Congenica

Enabling genomic medicine

Congenica Express™

Less work, more results

Recurrent variants have long been implicated in both ultra-rare and 'common' monogenic disorders. These variants may be population-specific – caused by founder effects (e.g. Cystic Fibrosis, Tay Sachs, hereditary breast cancer, hypertrophic cardiomyopathy) – or introduced at easily mutable sites in the genome (e.g. Noonan syndrome).

Known variants - a common cause

Recurring 'known' pathogenic and likely pathogenic variants are reported in a wide range of disorders, including:

- **>70%** of pathogenic variants in cardiomyopathy patients[1]
- **35%** of pathogenic variants in cardiac arrhythmia patients[1]
- **> 50%** of de novo missense variants in neurodevelopmental patients[2]
- Recurrent PAX6 variants resulting in ophthalmic malformations in **15 families**[3]
- **> 15,600** Pathogenic or Likely Pathogenic SNVs and indels in ClinVar reported in multiple individuals with no conflicting interpretations

Automated classification, annotation, and reporting of known variants

Congenica decision support software features Automated Classification of Known Variants to instantly pre-classify variants observed in your rare disease cases, significantly saving time to maximize your yield and throughput.

The Automated Classification of Known Variants feature uses your high-quality curations or data sets that you select from external knowledgebases to put you in control of variant classification while minimizing the effort and time required review, interpret and report data.

Congenica Express functionality also enables you to include ACMG criteria, literature articles and interpretive statements for your report collated during previous interpretations of a variant. This means less duplicated work and more rapid analysis for recurrent variants.

Key benefits of Congenica Express:

- ✓ Get Started Easily
- ✓ Accelerate Turnaround Times
- ✓ Increase Case Throughput
- ✓ Improve Safety & Quality
- ✓ Maximize Analytical Yield

Automate your workflows

The Automated Classification of Known Variants feature has been designed to be easy to set-up to deliver value to you as quickly as possible. To get you going with your specific automation setup we will support you with the following to enable rapid analysis without human interpretation:

1. Pre-curated variants list from your external or in-house curations -
    - Congenica customers can generate lists from their existing classifications of recurrent variants in the platform to automatically interpret the variants that they choose.
    - Data from Congenica's supported knowledgebases, including ClinVar and Decipher, can also be used if you do not have a historic set of classified variants.
2. Gene panels for each case – define which genes are phenotypically-relevant and specify their expected mode of inheritance.
3. A custom report template (optional with our Professional Services) – design the report format exactly how you want your data to be presented.

The Congenica Support and Professional Services Teams will be on hand to help during configuration. Once set up, simply load your samples and let Congenica do the rest.

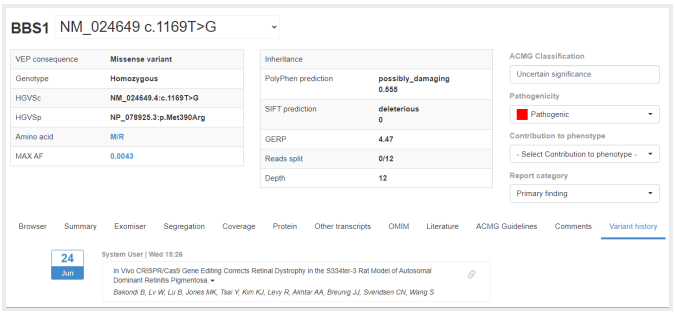
Achieve 5-minute turnaround times

From analyzing thousands of cases ourselves, we know all about the challenges of variant interpretation. Without Congenica, even simple cases can take 11-12 hours to complete at a staffing cost of over $500 per case[4].

Congenica reduces the working time for interpretation and reporting by 90%, but repeated manual classification of recurrent pathogenic or likely pathogenic variants can be frustrating and a poor use of your precious analytical and clinical resources.

