

Germline Assay Guide



This is data-driven precision medicine.
This is the future of healthcare.

tempus.com/oncology/ →

xG Validated Hereditary Cancer Testing

(powered by GeneDx)

xG+ (extended hereditary cancers)

- Covers 88 genes providing risk assessment for both common and rare hereditary cancer types.
- Confirmatory testing for all xT incidental germline genes (excluding EGFR).

xG (common hereditary cancers)

- Covers 52 genes associated with breast, ovarian, colorectal, endometrial, prostate, pancreatic cancers.

xT Solid Tumor/Normal Match

648 gene somatic panel utilizing a normal match to enhance the accuracy of somatic variant calls by filtering out germline variants.

Based on the xT normal match, incidental germline findings from a select list of 65 hereditary cancer genes may be reported on xT, if present. These findings may or may not be related to the patient's current cancer diagnosis.

What Are The Differences Between xG/xG+ Hereditary Cancer Testing and xT Tumor/Normal Match?

xG xG and xG+ are stand-alone validated germline tests that identify various types of germline alterations, including single and multi-exon deletions/duplications and gene rearrangements.

xG xG and xG+ are specifically designed to provide hereditary cancer risk assessment and as such, sensitivity and specificity have been rigorously assessed.

xT Incidental germline reporting through xT tumor/normal matched testing assists in the identification of patients who may benefit from follow-up testing with xG or xG+.

**xG & xG+ Validated Hereditary Cancer Testing****xT Tumor/Normal Match**

Genes Assessed	52 common hereditary cancer genes (xG) 88 extended hereditary cancer genes (xG+)	65 hereditary cancer genes
Types of Variants Detected	SNVs, indels, large deletions/duplications, rearrangements/inversions	SNVs, indels
Possible Results Included on Report	Pathogenic variants, likely pathogenic variants, variants of uncertain significance (VUS)	Pathogenic variants, likely pathogenic variants
Validation	Rigorous validation process for hereditary cancer risk assessment	Validated for somatic testing; no specific hereditary validation
Secondary Confirmation	Performed for regions of inadequate NGS sequencing coverage (Sanger seq, MLPA, arrayCGH)	Not performed
Sample Types Accepted	Blood, buccal swab, cultured fibroblasts*	Blood, Saliva
Familial Variant/Cascade Testing	Available for pathogenic/likely pathogenic variants	Not available
Variant Reclassification	GeneDx reclassifies; amendments issued through Tempus	Not available
Therapeutic Implications	Not included on report	FDA/NCCN/OncoKB supported therapies included on report
Patient Genetic Counseling Services	Available with ordering provider referral	Not available

* Requires special approval

The reportable findings for the genes included on the above panels are based upon recommendations from the ACMG, the NCCN, and other published literature. The clinical significance of reported variants are based on germline classification criteria created by the American College of Medical Genetics (ACMG) and Association for Molecular Pathology (AMP).

This is data-driven precision medicine.
This is the future of healthcare.

tempus.com/oncology/