Agilent CytoGenomics Software

Learn how to analyze chromosomal microarray data from blood, single cell, hematological and solid tumor samples

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Agenda

1. Introduction

2. Live analysis of microarray data in CytoGenomics software:

- Blood
- Hematological tumor sample
- FFPE tumor sample
- Single cell

3. Q&A

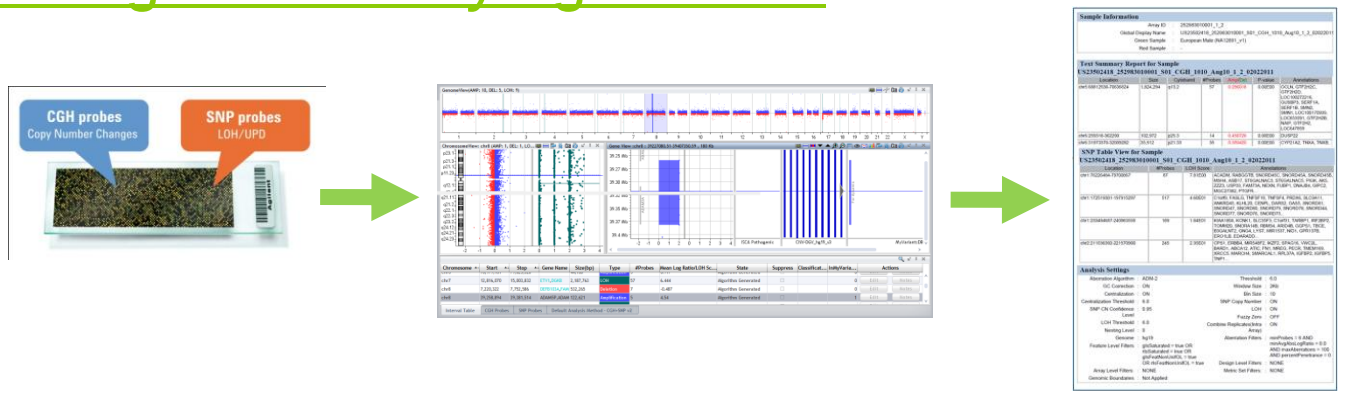
What is CytoGenomics?

