

Hereditary Cancer Risk, Diagnostics, and Treatment Strategies Practice Test (Sample)

Study Guide



Everything you need from our exam experts!

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Introduction

Preparing for a certification exam can feel overwhelming, but with the right tools, it becomes an opportunity to build confidence, sharpen your skills, and move one step closer to your goals. At Examzify, we believe that effective exam preparation isn't just about memorization, it's about understanding the material, identifying knowledge gaps, and building the test-taking strategies that lead to success.

This guide was designed to help you do exactly that.

Whether you're preparing for a licensing exam, professional certification, or entry-level qualification, this book offers structured practice to reinforce key concepts. You'll find a wide range of multiple-choice questions, each followed by clear explanations to help you understand not just the right answer, but why it's correct.

The content in this guide is based on real-world exam objectives and aligned with the types of questions and topics commonly found on official tests. It's ideal for learners who want to:

- Practice answering questions under realistic conditions,
- Improve accuracy and speed,
- Review explanations to strengthen weak areas, and
- Approach the exam with greater confidence.

We recommend using this book not as a stand-alone study tool, but alongside other resources like flashcards, textbooks, or hands-on training. For best results, we recommend working through each question, reflecting on the explanation provided, and revisiting the topics that challenge you most.

Remember: successful test preparation isn't about getting every question right the first time, it's about learning from your mistakes and improving over time. Stay focused, trust the process, and know that every page you turn brings you closer to success.

Let's begin.

How to Use This Guide

This guide is designed to help you study more effectively and approach your exam with confidence. Whether you're reviewing for the first time or doing a final refresh, here's how to get the most out of your Examzify study guide:

1. Start with a Diagnostic Review

Skim through the questions to get a sense of what you know and what you need to focus on. Your goal is to identify knowledge gaps early.

2. Study in Short, Focused Sessions

Break your study time into manageable blocks (e.g. 30 - 45 minutes). Review a handful of questions, reflect on the explanations.

3. Learn from the Explanations

After answering a question, always read the explanation, even if you got it right. It reinforces key points, corrects misunderstandings, and teaches subtle distinctions between similar answers.

4. Track Your Progress

Use bookmarks or notes (if reading digitally) to mark difficult questions. Revisit these regularly and track improvements over time.

5. Simulate the Real Exam

Once you're comfortable, try taking a full set of questions without pausing. Set a timer and simulate test-day conditions to build confidence and time management skills.

6. Repeat and Review

Don't just study once, repetition builds retention. Re-attempt questions after a few days and revisit explanations to reinforce learning. Pair this guide with other Examzify tools like flashcards, and digital practice tests to strengthen your preparation across formats.

There's no single right way to study, but consistent, thoughtful effort always wins. Use this guide flexibly, adapt the tips above to fit your pace and learning style. You've got this!

Questions

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- 1. Which statement correctly describes the impact of whole genome sequencing on MRD sensitivity?**
 - A. It reduces the number of detectable variants**
 - B. It provides identical results to exome sequencing**
 - C. It identifies significantly more tumor variants than exome sequencing**
 - D. It cannot detect circulating tumor DNA**

- 2. Which statement is true about MRD and imaging?**
 - A. MRD testing is more sensitive than imaging**
 - B. Imaging is more sensitive than MRD**
 - C. MRD and imaging have identical sensitivity**
 - D. MRD is not used for recurrence detection**

- 3. Which testing method is commonly used to identify protein expression such as ER and HER2 in tumor tissue?**
 - A. Genetic sequencing**
 - B. Ultrasound**
 - C. Immunohistochemistry (IHC)**
 - D. CT scan**

- 4. Which phenotype corresponds to absence of ER, PR, and HER2 expression?**
 - A. Triple-negative breast cancer**
 - B. Luminal B**
 - C. HER2-enriched**
 - D. Luminal A**

- 5. Which sequencing approach yields greater breadth of tumor variant detection, enhancing MRD sensitivity?**
 - A. Whole genome sequencing**
 - B. Targeted panel sequencing**
 - C. Sanger sequencing**
 - D. RNA sequencing**

- 6. How many genes are included in the MyRisk test?**
- A. 63 genes**
 - B. 50 genes**
 - C. 100 genes**
 - D. 25 genes**
- 7. Which statement about EOBs is accurate based on the information?**
- A. They indicate the amount billed to the patient**
 - B. They are a bill**
 - C. They are a formal notification of payment**
 - D. They are not a bill**
- 8. In which cancer is MyChoice CDx used?**
- A. Breast cancer**
 - B. Prostate cancer**
 - C. Pancreatic cancer**
 - D. Ovarian cancer**
- 9. Which Myriad test determines HRD status?**
- A. BRACAnalysis**
 - B. MyChoice CDx**
 - C. OncoVantage**
 - D. HRDSense**
- 10. What sample type is required for MRD monitoring tests?**
- A. Tumor tissue**
 - B. Blood only**
 - C. Saliva**
 - D. Urine**

Answers

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1. C
2. A
3. C
4. A
5. A
6. A
7. D
8. D
9. B
10. B

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Explanations

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1. Which statement correctly describes the impact of whole genome sequencing on MRD sensitivity?

