

# Swiss Genomics Association consensus guideline for evidence-based genomic variant interpretation in Mendelian disease

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## Abstract

**Background:**

**Methods:**

**Results:**

**Conclusions:** <sup>1</sup>

## LIVE PUBLIC WORKING DRAFT – NOT FINAL

This document is a **live public working draft** and does not represent a completed or officially endorsed release. All statements, analyses, and opinions are those of the authors and have not yet undergone joint committee review or external peer review. Content is provided for transparency and collaborative development and may be revised substantially prior to publication.

## 1 QV set preparation

Qualifying Variant (QV) sets define structured, reproducible variant interpretation rules using a transparent, machine-readable YAML format. Each QV file specifies metadata, filters, and evidence-based criteria in a simple key–value syntax, enabling precise replication of variant selection and interpretation logic across studies. QV sets can be composed interactively using the online [https://switzerlandomics.ch/pages/qv\\_builder/](https://switzerlandomics.ch/pages/qv_builder/), which provides an intuitive interface for defining rules, previewing YAML output, and ensuring consistency with established standards. This framework promotes FAIR data principles and harmonised variant interpretation for both research and clinical applications.

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**Availability:** This data is integrated in <https://iei-genetics.github.io>.

## 2 QV set for reporting

The `gnomad_flags` rule ensures that all variants are retained for review rather than automatically excluded. For each variant in the patient-level dataset, the rule checks whether a gnomAD flag is present. Variants with no flag (`NA`) pass directly, while those carrying any recognised gnomAD flag (for example, `AS-VQSR`, `RF`, `LC pLoF`, or `SEGDUP`) also pass but are explicitly marked for downstream review. These flagged variants are not filtered out but instead require justification or comment in the final Mendelian report, ensuring transparency and traceability of interpretation decisions. Variants carrying unexpected or unlisted flags are held for manual inspection. This approach prevents premature exclusion of potentially causal variants while maintaining auditability of quality annotations.

<code>variant_id</code>	<code>gnomad_flag</code>	<code>outcome</code>	<code>report_action</code>
1	<code>NA</code>	pass	include normally
2	<code>LC pLoF</code>	pass (flagged)	include with note: “gnomAD LC pLoF – review interpretation.”
3	<code>UnknownFlag</code>	fail	hold for manual review

Table 2: Example application of the `gnomad_flags` rule to patient variants. Long entries automatically wrap within the column width for compact layout.

The `acmg_criteria` rule interprets the condensed ACMG criteria column for each variant and flags variants that carry benign evidence. When a variant has passed upstream prioritisation tools such as Exomiser, the ACMG criteria are typically recorded in a single column as a list of applied evidence codes (for example, `PVS1`, `PM2`, `PP3`, or `BA1`). The downstream rule inspects this condensed string to determine whether it contains any benign evidence codes, recognised by the presence of the letter “B” (for example, `BA1`, `BS1--BS4`, or `BP1--BP8`). Variants with such codes are retained but marked for review, similar to those carrying gnomAD quality flags. This ensures that variants with benign evidence are not automatically excluded but instead require explicit assessment or justification in the final clinical interpretation.

## 3 Pedigree and inheritance information

When pedigree data are available, Whole Genome Sequencing (WGS) enables direct evaluation of inheritance models for each variant. Genotypes are interpreted across

<b>variant_id</b>	<b>ACMG_criteria</b>	<b>outcome</b>	<b>report_action</b>
1	PVS1, PM2, PP3	pass	include normally
2	PVS1, PM2, BA1	pass (flagged)	include with note: “contains benign ACMG evidence (BA1) – review interpretation.”
3	BP4	pass (flagged)	include with note: “benign supporting evidence – verify consistency with phenotype.”
4	PS2, PM5	pass	include normally

Table 4: Example application of the `acmg_criteria` rule to patient variants. Variants containing benign ACMG evidence codes are retained but flagged for explicit review in the final report. Long entries automatically wrap within the column width for compact layout.

proband and parents using standard representations such as `REF`, `HET`, and `HOM`, or equivalent encodings used in variant data formats (`0,1,2` in PLINK, `0/0, 0/1, 1/1`, or phased forms such as `0|1` in VCF). From these data, the inheritance pattern for each variant is determined, such as de novo, homozygous, heterozygous, or compound heterozygous, and this information is then evaluated in relation to the known gene–disease relationship. For example, the observed segregation pattern may provide supporting or contradictory evidence for an Autosomal Dominant (AD), Autosomal Recessive (AR), or X-Linked (XL) disease mechanism.