INTRODUCTION

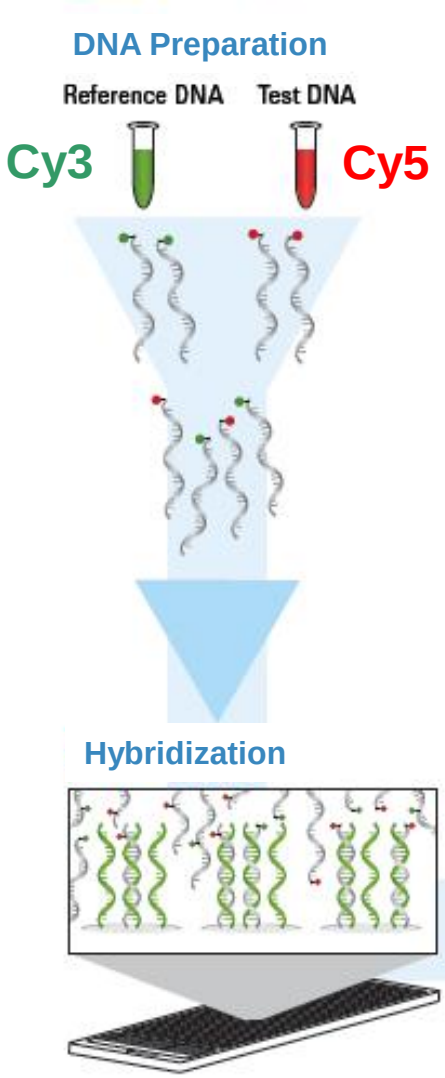
Agilent CytoGenomics Software

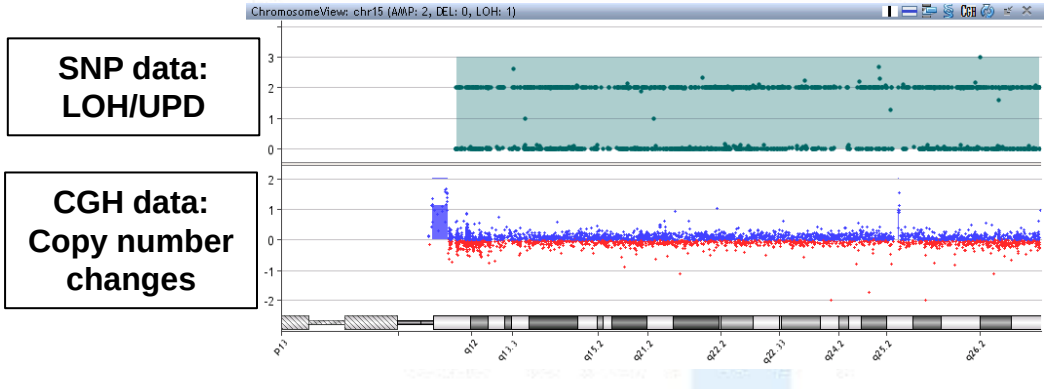
Analyze, monitor, review all your samples in a few steps

- Workflow-based analysis tool for CGH and CGH+SNP microarray analysis
- Powerful algorithms: Accurate copy-number & LOH calls
- Designed specifically for cytogenetic research
- Available at no charge to all Agilent microarray customers
  www.agilent.com/cytogenomics



