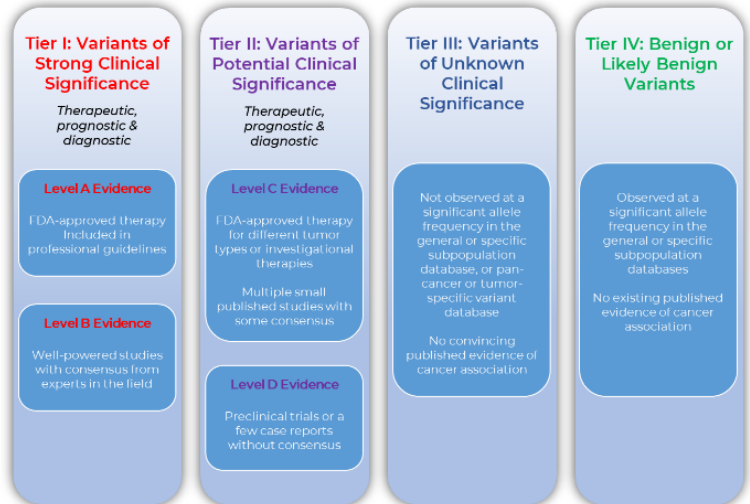


## FOCUS ON Pathogenicity of somatic sequence variants

The introduction of next generation sequencing of multiple tumour types into the clinical pathway has led to an increase in detection of variants outside the classical hotspot regions of tumour genes.

Therefore there is an increased requirement to classify and interpret the actionability of somatic variants in terms of diagnosis, prognosis and therapeutic intervention. Various classification systems are available and will be discussed during the webinar.



In 2020 GenQA introduced an EQA to assess the classification of somatic sequence variants with 24 laboratories participating. The results of the EQA and the evidence used to classify the variants will be presented.

After the seminar there will be a LIVE Question and Answer session.

### Pathogenicity of somatic sequence variants webinar Monday 24th May 2021, 2pm BST

- Introduction to classification of somatic variants
- Examples of variant classification
- Results of 2020 GenQA EQA for pathogenicity of somatic sequence variants
- LIVE question and answer session

Register for the free webinar and live Q&A session before **24<sup>th</sup> May 2021** at:

<https://attendee.gotowebinar.com/register/3577365948727167755>

**FOCUS ON next month:**

**Pathogenicity of postnatal copy number variants**