By automating the classification of previously interpreted variants, Congenica automatically performs the analysis for cases with recurring variants for you.

In internal testing, **Automated Classification of Known Variants reduces time to report by an additional 90% - achieving complex genomic data interpretation in only 5-minutes when a recurring causal variant is identified.**



Congenica automatically interpreted and classified this BBS1 variant as pathogenic. The software has also highlighted relevant literature articles supporting the interpretation of the variant and marked the variant as a 'Primary Finding' for reporting.

Case Study: Driving down turnaround times and costs

In a study analyzing 19,000 cases from the Congenica Knowledgebase a team of Registered Clinical Scientists identified nearly 4,000 cases with recurrent pathogenic or likely pathogenic variants, which Congenica Express of Known Variants would have automatically classified, increasing throughput significantly.

Using the Congenica Automated Classification of Known Variants pipeline, interpretation and reporting of each of these 4,000 cases could be completed in under 8 minutes, saving almost 5,500 hours (91%) of combined interpretation effort and saving 98% of staff costs.

Increase your case throughput

Staffing shortages in genetic analysis departments significantly impacts access to genetic services with 71% of clinical laboratories reporting that they are nearly or completely at capacity[5]. Increasing case throughput by reducing interpretation time is therefore essential.

Congenica software already enables the fastest analysis and highest throughput of complex genomic cases[6]. **With Congenica Automated Classification of Known Variants, labs can increase their throughput by a further 20% to 60%,** depending on the frequency of recurrent variants. This means quicker report turnarounds and the ability to process significantly more tests, returning more results in a shorter timeframe.

Labs using Congenica for high sample volumes of routine tests will see throughput continue to increase over time as their clinical teams build and benefit from curated variant lists, interpretations, and report comments within the software. And, by clearing recurring variant cases, Congenica Express lets Clinical Geneticists focus their attention on solving their most complex cases.

Maximize your analytic yield

Compared to industry averages, Congenica decision support software enables laboratories to reach actionable insights from their analysis in 30% more cases[7].

With Automated Classification of Known Variants, Congenica will detect and classify previously curated variants present in your chosen dataset. It will pick out the “easy wins” and highlight them for you, to avoid repetitive work. For cases where no known variants are identified, the full functionality of Congenica still enables clinicians to perform detailed in-depth analysis to identify novel causes of disease, faster and with a higher yield than ever before.

Have complete confidence in the quality of your automated analysis

We understand the importance of reliable, high quality and safe reporting that you can have complete confidence in. Congenica Express features built-in functionality to safeguard against issues such as false negative reporting and unmasking carrier status in unconsented individuals:

- The Automated Classification of Known Variants pipeline uses the mode of inheritance of each gene in your panels to restrict classification of variants to those consistent with the mode of inheritance of a gene. For example, only compound heterozygous or homozygous variants in the CFTR gene would be classified in a case referred for Cystic Fibrosis testing.
- Congenica fully supports both single and double-user-check workflows, recommended by international best practices. This enables a second clinician to check and approve automated decisions and record a full audit trail within the platform.
- Genotype data for each site of interest in your curated variant data is available to review within the Congenica software in a new Genotype tab, to exclude the possibility of a missed variant (NOCALL) affecting your results.

Congenica Express achieves complex genomic data interpretation in as little as 5-minutes when a recurring causal variant is identified, maximizing lab throughput

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Is your lab running as efficiently as possible?

- Automate the analysis of your simpler cases
- Improve the consistency and quality of your variant interpretation
- Maximize the efficiency of your analysis workflows and increase case throughput
- Increase the time available to dedicate to the most complex, ultra-rare disease cases
- Scale-up analysis and drive-down costs

Congenica® is the world's leading software for the analysis of complex genomic data. The platform accelerates the interpretation of whole genome, whole exome and gene panel data to increase diagnostic yield, maximize workflow efficiency and improve confidence in every case.

Request a demo

www.congenica.com/demo

References

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