Hereditary Prostate Cancer Panel, Sequencing and Deletion/Duplication

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Pathogenic germline variants in multiple genes have been implicated in hereditary prostate cancer. Hereditary cancer syndromes are often characterized by the onset of cancer at an early age (typically before 50 years of age) and multiple, multifocal, and/or similar cancers in a single individual or in one or more closely related family members. Refer to the Genes Tested table below for more details regarding the genes and syndromes included on the Hereditary Prostate Cancer Panel. Genes included on this panel are also included in other ARUP hereditary cancer tests. For more information, refer to the ARUP Hereditary Cancer Panel Comparison table.

Featured ARUP Testing

To compare directly to other hereditary cancer panels offered by ARUP Laboratories, refer to the ARUP Hereditary Cancer Panel Comparison table.

Hereditary Prostate Cancer Panel, Sequencing and Deletion/Duplication 3005686

Method: Massively Parallel Sequencing/Sequencing/Multiplex Ligation-Dependent Probe Amplification (MLPA)

- Recommended test to confirm a hereditary cause of prostate cancer in individuals with a personal or family history
- Testing minors for adult-onset conditions is not recommended and will not be performed without prior approval. For additional information, please contact an ARUP genetic counselor at 800-242-2787.

If a familial sequence variant has been previously identified, targeted sequencing for that variant may be appropriate; refer to the Laboratory Test Directory for additional information.

Genetics

Genes

Refer to the Genes Tested table for genes included in the panel.

Etiology

Approximately 10% of prostate cancers are associated with a hereditary cause.[1]

Inheritance

- Autosomal dominant
- Some genes are also associated with autosomal recessive childhood cancer predisposition or other syndromes.

Test Interpretation

Contraindications for Ordering

- For individuals with a suspected diagnosis of Lynch syndrome, consider testing specific to Lynch syndrome as some relevant variants are not included on this panel. Refer to Lynch Syndrome - Hereditary Nonpolyposis Colorectal Cancer (HNPCC) for more information.
- The test should not be ordered to detect somatic variants associated with malignancy because sensitivity for mosaic variants is low with methodology used for germline assays.
- Individuals with hematological malignancy and/or a previous allogeneic bone marrow transplant should not undergo molecular genetic testing on peripheral blood specimen.
  - Testing of cultured fibroblasts is required for accurate interpretation of test results.

Methodology

This test is performed using the following sequence of steps:

- Selected genomic regions, primarily coding exons and exon-intron boundaries, from the targeted genes are isolated from extracted genomic DNA using a probe-based hybrid capture enrichment workflow.
- Enriched DNA is sequenced by massively parallel sequencing (MPS; also known as next generation sequencing [NGS]) followed by paired-end read alignment and variant calling using a custom bioinformatics pipeline. The pipeline includes an algorithm for detection of large (single exon-level or larger) deletions and duplications.
- Sanger sequencing is performed as necessary to fill in regions of low coverage and in certain situations, to confirm variant calls.
- Large deletion/duplication calls made using MPS are confirmed by an orthogonal exon-level microarray when sample quality and technical conditions allow.
- Long-range polymerase chain reaction (PCR) followed by nested Sanger sequencing is performed on the following gene(s) and exon(s):
  - *PMS2* (NM_000535) 11, 12, 13, 14, 15

- Bidirectional Sanger sequencing is performed on the following gene(s) and exon(s):
  - *MSH2* (NM_000251) 5
  - *PMS2* (NM_000535) 7
- Multiplex ligation-dependent probe amplification (MLPA) is performed on the following genes to call exon-level deletions and duplications:
  - *PMS2* (NM_000535)

Sensitivity/Specificity

Clinical Sensitivity

Variable, dependent on phenotype/condition

Analytic Sensitivity

Variant Class	Analytic Sensitivity (PPA) Estimate[a] (%) and 95% Credibility Region	Analytic Specificity (NPA) Estimate (%)
SNVs	>99 (96.9-99.4)	>99.9
Deletions 1-10 bp[b]	93.8 (84.3-98.2)	>99.9
Insertions 1-10 bp[b]	94.8 (86.8-98.5)	>99.9
Exon-level[c] deletions	97.8 (90.3-99.8) [2 exons or larger] 62.5 (38.3-82.6) [Single exon]	>99.9
Exon-level[c] duplications	83.3 (56.4-96.4) [3 exons or larger]	>99.9
Exon-level deletions/duplications (MLPA)	>99	>99

[a]PPA values are derived from larger methods-based MPS and/or Sanger validations. These values do not apply to testing performed by multiplex ligation-dependent probe amplification (MLPA) unless otherwise indicated.

[b]Variants greater than 10 bp may be detected, but the analytic sensitivity may be reduced.

