)-indexed reference, and known-sites resources (docs.nvidia.com). Its DeepVariant tool identifies a specific deep-learning caller, with separate WGS and WES model options (docs.nvidia.com). These are distinct accuracy experiments even when executed through the same GPU software suite.

For pangenome analysis, **pangenome_germline** uses Giraffe alignment and Pangenome-aware DeepVariant (docs.nvidia.com). The reference FASTA must derive from the same graph (docs.nvidia.com). Reference-path compatibility is therefore a precondition for interpreting the resulting coordinates, not merely a packaging detail.

Adoption

GPU availability is only part of deployment readiness. NVIDIA specifies at least **16 GB of GPU memory per GPU** and, for a two-GPU host, at least **100 GB host memory and 24 CPU threads** (docs.nvidia.com) (docs.nvidia.com). Driver compatibility is tied to **CUDA 12.9.1** in the retrieved requirements (docs.nvidia.com). These are documentation requirements, not measured resource consumption for every germline job.

Amazon Web Services (AWS) HealthOmics also lists managed Parabricks WGS workflows (docs.aws.amazon.com). Its Ready2Run definition is preconfigured and cannot be edited (docs.aws.amazon.com). A managed option can simplify operation, but its configuration boundary should be evaluated separately from a laboratory-controlled container.

Strengths and Limitations

NVIDIA documents functional equivalence to CPU-native GATK for the relevant GATK workflows (docs.nvidia.com). That statement should not be generalized to every DeepVariant or pangenome output.

- **Caller identity:** Record the caller, model, and complete execution command explicitly.

- **Storage placement:** Test fast local solid-state drive (SSD) storage for inputs, outputs, and temporary files (docs.nvidia.com).
- **Reference preflight:** Enable and record graph/FASTA verification for the pangenome workflow where appropriate (docs.nvidia.com).
- **WES settings:** Follow the selected release's model flags; the retrieved release notes specify an additional small-model setting for WES consistency (docs.nvidia.com).
- **License boundary:** NVIDIA states that no Parabricks license is required to run the software; optional enterprise support is separate (docs.nvidia.com).

A zero required runtime-license charge does not make an analysis free. GPUs, host resources, storage, support, and operational work still belong in the cost model. This research did not establish diagnostic authorization for the ordinary container configuration; diagnostic suitability requires evidence for the complete intended test.

Feature Comparison

Table 1 compares **documented configurations**, not interchangeable product badges. It separates dated release evidence from undated current documentation and identifies where a laboratory must narrow the workflow before measurement.

Decision axis	Illumina DRAGEN	Sentieon DNaseq / DNAscope	NVIDIA Parabricks
Version evidence	Server 4.6.2 listed September 30, 2026 (support.illumina.com).	Dated vendor benchmark uses 202503.03 ; observed installation docs identify 202503.04 , without a verified release day (www.sentieon.com) (support.sentieon.com).	Latest fetched artifact 4.8.0-1 , updated October 13, 2026 (catalog.ngc.nvidia.com); capability discussion uses the reviewed documentation baseline.
Compute boundary	FPGA deployment plus supported CPU Software Mode (help.dragen.illumina.com).	CPU-based deployment without required GPUs or FPGAs (www.sentieon.com).	GPU acceleration with explicit host-memory and driver requirements (docs.nvidia.com).
Small-variant caller	Integrated germline analysis (help.dragen.illumina.com).	DNaseq versus DNAscope, with different calling approaches (www.sentieon.com).	Caller-specific workflows; test each enabled pipeline (docs.nvidia.com).
Pangenome control	DRAGEN-built reference resources (help.dragen.illumina.com).	Personalized-reference workflow with matched population VCF and model bundle (support.sentieon.com).	Giraffe graph with matching reference FASTA and Pangenome-aware DeepVariant (docs.nvidia.com).
SV/CNV boundary	Documented within germline application; verify chosen mode (help.dragen.illumina.com).	Pangenome SV/CNV feature status is release-specific (support.sentieon.com).	Require workflow-specific SV/CNV evidence before including these outputs.