Where genotype data are incomplete, inheritance may be inferred from clinical features, family history, or segregation information, but such cases are explicitly flagged as uncertain. Scenarios of incomplete penetrance, such as a heterozygous variant inherited from an unaffected parent, are also recorded because they influence the strength of causal interpretation. Each inheritance assessment includes both the inferred pattern and the type of supporting evidence, ensuring that interpretative conclusions in the genetic report transparently reflect the available data and its confidence level.

## 4 Functional evidence databases

Functional evidence from UniProt is integrated by detecting positional overlap between variant amino acid coordinates and annotated protein features recorded in UniProt GFF files. Each UniProt entry provides structured annotations describing biochemical,

structural, and functional properties of the protein. For each variant, the affected residue position is compared against these annotated intervals, and any intersection is recorded as supporting evidence in the QV interpretation framework. This approach ensures that experimental and curated protein-level information contributes directly to variant interpretation and reporting (Fig. 1).

The annotated features used as evidence sources include catalytic and binding sites, metal and nucleotide binding regions, and other experimentally defined functional motifs. Structural features such as helices, beta strands, and coiled coils provide spatial context for potential conformational disruption. Domain- and family-level annotations, including domains, motifs, and topological regions, capture conserved structural organisation and functional domains. Additional layers include post-translational modification sites, mutagenesis data, and known sequence variants curated in UniProt. Processing and localisation signals (such as signal peptides, transit peptides, and cleavage products) and cautionary sequence annotations (for example, frameshifts or sequence uncertainty) are also recorded.

By systematically linking these feature classes to variant coordinates, the framework records not only where functional or structural evidence exists, but also the type of information present—whether experimental, inferred, or computational. This enables each variant interpretation to transparently reflect the available molecular evidence supporting its classification.

## 5 Preference for established standards

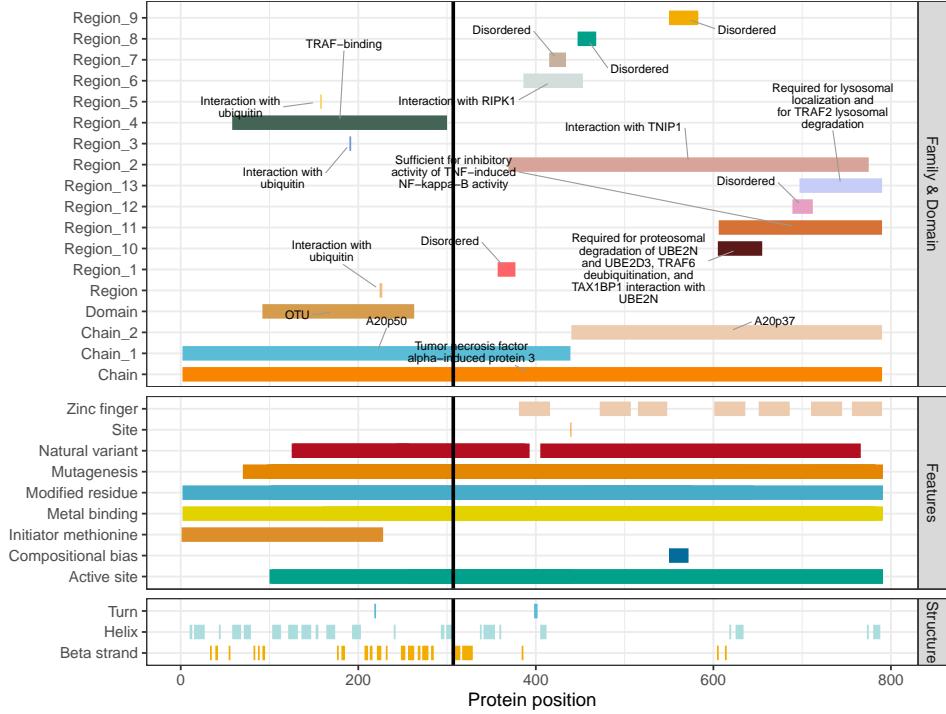
Automation, interoperability, and reproducibility in genomics rely on the use of internationally recognised standards rather than isolated or proprietary tools. Validated frameworks enable traceable, comparable, and scalable handling of genomic and phenotypic data across research and clinical contexts (? ).