CGH+SNP wet lab and analysis workflow



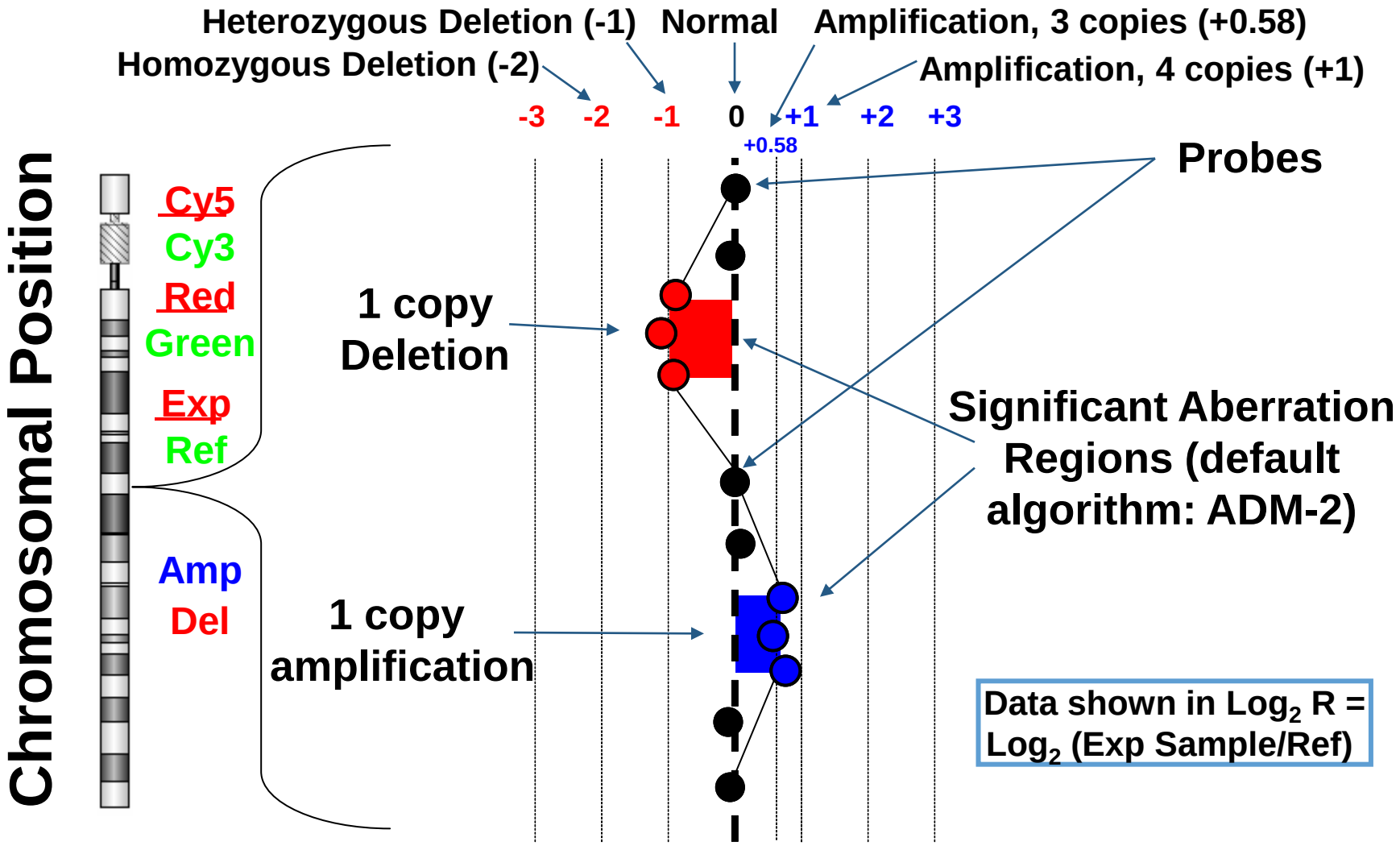


Data Analysis

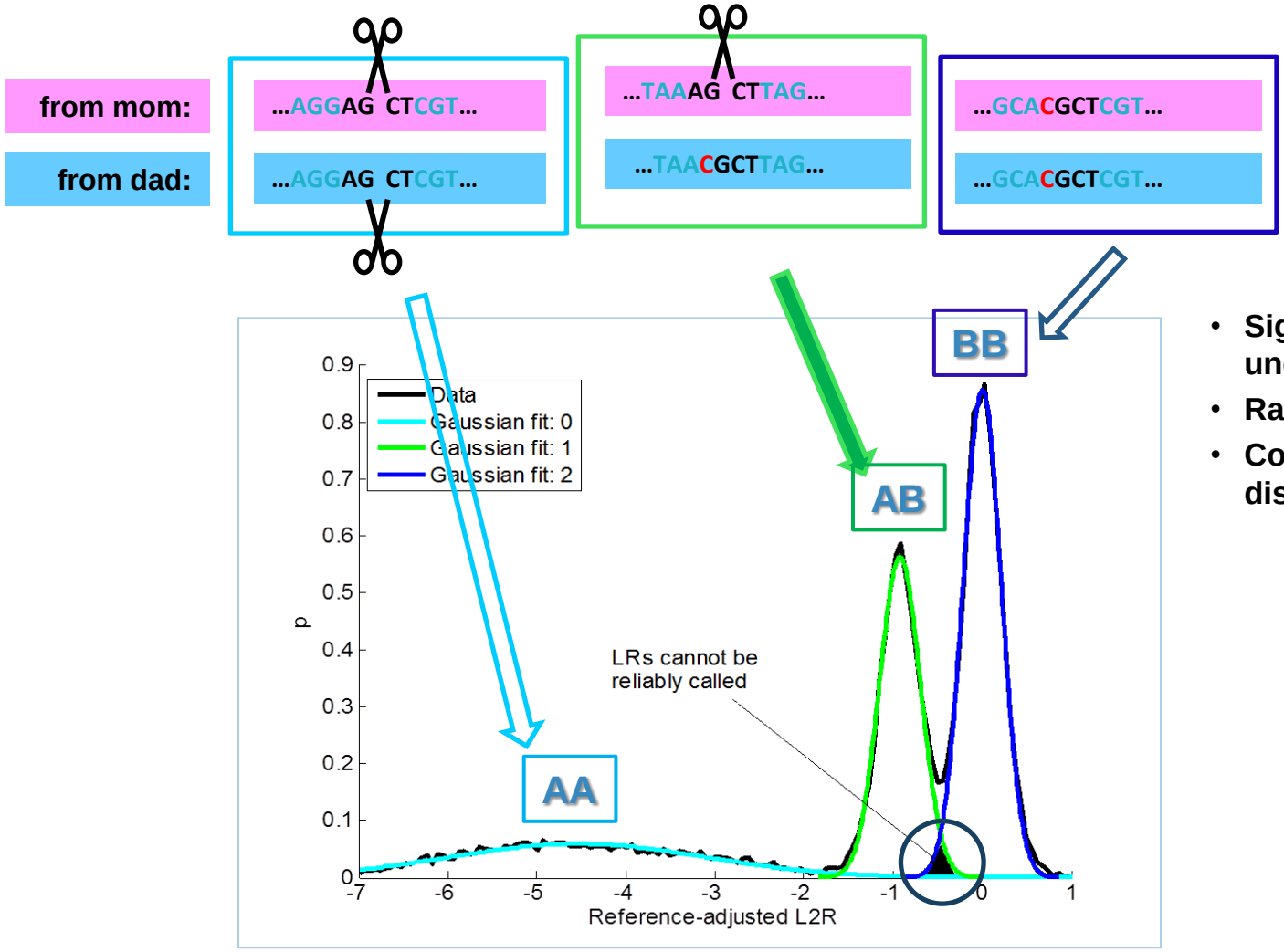
Scanning

Software

Schematic view of CGH data output



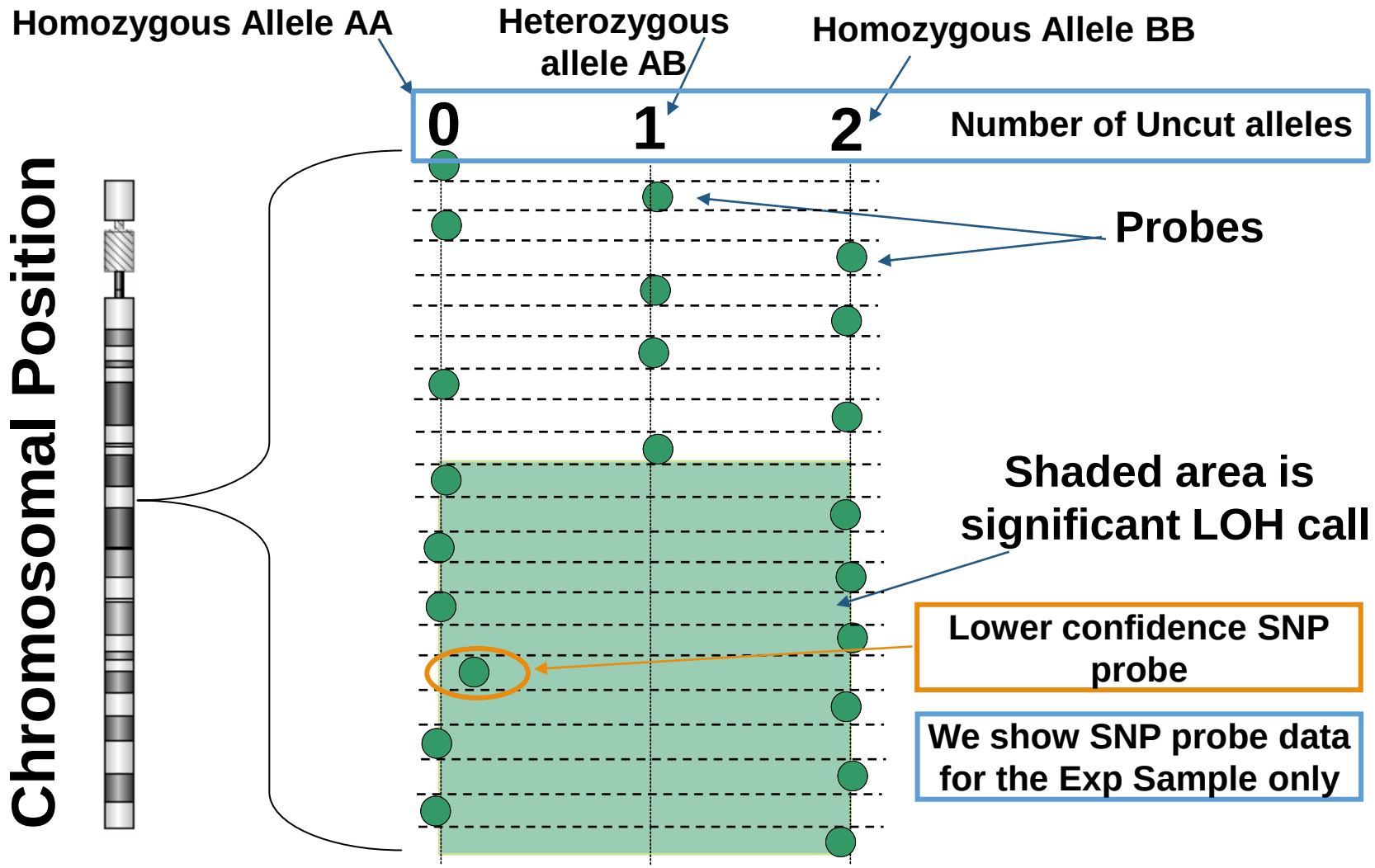
Mechanism of Agilent SNP Probes



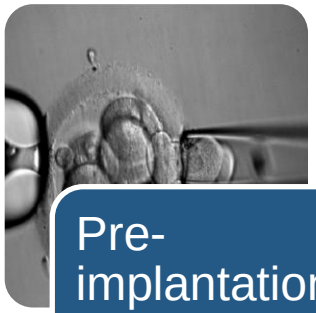
***AluI* cuts: AGCT**

- **Signal measures copies of uncut allele**
- **Raw SNP data: black curve**
- **Colored Gaussians: fits to distributions**