Decision axis	Illumina DRAGEN	Sentieon DNaseSeq / DNAscope	NVIDIA Parabricks
Charging boundary	Applicable v4.6+ BioInsight-connected human analyses: per-sample pricing; installed DRAGEN Server licenses and legacy Cloud FPGA BYOL credentials: separate prepaid gigabase quotas (help.dragen.illumina.com). Infrastructure excluded (www.illumina.com).	Annual flat-fee commercial license; obtain a usage-matched quote (www.sentieon.com).	No required runtime license; optional support and infrastructure remain (docs.nvidia.com).

The practical distinction is **configuration completeness**. A shortlist is not ready for a benchmark until the laboratory can name the exact caller, model, reference, variant outputs, and deployment mode. The table deliberately avoids a single accuracy score: its rows describe different experiments, not results from one common test.

WGS and WES should also have separate acceptance envelopes. Broad's interval guidance ties exome intervals to the capture targets (gatk.broadinstitute.org), while Sentieon's tutorial recommends explicit WES target restriction (support.sentieon.com). The protocol should freeze capture-kit version, interval padding, coverage requirements, and the denominator used for scoring. A workflow can perform well inside well-covered targets while leaving a different fraction of the intended assay unassessed.

Outputs need a **downstream contract**. Broad distinguishes per-sample gVCF creation from cohort joint genotyping (gatk.broadinstitute.org); simply merging gVCFs is not equivalent to jointly calling the cohort (gatk.broadinstitute.org). Specify whether the pilot ends at individual VCF, gVCF, joint-genotyped cohort, or downstream annotation. Include sample identifiers, contig naming, reference identity, filter semantics, and audit metadata in acceptance checks.

Chemistry support must be demonstrated at the workflow and model level. Examples include DRAGEN's documented TruPath analytical support (www.illumina.com), Sentieon's chemistry-specific models (www.sentieon.com), and Parabricks' release-specific Roche SBX additions (docs.nvidia.com). None of those examples establishes blanket support across every short-read instrument or library preparation.

Performance and Benchmarks

What published comparisons establish

The **2025 GCP benchmark** used DNaseSeq **v202308** and Parabricks Germline **v4.0.1-1**, launched with default execution steps (ascpt.onlinelibrary.wiley.com). WES took approximately **10 to 14 minutes** on Parabricks and **14 to 16 minutes** on Sentieon (ascpt.onlinelibrary.wiley.com); WGS took **4.1 to 4.7 hours** and **3 to 3.8 hours**, respectively (ascpt.onlinelibrary.wiley.com). It did not include DRAGEN or current DNAscope.

The separate accelerated-pipeline study analyzed **10 WGS samples** (pmc.ncbi.nlm.nih.gov). It used DRAGEN **4.2** and Parabricks **4.3.0-1** (pmc.ncbi.nlm.nih.gov) (pmc.ncbi.nlm.nih.gov), with accuracy assessed inside specified high-confidence intervals (pmc.ncbi.nlm.nih.gov). Its total-runtime comparison excluded Parabricks DeepVariant (pmc.ncbi.nlm.nih.gov), and filtered callsets were not validated (pmc.ncbi.nlm.nih.gov). Its conclusions therefore need those boundaries when cited.

These studies answer different experimental questions. Their runtimes cannot be joined into a three-way league table. Nor does GATK equivalence establish superiority over a different caller. NVIDIA itself documents reasons why Pangenome-aware DeepVariant output can differ from Google's implementation (docs.nvidia.com). The relevant buyer question is whether the selected workflow meets the assay's predefined analytical requirements.

Truth sets, references, and difficult regions

Use **GIAB** as a versioned benchmark resource, not an unqualified synonym for truth. NIST supplies small-variant VCFs and associated benchmark-region BEDs for different reference builds (www.nist.gov). The benchmark BED determines which evaluated positions contribute to the primary metrics.

For historical replication, **v4.2.1** remains available for the GIAB samples (www.nist.gov). For a fresh HG002 assessment, NIST lists **v5.0q** and marks the older HG002 benchmark deprecated (www.nist.gov). Its challenging medically relevant gene benchmarks are also labeled deprecated (www.nist.gov). Record which benchmark supports each result; do not silently change the truth set halfway through vendor testing.