Core standards include the **Variant Call Format (VCF)**, **Binary Alignment Map (BAM/CRAM)**, and the **Phenopacket Schema** from the **Global Alliance for Genomics and Health (GA4GH)**. The **Human Phenotype Ontology (HPO)** and **Orphanet Rare Disease Ontology (ORDO)** support structured phenotyping and disease mapping, while the **Beacon protocol** enables federated search across distributed datasets without sharing raw data.

Using such standards ensures long-term compatibility, supports automation, and

### TNFAIP3 evidence tracks

6–137877190 T>A (GRCh38); SNV. Gene: TNFAIP3; Transcripts affected: ENST00000612899.5 (MANE Select), ENST00000237289.8, ENST00000485192.1. Consequence: stop\_gained (p.Leu307Ter, c.920T>A); pLoF High-confidence. Reference population gnomAD v4.1.0: AC=1, AN=1613922, AF=6.2e-07; Homozygotes=0; Filter=PASS.



**Figure 1: Functional evidence tracks from UniProt annotations.** The example illustrates how protein-level features such as domains, motifs, and catalytic sites provide structured evidence supporting interpretation of coding variants. Overlaps between variant positions and curated functional regions indicate potential mechanistic relevance, while the absence of overlap suggests limited or indirect evidence. This evidence framework guides the strength of interpretation in clinical reporting, ensuring that well-supported variants are highlighted and uncertain findings are transparently qualified.

improves accuracy through consistent validation and version control. Tools such as *Exomiser*, *LIRICAL*, and *PhenIX* show how ontology-based approaches enable automated, phenotype-driven variant prioritisation. For cloud analysis, platforms like **Terra** and pipelines such as **GATK** provide transparent, reproducible environments aligned with GA4GH and international data-sharing frameworks.

## 6 Structured variant annotation and automation of interpretation

Variant interpretation has traditionally relied on expert review and rule-based systems such as the ACMG/AMP criteria, where evidence is manually classified into discrete levels (e.g. “strong”, “moderate”, “supporting”). While this provides clinical transparency, it limits scalability and does not easily incorporate quantitative or experimental data generated outside the sequencing pipeline.

Structured annotation frameworks, such as the **GA4GH Variant Annotation (VA) specification**, provide a way to formalise how evidence supports or refutes pathogenicity, linking statements to their provenance and strength. Rather than a human-readable label alone, each assertion is represented as a computable object that connects a variant, a condition, and all supporting evidence lines. These may include cohort allele frequencies, functional assays, or other study results, each qualified by method, direction, and strength of support. This structure allows integration of diverse evidence types while retaining traceability to original data sources.

Such a model enables a shift from categorical to quantitative reasoning. A variant’s pathogenicity statement can accumulate weighted evidence from multiple domains: ACMG-derived criteria, *in vitro* functional data (e.g. MAVE), RNA and protein evidence, population studies, or model organism data. Each evidence line can be standardised using controlled vocabularies and shared identifiers, allowing aggregation across studies and automated computation of posterior probabilities.

Tools such as *Exomiser* and *LIRICAL* illustrate early automation based on ACMG-compatible logic and phenotype-driven scoring. Extending these with the GA4GH VA model allows incorporation of continuous, probabilistic evidence rather than threshold-based categories. This approach transforms variant classification from interpretive judgment into quantifiable inference, reducing subjective variability and supporting automated re-evaluation as new evidence emerges.

By representing all evidence as structured, machine-interpretable data with defined provenance, the GA4GH framework provides a foundation for fully automatable, transparent, and continuously updatable variant interpretation.

