Migrating to SeqOne Platform
Workflow Mapping

Congenica
A SeqOne Company

Your germline analysis workflow, enhanced.

Moving from Congenica Rare Disease (CRD) to GermVar doesn't mean starting from scratch. These step-by-step guides show you how your familiar germline workflows carry over to GermVar on the SeqOne Platform, so you can pick up right where you left off. **Green highlights throughout will flag the improvements as you go.**

The following tutorials are covered in this guide:

1. Sample Upload & Project Setup
2. Variant Analysis & Review
3. Family & Trio Analysis
4. Filtering & Panels
5. ACMG Classification & Curation
6. Reporting & Quality Control

Tutorial 1: Sample Upload & Project Setup

1 Create a project

Projects organize your samples, panels, and analysis settings in both platforms.

IN CRD	IN GERMVAR
Navigate to **Projects → Create Project.** Assign project admin, set default panels and presets.	Navigate to **Projects → New Project** on **the SeqOne platform. Configure project** settings, assign default in silico panels and filter profiles.

2 Upload Sample Data

Both platforms support FASTQ, BAM, and VCF upload.

IN CRD	IN GERMVAR
Use the **Congenica Upload Client** or SFTP to upload FASTQ/BAM/VCF files. **Create an Interpretation Request (IR) for each patient.**	Use **SeqOne Data Sync (SDS)** to upload files. Create a **Sample** entry with metadata. The SeqOne platform auto-detects file types.

Improvement
GermVar also supports long-read FASTQ data — a capability not available in CRD.

3 Select Analysis Workset

Choose the appropriate pipeline for your data type.

IN CRD	IN GERMVAR
Select from: **Single sample, Trio, or Family** analysis. Pipeline is largely automatic based on input data.	Select a specific workset: **GermlineVar** (standard), **GermVar** (flexible), **GermlineFamily** (trio), **CNVCapture**, **CNVExome**, or **GermVar Tertiary** (VCF only, with WES capture-kit selection on import).

Improvement
GermVar offers more granular workset selection, giving you precise control over which pipeline runs on your data.

4 Add Phenotype Information

Attach HPO terms to guide AI-assisted variant prioritization.

IN CRD	IN GERMVAR
In the Interpretation Request, search and add **HPO terms** manually (up to 20 for AI analysis).	Add HPO terms manually or **auto-extract them from clinical text via DiagAI** (Phenogenius v3.1: 6,181 genes, 19,409 HPO terms), then filter using **Recommended or Union Mode.**

Major improvement
DiagAI's automatic HPO extraction from clinical narratives eliminates tedious manual phenotype coding and reduces human error.

Tutorial 2: Variant Analysis & Review

1 Open the Variant List

IN CRD	IN GERMVAR
Open an Interpretation Request → **Variants tab**. View the SNV/Indel list with annotation columns.	Open a Sample analysis → **Variant list view**. Variants are pre-ranked by DiagAI with SmartPick and Short list indicators.

2 Review AI Prioritization

IN CRD	IN GERMVAR
Review **Congenica AI scores** (Pathogenicity, Confidence, Contribution) and Exomiser gene-phenotype matching. Scores based on historical interpreted cases.	AI Prioritization: **DiagAI score** 0–100 + **UP^2** (-1 to 1, 3M+ variants, GPN-MSA) + **PhenoGenius.** Diagnostic variants are typically ranked in the **top 3.**

3 Inspect Variant Details

IN CRD	IN GERMVAR
Click a variant to see annotation details: gnomAD, UK10K, 1000G, ClinVar, OMIM, splicing predictions (5 algorithms), and genome browser.	Click a variant to see details: gnomAD v4.1 (LOEUF slider, Z-missense, Intolerant/Tolerant badges), ClinVar, OMIM, splicing viewer, read alignment, coverage.

4 Apply Filters

IN CRD	IN GERMVAR
Open the filter panel. Apply saved **SNV/SV** presets. Filter by gene, frequency, consequence, quality, inheritance.	Open the filter panel. Apply saved **filter profiles.** Combine multiple **profiles for complex queries**. Mark profiles as favorites for **quick access**.

Improvement
GermVar lets you combine multiple filter profiles and save favorites, offering more flexibility than CRD's single-preset approach.

Tutorial 3: Family & Trio Analysis

1 Set Up a Trio/Family Case

IN CRD	IN GERMVAR
Create a Trio Interpretation Request. Upload proband, mother, and father samples. CRD uses DeNovoGear for de novo calling.	Select the GermlineFamily or GermVar Family workset. Upload family samples and define relationships. GermVar calculates relationship coefficients to verify family links.