Pangenomes require another layer of control. The initial Human Pangenome Reference Consortium release represented **94 distinct genome sequences** (www.genome.gov). That historical resource count is context, not the composition of every vendor reference. Sentieon's population VCF must match its model bundle (support.sentieon.com), while NVIDIA requires the graph-derived FASTA to match the alignment graph (docs.nvidia.com). Keep the coordinate reference separate from the larger representation used during alignment.

Matched FASTQ-to-VCF pilot

The following is a proposed procurement protocol. It intentionally leaves sample count and acceptance limits to the assay's scope and statistical plan.

- **Freeze inputs:** Use identical FASTQ files, checksums, read groups, sample identities, and preprocessing boundaries.
- **Separate experiments:** Test linear-reference workflows together, then run a separately labeled pangenome comparison.
- **Freeze resources:** Retain assembly files, decoys, alternate contigs, graph resources, known sites, interval files, and model checksums.
- **Check training/evaluation independence:** Sentieon reports training its new model using GIAB v4.2.1 and v5.0 (Q100-T2T) benchmarks ([Sentieon Q2 update](#)). As a proposed pilot requirement, request training-sample and training-region disclosures for each model, compare them with the evaluation genomes and regions, and evaluate held-out genomes or regions wherever possible. Label any training overlap or unknown independence in the reported results. Do not label a newer truth-set version as independent validation unless training/evaluation independence has been established.
- **Declare outputs:** State which SNVs, indels, SVs, CNVs, repeat calls, gVCFs, and quality metrics are required.

- **Stratify results:** Evaluate variant class and genomic context, following GA4GH's benchmarking framework (www.ga4gh.org).
- **Exercise failures:** Test interrupted jobs, full temporary storage, invalid reference inputs, and license-service unavailability.
- **Check reproducibility:** Repeat representative inputs and compare biological calls, filters, and provenance, using appropriate output-specific comparison procedures (docs.nvidia.com).
- **Measure operations:** Capture queueing, staging, computation, export, retries, and operator intervention as separate events.

A common coordinate system does not guarantee comparable calls. GA4GH identifies **different variant representations** as a benchmarking problem (www.ga4gh.org). Use a haplotype-aware comparison process and record its settings. Retain PASS-only results alongside the broader unfiltered analysis where appropriate; the published benchmarking framework distinguishes those precision-recall views (www.nature.com).

Data Analysis and Evidence

Define the accuracy denominator

Precision and recall should be calculated independently for SNPs and indels, rather than compressed into a single product score. The peer-reviewed accelerated-pipeline study uses the standard precision, recall, and F1 definitions (pmc.ncbi.nlm.nih.gov). GA4GH also emphasizes the limits of high-confidence calls and regions (www.ga4gh.org).

Table 2 states the proposed scorecard. **TP**, **FP**, and **FN** mean true positives, false positives, and false negatives. The equations are the simplified definitions; a representation-aware tool can maintain distinct query-side and truth-side TP counts.

Measure	Definition or calculation	Required reporting split
Precision	$TP / (TP + FP)$ (pmc.ncbi.nlm.nih.gov).	SNPs and indels separately; PASS and broader callsets distinguished.
Recall / sensitivity	$TP / (TP + FN)$ (pmc.ncbi.nlm.nih.gov).	Same truth set, reference build, and benchmark BED for every workflow.
F1 score	$2TP / (2TP + FP + FN)$ (pmc.ncbi.nlm.nih.gov).	Publish alongside precision and recall, preserving each error direction.
Context-specific performance	Recompute metrics within predefined regional strata (www.nature.com).	Repeats, homopolymers, segmental duplications, low-complexity and medically relevant regions, where supported.
Assay callability	Proposed operational metric: assessed target bases divided by intended target bases.	WES target and padding policy; WGS assay scope; excluded regions listed.
Operational yield	Proposed service metric: accepted outputs divided by attempted samples.	First attempt and eventual completion, with retry causes retained.