## 7 Qualifying variant protocol design and standardised approaches

Variant interpretation depends on how whole genome data are prepared and analysed. Each step, from sequencing and variant calling to annotation and filtering, defines what can be detected or missed. A qualifying variant (QV) protocol makes these steps explicit by describing the rules that determine variant inclusion and interpretation (?).

A standard QV protocol should specify the sequencing method, genome build, and tools used; the quality thresholds for coverage and genotype confidence; the genomic regions or panels considered; and the annotation or classification systems applied. Defining these parameters in a structured QV file separates logic from execution, allowing reproducible, auditable workflows. Each file has a version and checksum, linking it directly to analysis outputs.

This standardisation ensures that variant findings are traceable and comparable across studies. It also supports automated pipelines that integrate multiple evidence sources, such as population, functional, and multiomic data, in line with frameworks like the GA4GH Variant Annotation model. The result is consistent, transparent, and quantifiable variant interpretation.

## 8 Compliance and accreditation framework

Genomic data processing and analysis in Switzerland are governed by national and international legal standards designed to ensure data protection, traceability, and clinical reliability. The primary legal framework is the **Federal Act on Data Protection (FADP, SR 235.1)**, which regulates the processing of personal and sensitive data, including genetic information. Key obligations under the FADP include lawful processing (Arts. 6, 31), the establishment of Data Processing Agreements between controllers and processors (Art. 9), the implementation of technical and organisational safeguards such as encryption and access logging (Art. 8), maintenance of records of processing activities (Art. 12), breach notification procedures (Art. 24), and regulated cross-border data transfers requiring adequacy decisions or safeguards (Arts. 16–18).

Under Swiss law, platforms that store or share genomic data are typically considered

*data processors*, not *medical devices*, unless marketed for diagnostic, therapeutic, or monitoring purposes. In such cases, the regulatory scope shifts from the FADP to the **Medical Devices Ordinance (MedDO, SR 812.213)** or the **In Vitro Diagnostic Medical Devices Ordinance (IvDO, SR 812.219)**, corresponding to the EU's **MDR 2017/745** and **IVDR 2017/746**. Medical device classification is determined by intended use and requires conformity assessment, a Technical File, risk management under **ISO 14971**, and registration in **swissdamed**.

For non-medical genomic infrastructure, compliance with FADP and, where applicable, the **General Data Protection Regulation (GDPR)** is sufficient. GDPR may apply when data from EU subjects are processed (Art. 3). Voluntary alignment with international standards such as **ISO 27001** for information security and **ISO 15189** for quality management in medical laboratories is recommended to enhance transparency and interoperability across research, clinical, and industrial settings.

## 8.1 Accreditation standards

Accreditation provides verifiable assurance that laboratory and computational processes meet international quality benchmarks. The **ISO 15189** standard defines competence and quality management requirements for medical laboratories, encompassing both wet-lab and analytical bioinformatics activities. Laboratories accredited under ISO 15189 operate with validated procedures, documented workflows, and reproducible performance metrics suitable for clinical-grade diagnostics.

Within Switzerland, the *Health 2030 Genome Center* represents a reference implementation. Its ISO 15189-accredited Diagnostic Sequencing Platform (DSP) delivers whole-genome, whole-exome, and RNA-seq services under a certified quality system, including validated fast-turnaround workflows capable of data delivery within seven days of sample receipt. This demonstrates that high-quality accreditation and rapid clinical response can be achieved concurrently.

Accreditation should extend beyond laboratory sequencing to cover computational analysis, data management, and quality assurance frameworks. Validation, reproducibility testing, version control, and full documentation of pipelines must form part of the accredited quality management system. Laboratories and institutions that align with ISO 15189 or equivalent frameworks ensure that genomic data in Switzerland remain verifiable, comparable, and suitable for both clinical and research integration at national and international levels.

