Germline Assay Guide

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

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+.

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This is the future of healthcare.
## xG & xG+ Validated Hereditary Cancer Testing

### Genes Assessed
- 52 common hereditary cancer genes (xG)
- 88 extended hereditary cancer genes (xG+)

### Types of Variants Detected
- SNVs, indels, large deletions/duplications, rearrangements/inversions

### Possible Results Included on Report
- Pathogenic variants, likely pathogenic variants, variants of uncertain significance (VUS)

### Validation
- Rigorous validation process for hereditary cancer risk assessment

### Secondary Confirmation
- Performed for regions of inadequate NGS sequencing coverage (Sanger seq, MLPA, arrayCGH)

### Sample Types Accepted
- Blood, buccal swab, cultured fibroblasts*

### Familial Variant/Cascade Testing
- Available for pathogenic/likely pathogenic variants

### Variant Reclassification
- GeneDx reclassifies; amendments issued through Tempus

### Therapeutic Implications
- Not included on report

### Patient Genetic Counseling Services
- Available with ordering provider referral

## xT Tumor/Normal Match

### Genes Assessed
- 65 hereditary cancer genes

### Types of Variants Detected
- SNVs, indels

### Possible Results Included on Report
- Pathogenic variants, likely pathogenic variants

### Validation
- Validated for somatic testing; no specific hereditary validation

### Secondary Confirmation
- Not performed

### Sample Types Accepted
- Blood, Saliva

### Familial Variant/Cascade Testing
- Not available

### Variant Reclassification
- Not available

### Therapeutic Implications
- FDA/NCCN/OncoKB supported therapies included on report

### Patient Genetic Counseling Services
- Not available

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* Requires special approval

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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).

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[link to tempus.com oncology]