The interpretation depends on **scope**. High recall inside a benchmark BED does not measure every position in the genome. The scorecard should therefore include callable territory and out-of-benchmark findings as separate evidence streams. A small difference in aggregate F1 may matter less than a reproducible difference in a required difficult-region stratum.

Report costs without turning estimates into prices

The GCP paper reported WES costs of **\$0.71 to \$0.93** for Parabricks and **\$0.82 to \$1.03** for Sentieon (ascpt.onlinelibrary.wiley.com). Its WGS ranges were **\$8.13 to \$10.63** and **\$8.02 to \$10.67** (ascpt.onlinelibrary.wiley.com). Licensing was excluded (ascpt.onlinelibrary.wiley.com). These are historical experiment costs, not current all-inclusive quotations.

A separate Sentieon vendor example reports approximately **\$4.10** on-demand compute cost for its specified WGS configuration (www.sentieon.com). Intel's historical material attributes measurements to Sentieon and imports Parabricks timings from earlier published results (cdrdv2-public.intel.com) (cdrdv2-public.intel.com). AMD's corresponding material identifies limits on independent verification (docs.amd.com). Keep such vendor-aligned evidence separate from the laboratory's matched pilot.

For procurement, calculate:

Cost per accepted sample = (compute + analysis licenses + storage + transfer + orchestration + support allocation + operating labor) / accepted samples.

This is a proposed accounting formula. Charge failed attempts and retries to the numerator, and use accepted deliverables in the denominator. For on-premises deployment, add an allocated share of hardware, maintenance, power, and capacity reservation. For cloud compute, use billed usage from the measured run and the reader's actual region, instance, and contracted rate.

Google Cloud Storage separately prices storage, processing, and network usage (cloud.google.com), with rates varying by storage class and location (cloud.google.com). Internet export can attract network charges (cloud.google.com). DRAGEN likewise excludes infrastructure from its analysis pricing (www.illumina.com). A runtime-only comparison omits real cost categories.

For each metered resource, compute cost equals its measured billed hours multiplied by the applicable hourly rate, summed across resources. Proposed end-to-end turnaround equals queue time plus input staging, processing, and output delivery. Record both turnaround and active processing time. Contract-specific export and retention assumptions should accompany the result; published cloud network charges depend on the data movement involved (cloud.google.com).

Implications and Future Directions

Change control belongs in the buying decision

FDA's germline NGS guidance recommends documenting software and its source (www.fda.gov) and preparing a procedure for revalidation after anticipated modifications (www.fda.gov). These are attributed analytical recommendations from **2018**, not a statement that any compared product has regulatory

authorization (www.fda.gov). A laboratory's quality team should determine the applicable requirements for its jurisdiction and intended test.

Table 3 converts that principle into a proposed change-control checklist. Approve acceptance criteria before introducing changes.

Change trigger	Evidence to preserve	Proposed verification
Caller or container release	Installer, digest, release notes, command line and prior baseline.	Re-run representative samples; inspect discordant calls and filter changes.
Reference or graph update	Source assembly, generated indices, population resources and checksums.	Check contig compatibility, liftover behavior and difficult-region metrics.
Sequencing chemistry or model	Instrument configuration, library preparation and exact model bundle.	Repeat chemistry-matched controls and inspect coverage-related changes.
Hardware, driver or mode	CPU/GPU identifiers, driver stack, host memory and storage layout.	Measure reproducibility, resource use, completion and turnaround.
Interval or filter change	Capture targets, padding, filters and previous scoring denominator.	Recalculate callability and class-specific precision/recall.
License or orchestration change	Entitlement configuration, scheduler, retry policy and audit records.	Test startup, interruption, resumption and prevention of partial-result release.

FDA recommends sufficient well-characterized samples with justification of their number and type (www.fda.gov), and assessment of modifications both individually and together (www.fda.gov). Check outputs and provenance even when calls are unchanged.

Assign operating owners:

- **Resource owner:** Approves analytical bundles.
- **Workflow owner:** Maintains configuration and rollback.
- **Infrastructure owner:** Maintains compute and monitoring.
- **Validation owner:** Defines acceptance and discrepancy review.
- **Cost owner:** Reconciles total service cost.
- **Release owner:** Authorizes controlled promotion.