## 9 Recommendations for bioinformatics in clinical practice

Clinical bioinformatics forms the analytical backbone of genomic medicine. It bridges raw sequencing data and clinical interpretation, and its reliability determines the accuracy of every downstream result. To maintain national consistency and international credibility, Switzerland should adopt a harmonised framework for sequencing-based clinical bioinformatics aligned with the recommendations of the Nordic Alliance for Clinical Genomics (NACG) (? ). While the NACG framework was developed for the Nordic region, its principles provide an appropriate foundation for Swiss implementation. The key recommendations, summarised in their Table 1, outline the operational, technical, and quality criteria expected of any accredited clinical bioinformatics unit.

The Swiss Genomics Association endorses the core sentiment of these recommendations: that clinical bioinformatics must operate at the same professional and regulatory standards as accredited medical laboratories. Bioinformatics pipelines should be validated, reproducible, and transparent, with defined responsibilities for quality management, data integrity, and patient safety. Use of the GRCh38/hg38 reference genome, strict version control, and structured documentation of analytical steps are expected across all clinical operations. Pipelines must be tested systematically, covering unit, integration, and end-to-end validation, and benchmarked against established reference datasets such as Genome in a Bottle (GIAB) and SEQC2, supplemented by local recall testing of verified clinical samples.

From an infrastructure perspective, secure, isolated computing environments are essential, with preference for air-gapped, clinical-grade high-performance systems. Software should be encapsulated in containerised or environment-controlled frameworks to ensure reproducibility and auditable traceability. Version-controlled source code, accompanied by peer-reviewed updates and complete change logs, is mandatory for clinical deployment.

Data integrity and identity verification are further non-negotiable components. File hashing, sample fingerprinting, and checks for sex, ancestry, and relatedness provide safeguards against sample mix-ups or data corruption. In-house databases of recurrent or artefactual variant calls should be maintained to filter false positives, particularly for structural variants.

Finally, the Association emphasises that clinical bioinformatics is not solely a

computational discipline but a multidisciplinary field requiring expertise in software engineering, data management, human genetics, and quality assurance. Sustainable national implementation depends on cross-site collaboration, shared reference datasets, and continual alignment with evolving ISO and GA4GH standards.

Together, these principles define the expected Swiss standard for clinical bioinformatics: evidence-based, reproducible, securely managed, and accredited under frameworks equivalent to ISO 15189. Adhering to these practices will ensure that genomic analysis in Switzerland remains accurate, auditable, and of enduring public value.

Table 5: Recommendations for sequencing-based clinical bioinformatics. Reproduced based on ? ).

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1. Genome build **hg38** is the national reference for alignment.
  2. Standard analyses: SNV, CNV, SV, STR, LOH, variant annotation, PRS (optional), and for cancer, TMB, HRD, MSI.
  3. Use multiple tools for structural variant calling.
  4. Apply in-house datasets to filter recurrent or false-positive SV calls.
  5. Use air-gapped, clinical-grade HPC and IT systems.
  6. Operate under ISO 15189 or equivalent accreditation.
  7. Employ standardised file formats and terminologies.
  8. Document and test pipelines for accuracy and reproducibility.
  9. Subject production code to manual review and testing.
  10. Manage all code and documentation under strict version control (e.g. Git).
  11. Validate pipelines with GIAB (germline) and SEQC2 (somatic) truth sets, plus local recall tests.
  12. Conduct unit, integration, system, and end-to-end tests.
  13. Verify data integrity using file hashing (e.g. MD5, SHA1).
  14. Confirm sample identity via fingerprinting or inferred traits.
  15. Encapsulate software using containers or controlled environments.
  16. Maintain multidisciplinary teams covering software, data, QA, and human genetics expertise.
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## **10 Conclusion**

### **Acknowledgements**

### **Contributions**

DL designed the analyses and wrote the manuscript.

### **Competing interest**

The authors declare no competing interest.

### **Ethics statement**

This study only used data which was previously published and publicly available, as cited in the manuscript.

### **Data availability**

The data used in this manuscript is derived from open sources which are cited in methods. The data generated is available from ...

### **Funding**

### **Acronyms**

<b>AD</b> Autosomal Dominant . . . . .	4
<b>WGS</b> Whole Genome Sequencing . . . . .	3

## **11 Supplemental**

Supplemental data are presented under the same headings that correspond to their relevant main text sections.