

SPONSORED WORKSHOP:

Variant interpretation & reporting: what's best for your lab? Standalone databases or a decision support tool

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Interpretation and reporting of variants can be a labour intensive and time-consuming process. A range of different software applications are required to detect and filter variants. Information from a variety of sources can be needed to accurately classify each variant. This process can be further complicated if there is a need to provide up to date information on relevant treatments and clinical trials. The final step of collating and summarising findings in a clinical report completes the process.

In this interactive workshop we will compare and contrast the use of databases (COSMIC, HSMD and HGMD) to an on-line classification and reporting application, QIAGEN Clinical Insight Interpret (QCI I) to prioritise, filter, classify and report variants. We will be analysing a variety of different sample types and discuss how to:

- Generate a list of clinical relevant variants from WES, trios and targeted panels
- Use the ACMG Guidelines for classification
- Associate variants with up-to date treatment and clinical trial information
- Generate a comprehensive clinical report

The comparison of different approaches presented during this session will help your lab to identify the best path for variant interpretation and reporting. Regardless of whether you need extra help in specific stages of the process or a complete end-to-end pipeline, at QIAGEN we have a range of different solutions to help in the reliable identification, classification and reporting of clinically relevant variants.

Please join us for this interactive session.