IntuitionLabs describes advisory services in technology roadmapping and artificial intelligence (AI) adoption (intuitionlabs.ai).

A decision tree for the shortlist

Shortlist by requirements, then select using pilot results.

- **If integrated variant classes are essential:** Shortlist configurations whose documented output inventory covers the assay; validate each required class separately.
- **If existing CPU capacity is central:** Include newly available CPU deployment options such as DRAGEN Software Mode (help.dragen.illumina.com).

- **If GPU capacity is available:** Evaluate the caller-specific workflow together with its intended storage configuration.
- **If GATK continuity is a priority:** Test the selected equivalence-oriented workflows against the laboratory's baseline, accounting for variant representation (www.ga4gh.org).
- **If pangenome performance is the differentiator:** Compare complete reference/model bundles and difficult-region outcomes, with the same scoring scope.
- **If diagnostic reporting is intended:** Require end-to-end test evidence and intended-use documentation before operational release (www.fda.gov).

Apply the same framework to upgrades. The direction of reference development is broader representation, as described by the National Human Genome Research Institute (www.genome.gov). Measure each upgrade's effect on the assay. Retain inputs, manifests, truth resources, and reports for revalidation.

Conclusion

The defensible answer to **DRAGEN vs Sentieon vs Parabricks** is a conditional selection based on the required assay and operating environment. Choose a complete workflow configuration, then require evidence that it meets predefined analytical and service thresholds. A product-level ranking hides differences in callers, references, models, enabled outputs, and deployment modes.

For **DRAGEN vs Sentieon germline variant calling**, compare the specific DRAGEN application with DNaseq or DNAscope separately. For **DRAGEN vs Parabricks**, distinguish the selected Parabricks caller from the acceleration platform. For **Sentieon vs Parabricks accuracy**, test equivalence-oriented and model-based workflows as separate hypotheses. Those boundaries are prerequisites for interpreting the score, not secondary procurement details.

The evidence package should answer both laboratory and infrastructure questions: which variants were assessed, where precision and recall were measured, how much target territory was callable, how long accepted results took, and what the service actually cost after retries and support. Preserve per-class and regional results alongside aggregate metrics, following the established benchmarking approach (www.nature.com).

A successful pilot leaves a reusable record: immutable inputs, versioned resources, approved acceptance limits, measured outputs, documented discrepancies, and a change-control plan. That record supports research reproducibility and gives a diagnostic team material for its own end-to-end assessment (www.fda.gov). The preferred platform is the one that satisfies those requirements with an operating model the organization can sustain.

Source links

Links cited in this article, in order of first appearance. Full addresses are provided for readers using extracted text.

1. https://support.illumina.com/sequencing/sequencing_software/dragen-bio-it-platform/downloads.html
2. <https://developer.illumina.com/news-updates/dragen-v4-6-a-decade-of-genomic-software-innovation-now-available-where-your-data-lives>

3. <https://www.sentieon.com/products/>
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AI consulting and adoption

Our AI enablement services cover readiness assessments, use-case selection, governance and policies, team workshops, adoption measurement and ongoing advisory support. We help organizations structure the information layer behind AI: source material, context, permissions and maintained knowledge that make generated answers useful and reviewable. Private LLM inference and hosted AI options support teams evaluating how to operate AI with appropriate control over their data and infrastructure.

Software, data and life-science workflows

IntuitionLabs develops custom software for pharma and biotech, integrates enterprise systems, and builds data engineering and business intelligence solutions. Areas of focus include AI agents, regulatory research, medical writing, medical affairs, CMC information, competitive intelligence and clinical-document workflows. Our eTMF intelligence work includes cross-system reconciliation and inspection-readiness support.

Enterprise platforms and regulated delivery

We provide Veeva services, application support, managed services, integrations and custom applications, alongside enterprise content work involving platforms such as Egnyte. For regulated workflows, our services include GxP enablement, computer-system validation and software development addressing 21 CFR Part 11 requirements. The applicable controls, validation responsibilities and acceptance criteria are defined for each engagement.

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