- A. It reduces the number of detectable variants**
- B. It provides identical results to exome sequencing**
- C. It identifies significantly more tumor variants than exome sequencing**
- D. It cannot detect circulating tumor DNA**

Whole-genome sequencing expands the set of tumor variants used to track MRD, which boosts sensitivity. By surveying the entire genome, it captures not only coding mutations but also noncoding mutations, structural variants, and copy-number alterations that exome sequencing misses. Those additional variants provide more targets to monitor in circulating tumor DNA, so even if some subclones disappear or the tumor evolves, you have a richer signature to detect residual disease. In contrast, exome sequencing focuses on coding regions, leaving many potential MRD signals undiscovered. WGS can also detect ctDNA signals, including rearrangements and CNAs, that exome-based approaches might miss. Therefore, identifying significantly more tumor variants with whole-genome sequencing explains its higher MRD sensitivity.

2. Which statement is true about MRD and imaging?

- A. MRD testing is more sensitive than imaging**
- B. Imaging is more sensitive than MRD**
- C. MRD and imaging have identical sensitivity**
- D. MRD is not used for recurrence detection**

The main idea here is how sensitive different methods are at spotting cancer when it's very small or just beginning to come back. MRD testing detects cancer at the cellular or molecular level, far below what imaging can reveal. It uses techniques like flow cytometry, PCR, or next-generation sequencing to find one cancer cell among tens of thousands or even a million normal cells. Imaging, on the other hand, looks for visible masses or metabolic activity above certain thresholds, which means very small or dispersed disease can be missed. Because MRD can pick up tiny amounts of disease long before it forms a visible lesion, it often detects relapse earlier and with greater sensitivity than imaging. This is especially true in blood cancers like leukemias and lymphomas, where MRD status provides strong prognostic information. Of course, imaging remains important for locating disease and assessing anatomical spread, especially in solid tumors, but the sensitivity advantage of MRD for detecting minimal disease makes the statement true: MRD testing is more sensitive than imaging.

3. Which testing method is commonly used to identify protein expression such as ER and HER2 in tumor tissue?

- A. Genetic sequencing**
- B. Ultrasound**
- C. Immunohistochemistry (IHC)**
- D. CT scan**

Determining protein expression in tumor tissue is assessed most commonly with immunohistochemistry, which uses labeled antibodies to bind specific proteins in preserved tissue sections. In practice, pathologists apply antibodies against proteins like estrogen receptor (ER) and HER2 to a fixed tumor sample and visualize where and how strongly these proteins are present under a microscope. This approach directly shows whether tumor cells are expressing ER or HER2, which is essential for guiding treatment—ER positivity suggests potential benefit from hormone therapy, while HER2 positivity indicates likely responsiveness to anti-HER2 targeted therapy. Immunohistochemistry is preferred here because it reveals protein presence and localization within the actual tumor cells, providing a practical, tissue-based readout. If results for HER2 are uncertain (equivocal), additional reflex testing with a gene-based method like FISH may be used, but the primary and most widely used method to identify these protein expressions is IHC. Other options like imaging studies (ultrasound, CT) or genetic sequencing do not evaluate protein expression in tumor tissue in the same direct, routine way.

4. Which phenotype corresponds to absence of ER, PR, and HER2 expression?

- A. Triple-negative breast cancer**
- B. Luminal B**
- C. HER2-enriched**
- D. Luminal A**

Breast cancer subtypes are defined by receptor status for ER, PR, and HER2, which guides therapy choices. Absence of all three receptors—ER, PR, and HER2—defines the triple-negative phenotype. Without ER or PR, tumors won't respond to endocrine therapies; without HER2, they won't respond to HER2-targeted therapies. This makes triple-negative breast cancer the label for tumors that lack these receptors. In contrast, luminal A and luminal B cancers express estrogen receptor (and often progesterone receptor) and may have variable HER2 status, while HER2-enriched cancers overexpress HER2 and are typically ER/PR negative but HER2 positive, so they are not triple-negative.

5. Which sequencing approach yields greater breadth of tumor variant detection, enhancing MRD sensitivity?

- A. Whole genome sequencing**
- B. Targeted panel sequencing**
- C. Sanger sequencing**
- D. RNA sequencing**

Broad surveillance across the genome increases MRD sensitivity. Whole-genome sequencing surveys the entire genome, catching coding and noncoding regions and identifying a wide range of tumor-derived changes—single-nucleotide variants, small indels, copy-number alterations, and structural rearrangements—in one test. This breadth matters because minimal residual disease can consist of diverse clones with different mutations, so having a genome-wide view raises the chance of detecting a tumor-specific signal and strengthens confidence in MRD detection. In contrast, a targeted gene panel looks at a fixed set of loci, which means deep coverage for those sites but missing anything outside the panel, limiting breadth. Sanger sequencing is accurate but low-throughput and can only assess a few sites, making it insufficient for broad MRD detection. RNA sequencing focuses on expressed changes and may miss nonexpressed DNA alterations, making it less reliable for capturing residual tumor DNA. Therefore, whole-genome sequencing offers the broadest detection of tumor variants and the greatest potential to enhance MRD sensitivity.