[c]In most cases, a single exon deletion or duplication is less than 450 bp and 3 exons span a genomic region larger than 700 bp.

bp, base pairs; NPA, negative percent agreement; PPA, positive percent agreement; SNVs, single nucleotide variants

Limitations

- A negative result does not exclude a heritable form of cancer.
- Diagnostic errors can occur due to rare sequence variations.
- Interpretation of this test result may be impacted if this patient has had an allogeneic stem cell transplantation.
- The following will not be evaluated:
  - Variants outside the coding regions and intron-exon boundaries of targeted genes
  - Regulatory region and deep intronic variants
  - Breakpoints of large deletions/duplications
  - Sequence variants in *EPCAM*
  - The following exons are not sequenced due to technical limitations of the assay:
    - *BRCA1* (NM_007300) 13
    - *CHEK2* (NM_001005735) 3; (NM_001349956) 4
- The following may not be detected:
  - Deletions/duplications/insertions of any size by MPS
  - Large duplications less than 3 exons in size
  - Noncoding transcripts
  - Single exon deletions/duplications may not be detected based on the breakpoints of the rearrangement.
  - Some variants due to technical limitations in the presence of pseudogenes, repetitive, or homologous regions
  - Low-level somatic variants
  - Deletions/duplications in the following exons:
    - *BRCA1* (NM_007294, NM_007299, NM_007300) 2; (NM_007298) 1

- *CHEK2* (NM_007194) 11-15; (NM_001005735) 3,12-16; (NM_001257387) 12-16; (NM_001349956) 4,10-14; (NM_145862) 10-14

Genes Tested

To compare directly to other hereditary cancer panels offered by ARUP Laboratories, refer to the ARUP Hereditary Cancer Panel Comparison table.

Gene	MIM Number	Disorder/Associated Cancer(s)/Tumor(s)	Inheritance
ATM	607585	Breast, colorectal,[a] ovarian, pancreatic, prostate	AD
		Ataxia-telangiectasia	AR
BRCA1	113705	HBOC syndrome Breast, fallopian tube, ovarian, pancreatic, peritoneal, prostate	AD
		Fanconi anemia, complementation group S	AR
BRCA2	600185	HBOC syndrome Breast, fallopian tube, melanoma, ovarian, pancreatic, peritoneal, prostate	AD
		Fanconi anemia, complementation group D1	AR
CHEK2	604373	Breast, colorectal, prostate, thyroid[a]	AD
EPCAM (Exon 9 deletion/duplications only)	185535	Lynch syndrome/HNPCC Brain, colorectal, endometrial, ovarian, pancreatic, prostate, renal pelvis and/or ureter, stomach, and others	AD
HOXB13	604607	Prostate	AD
MLH1	120436	Lynch syndrome/HNPCC Brain, colorectal, endometrial, ovarian, pancreas, prostate, renal pelvis and/or ureter, stomach, and others	AD
		CMMRD	AR
MSH2	609309	Lynch syndrome/HNPCC Brain, colorectal, endometrial, ovarian, pancreas, prostate, renal pelvis and/or ureter, stomach, and others	AD
		CMMRD	AR
MSH6	600678	Lynch syndrome/HNPCC Brain, colorectal, endometrial, ovarian, pancreas, prostate, renal pelvis and/or ureter, stomach, and others	AD
		CMMRD	AR
NBN	602667	Breast,[a] ovarian,[a] prostate[a]	AD
		NBS	AR
PALB2	610355	Breast, ovarian, pancreas, prostate	AD

[a]Association is suggested but not well-established at this time

AD, autosomal dominant; AR, autosomal recessive; CMMRD, constitutional mismatch repair deficiency; CNS, central nervous system; HBOC, hereditary breast and ovarian cancer; HNPCC, hereditary nonpolyposis colorectal cancer; LFS, Li-Fraumeni syndrome; NBS, Nijmegan breakage syndrome

Gene	MIM Number	Disorder/Associated Cancer(s)/Tumor(s)	Inheritance
		Fanconi anemia, complementation group N	AR
PMS2	600259	Lynch syndrome/HNPCC Brain, colorectal, endometrial, ovarian, pancreas, prostate, renal pelvis and/or ureter, stomach, and others	AD
		CMMRD	AR
RAD51D	602954	Breast, ovarian, prostate	AD
TP53	191170	LFS Adrenocortical carcinoma, breast, choroid plexus carcinoma, CNS, colorectal, melanoma, osteosarcoma, pancreas, prostate, renal, rhabdomyosarcoma, soft tissue sarcoma, stomach, thyroid, and others	AD

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AD, autosomal dominant; AR, autosomal recessive; CMMRD, constitutional mismatch repair deficiency; CNS, central nervous system; HBOC, hereditary breast and ovarian cancer; HNPCC, hereditary nonpolyposis colorectal cancer; LFS, Li-Fraumeni syndrome; NBS, Nijmegan breakage syndrome

References

1. American Cancer Society. What causes prostate cancer? Accessed Jun 2022.

Related Information

Hereditary Cancer Germline Genetic Testing

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