

RTMS Article 37, October 2015 Microarray Techniques to Analyze Copy-Number Alterations in Genomic DNA: Array Comparative Genomic Hybridization and Single-Nucleotide Polymorphism Array

QUESTIONS

- 1. Comparative genomic hybridization is a tool that is suited to**

 - Detect copy-number alterations.
 - Detect translocations.
 - Give information about gene expression.
- 2. A genomic array-CGH profile without any detectable alteration indicates**

 - The lack of tumor cells.
 - Copy number—neutral LOH.
 - Balanced rearrangements.
 - Probe density that is too low.
- 3. Array CGH is preferably performed using DNA obtained from**

 - Frozen tissue with low tumor content.
 - Paraffin-embedded tissue with low tumor content.
 - Frozen tissue with high tumor content.
 - Paraffin-embedded tissue with high tumor content.
- 4. Major advances in array approaches do *not* include the following:**

 - Multiple genetic loci are investigated in one experiment.
 - A wide dynamic range in copy-number estimation allows for detection of gains and losses.
 - Array CGH can be performed on heterogeneous cell populations.
 - Information on spatial organization of the involved chromosomes.
- 5. The resolution for the detection of copy-number alterations depends largely on**

 - The probe density on a chip.
 - The software that is used.
 - The DNA quality of the samples.
 - The amount of available sample DNA.

ANSWERS

- A.
- A.
- C.
- D.
- A.