

Exception variant reporting

In UK labs, there are certain genes in which only certain types of (likely) pathogenic variants are reported when the indication for testing is cancer predisposition, because of the underlying mechanism of disease or low associated disease penetrance.

The table here below outlines gene-specific reporting, indicating those variants, or regions of the gene in question that are explicitly included or excluded from analysis, when testing is undertaken in a UK laboratory.

This list is dynamic, and will be updated in line with changing evidence, subject to review by Cancer Variant Group-UK (Can-VIG) Interpretation Steering and Advisory Group (CStAG) and/or UK Cancer Genetics Group Council as required.

Gene	Exceptions to variant reporting
<i>APC</i>	APC c.3920T>A; p.Ile1307Lys (I1307K) excluded from analysis/reporting
<i>ATM</i>	Reporting restricted to truncating variants and c.7271T>G
<i>CHEK2</i>	Reporting restricted to truncating variants and c.349A>G p.(Arg117Gly)
<i>EPCAM</i>	Reporting restricted to 3' CNV
<i>GREM1</i>	Copy number analysis only to check for duplication involving the 3' end of the <i>SCG5</i> gene & a region upstream of the <i>GREM1</i> gene
<i>POLE</i>	Reporting restricted to missense variants in exonuclease domain, exons 9-14 (cancer predisposition)
<i>POLD1</i>	Reporting restricted to missense variants in exonuclease domain, exons 6-13 (cancer predisposition)
<i>RAD51C</i>	Reporting restricted to truncating variants
<i>RAD51D</i>	Reporting restricted to truncating variants
<i>RET</i>	Reporting (for MEN2) restricted to exons 5, 7, 8, 10, 11,13-16