6. How many genes are included in the MyRisk test?

- A. 63 genes**
- B. 50 genes**
- C. 100 genes**
- D. 25 genes**

A broad hereditary cancer panel like MyRisk is designed to detect pathogenic variants across a wide set of genes that contribute to inherited cancer risk. The version most commonly used includes 63 genes, spanning high-penetrance genes such as BRCA1 and BRCA2 and many others involved in breast, ovarian, colorectal, endometrial, pancreatic, and prostate cancer predisposition. This breadth increases the chance of identifying an inherited risk, guides individualized screening and risk-reduction plans, and can influence treatment options in some contexts. Panels are updated over time as new evidence emerges, so the exact gene count can change, but this version reflects a comprehensive scope. The other options would imply panels that are notably smaller or larger than this current comprehensive set, which would miss or overextend the intended gene coverage.

7. Which statement about EOBs is accurate based on the information?

- A. They indicate the amount billed to the patient**
- B. They are a bill**
- C. They are a formal notification of payment**
- D. They are not a bill**

An Explanation of Benefits is a document from the insurer that shows how a submitted claim was processed. It details the amount the insurer allowed, what they paid, and what the patient is responsible for (such as deductible, coinsurance, or copay), along with any reasons for adjustments or denials. It is not a bill from a provider; it doesn't request payment. A separate bill from the provider may come for any charges not covered or remaining balance, but the EOB itself is a summary of benefits and payment decisions. The main point is that EOBs describe how the claim was handled and what's owed, not to bill you directly.

8. In which cancer is MyChoice CDx used?

- A. Breast cancer**
- B. Prostate cancer**
- C. Pancreatic cancer**
- D. Ovarian cancer**

The main idea is how a companion diagnostic like MyChoice CDx is used to identify tumors that may respond to targeted therapy. MyChoice CDx is designed to assess homologous recombination deficiency (HRD) and BRCA1/2 mutation status in tumor tissue. In ovarian cancer—especially high-grade serous cases—HRD is common and predicts sensitivity to PARP inhibitors. Because of this, MyChoice CDx is used to select ovarian cancer patients who are likely to benefit from PARP inhibitor therapy, guiding treatment decisions such as maintenance after platinum-based chemotherapy. While PARP inhibitors are also used in breast, prostate, and pancreatic cancers, those settings rely on different testing approaches (often BRCA1/2 mutation testing or other HRD assessments specific to those contexts). The MyChoice CDx test is specifically aligned with guiding PARP inhibitor use in ovarian cancer.

9. Which Myriad test determines HRD status?

- A. BRACAnalysis**
- B. MyChoice CDx**
- C. OncoVantage**
- D. HRDSense**

HRD status reflects a tumor's deficiency in homologous recombination repair, which makes it more likely to respond to PARP inhibitors. The test designed to determine this status is MyChoice CDx, as it specifically assesses tumor genomic instability to produce an HRD score (beyond just BRCA gene status) and is used as a companion diagnostic to guide PARP inhibitor therapy. The BRACAnalysis test looks for inherited BRCA1/2 mutations and does not measure tumor HRD. The other tests mentioned are not the standard HRD-determining assay in clinical use. So, the test that determines HRD status is MyChoice CDx.

10. What sample type is required for MRD monitoring tests?

- A. Tumor tissue
- B. Blood only**
- C. Saliva
- D. Urine

MRD monitoring requires a sample that accurately reflects residual cancer burden and can be collected repeatedly. Peripheral blood is the standard because it is easy to obtain with serial draws and often contains detectable cancer cells or tumor-derived DNA for many hematologic malignancies, allowing highly sensitive tests to track disease over time. While some diseases may use bone marrow for greater sensitivity, blood provides a practical and reliable basis for ongoing MRD assessment. Tissue (tumor), saliva, and urine generally do not reliably reflect systemic MRD in these settings and are not used for routine MRD monitoring.

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Next Steps

Congratulations on reaching the final section of this guide. You've taken a meaningful step toward passing your certification exam and advancing your career.

As you continue preparing, remember that consistent practice, review, and self-reflection are key to success. Make time to revisit difficult topics, simulate exam conditions, and track your progress along the way.

If you need help, have suggestions, or want to share feedback, we'd love to hear from you. Reach out to our team at hello@examzify.com.

Or visit your dedicated course page for more study tools and resources:

<https://hereditarycancerrisktreatmentstrat.examzify.com>

We wish you the very best on your exam journey. You've got this!

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