2 Review Inheritance & De Novo Variants

IN CRD	IN GERMVAR
Use the **Segregation tab** to review inheritance patterns. Filter by mode of inheritance. View compound heterozygous pairs. De novo variants are flagged automatically.	Filter by inheritance in the **Transmission & Phenotypes** section. Review de novo, **Grouped Compound Het** (small + large variants merged), and segregation data. The **Genotype & Inheritance** display adds trio colours, sex-chromosome inheritance, hemizygous labels, and Mendelian violation warnings. Filter with the **Genetics** section.

Tutorial 4: Filtering & Gene Panels

1 Apply Gene Panels

IN CRD	IN GERMVAR
Assign **virtual gene panels** to a project. Panels include gene lists with mode of inheritance annotations. Panels are versioned with Ensembl v109.	Assign **in silico panels** (gene lists) to a project. Import from **PanelApp** (UK, Australia, and more) or create custom lists. Panels include mode of inheritance per gene.

Improvement
GermVar integrates with multiple PanelApp sources for standardized, curated gene panels — a capability not available in CRD.

2 Create & Manage Filter Presets

IN CRD	IN GERMVAR
Create **SNV presets** or **SV presets**. Save to project or inherit from parent projects. Set a default preset for the project.	Create **filter profiles**. Save as **public or private.** Combine profiles for complex filtering. Mark as **favorites**. Set project defaults.

Tutorial 5: ACMG Classification & Variant Curation

1 Classify Variants with ACMG Criteria

IN CRD	IN GERMVAR
Open the **ACMG Evidence tab.** Review **heuristic Exomiser hints** (top 100 variants only, partial criteria coverage). Set the remaining criteria manually. System calculates pathogenicity class.	Open the **ACMG tab. AutoACMG** has already scored all 28 ACMG/AMP criteria for the variant and pre-computed the class. Auto-selected tags appear **pending. Validate or reject** each in **one click** in the interactive matrix. Adjust scoring points, or add criteria manually, then **Save Classification** to lock it and refresh the comment.

Improvement
GermVar automatically scores every variant against all 28 ACMG/AMP criteria, with clear per-criterion justifications. You review and sign off, instead of building each classification from scratch.

2 Manage Curated Variant Database

IN CRD	IN GERMVAR
Use **Curated Variant Lists (CVL)**. Add variants with include/exclude designations. CVLs can automate classification in future cases. Share across projects.	Use the **Variant Knowledge Base (VKB)** with both case-level and account-level classification. Curate variants with classifications. Use the VKB search to check previous evaluations. Include/exclude designations available.

Tutorial 6: Reporting & Quality Control

1 Review Quality Control

IN CRD	IN GERMVAR
Open the **QC tab**. Review coverage metrics at configurable depths. Check sequencing quality statistics.	Review **QC metrics** at both gene- and exon-level coverage, with XLS exports and WES coverage summaries now in clinical reports. Check **contamination status**, verify **sample identity (ID-Check)**, and review against **configurable QC thresholds.**

Major Improvement
GermVar adds contamination checking and sample identity verification (ID-Check) — critical QC capabilities not available in CRD.

2 Generate Clinical Reports

IN CRD	IN GERMVAR
Select reported variants → **Generate report**. Choose from report templates. Export as PDF. Additional outputs: VCF, BAM, gVCF.	Select reported variants → **Create report** from a streamlined single-page form with custom sections. Also available: **Technical report** and **ID-Check report**. Export in multiple formats.

Improvement
GermVar provides dedicated Technical and ID-Check reports in addition to the clinical report.

Terminology Mapping: CRD → GermVar

CRD Terminology	GermVar Terminology
Patient	Sample
Interpretation Request	Analysis
Sub-project	entity-level sharing
Pipeline	Workset
Curated Variant List	Variant Knowledge Base
Variant Decision	Variant Evaluation
Congenica AI	DiagAI
Exomiser	DiagAI + PhenoGenius
Pathogenicity score	DiagAI score (0–100)
New	SmartPick
New	UP^2 score
SNV/SV Preset	Filter Profile
New	Preset Combos
Gene Panel	In Silico Panel
New	PanelApp import
Congenica Upload Client	SeqOne Data Sync (SDS)
Genome Browser	IGV tab
CNV viewer	Large Variant viewer
Generate report	Create report
New	Technical report
New	ID-Check report
QC tab	QC metrics panel
New	Contamination check
New	ID-Check

Ready for the next step? Contact us

SeqOne Platform is a software-based in vitro diagnostic medical device, CE-marked as a Class C under the Regulation (EU) 2017/746, designed to support healthcare professionals in analyzing and interpreting raw genomic and sequencing data from patients undergoing NGS or CGH array analysis. By providing qualitative and actionable insights, the platform functions as a decision support system, aiding healthcare professionals in making clinical decisions. GermVar is a feature of SeqOne Platform. Find out more about our compliance and security framework at trust.seqone.com. Manufacturer: SeqOne (France)

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