Schematic view of SNP data output



Clinical research on different sample types using SurePrint CGH microarrays and CytoGenomics



Pre-implantation

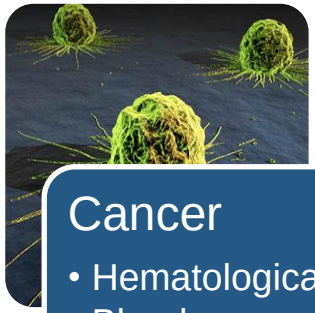
- One-two cells
- Parental samples

Pre-natal

- Amniotic Fluid
- Chorionic Villi
- Products of Conception

Post-natal

- Blood
- Saliva



Cancer

- Hematological
- Blood
- Bone marrow
- Solid tumor:
  - Frozen
  - FFPE

CYTOGENOMICS LIVE DEMO

CGH math: We measure the difference between 1 sample and 1 reference DNA, usually expressed as log(2) (Sample/reference). Actual data are slightly compressed from ideal values.

Description	Average Sample CN	Ref CN	Ratio (S/R)	Ideal Log2(Ratio)	Actual data
Diploid	**2**	**2**	1	0	0
Deletion	**1**	**2**	0.5	-1	-0.9
Trisomy	**3**	**2**	1.5	+0.58	+0.53
50% mosaic deletion	**1.5**	**2**	0.75	-0.41	-0.37
50% mosaic trisomy	**2.5**	**2**	1.25	+0.32	+0.29
20% mosaic deletion	**1.8**	**2**	0.9	-0.15	-0.13

Questions