OncoScan™ FFPE Express 2.0 Performance Data

OncoScan FFPE Express was developed specifically for FFPE sample analysis

Copy number, allelic ratio, and somatic mutation data in one experiment

FFPE challenges	OncoScan benefits
Short DNA fragments	Small binding footprint of 40 bp
Low DNA yields	Arrays accommodate DNA inputs as low as 75 ng
Old, degraded samples	Oldest successful samples to date: 28 years old
Variable fixing/collection methods	Success with thousands of samples from many different labs and sources
Genomic complexity	Three types of data, unparalleled data quality, and broadest linear dynamic range

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OncoScan FFPE Express 2.0 offers whole-genome, high-resolution coverage

Specifications – 300K MIP Copy Number	
Total number of copy number markers	334,183
Number of non-polymorphic markers	50,477
Intragenic markers	176,318
Intergenic markers	157,865
Median marker spacing	**Base pairs**
Intragenic	2,787
Whole-genome backbone	8,974

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OncoScan™ FFPE Express 2.0:
Excellent sample pass rates

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Excellent pass rates with FFPE samples from various study collections

	Tissues tested	Number submitted samples	Number passing samples	Sample success rate
Collaborator 1	Breast	42	42	**100%**
Collaborator 2	Bone marrow, Ewing's sarcoma, brain	77	74	**96%**
Collaborator 3	Breast, colon, brain	1,320	1,215	**92%**
Total		**1,439**	**1331**	**92%**

Robust performance across multiple tissue types

- 98 FFPE samples, 7 different collections
  - Breast cancer, invasive breast cancer, liver primary, liver metastases, colorectal, bladder, kidney
  - Age of samples: 1-28 yrs
  - Included 38 with matched fresh frozen samples

Performance parameter	Result
FFPE sample pass rate	88%
FF sample pass rate	100%
Genotype concordance – FFPE vs. FF	99.9%

Wang *et al*., *BMC Medical Genomics* 2009, 2:8

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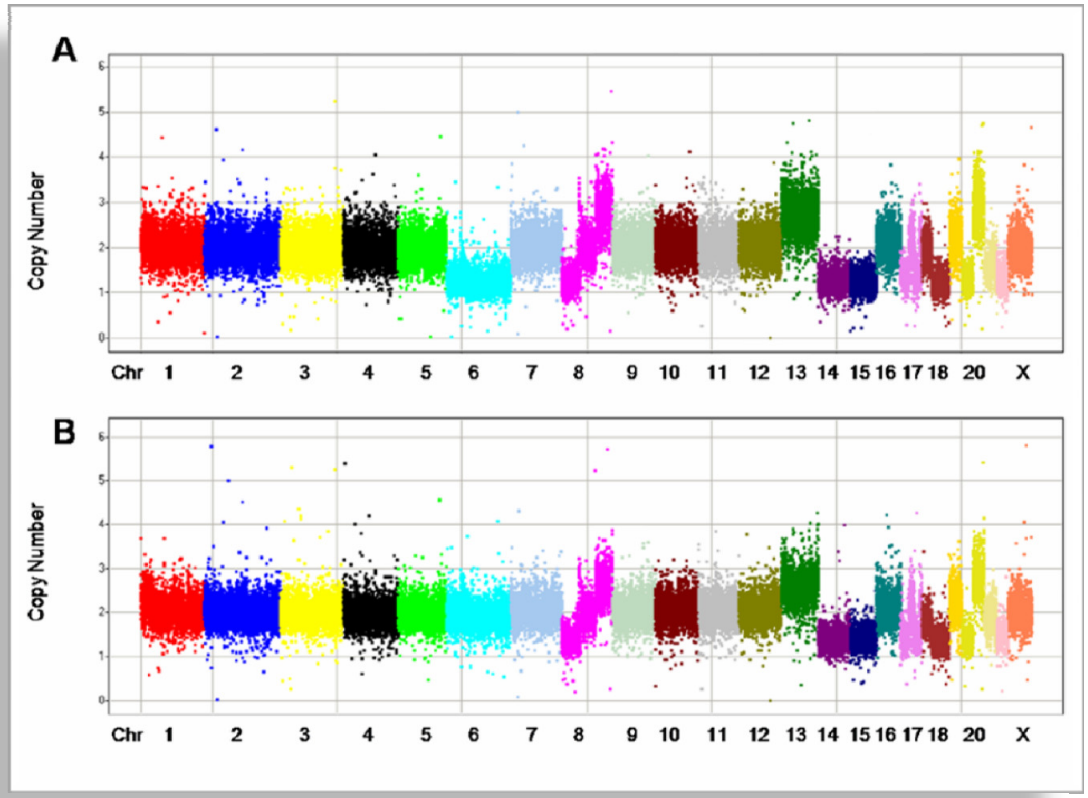
Consistent copy number from fresh frozen to FFPE sample



Copy number in matched FFPE (A) and fresh frozen (B) samples

Wang *et al.*, *BMC Medical Genomics* 2009, 2:8

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OncoScan™ FFPE Express 2.0:
Linear dynamic range and high resolution

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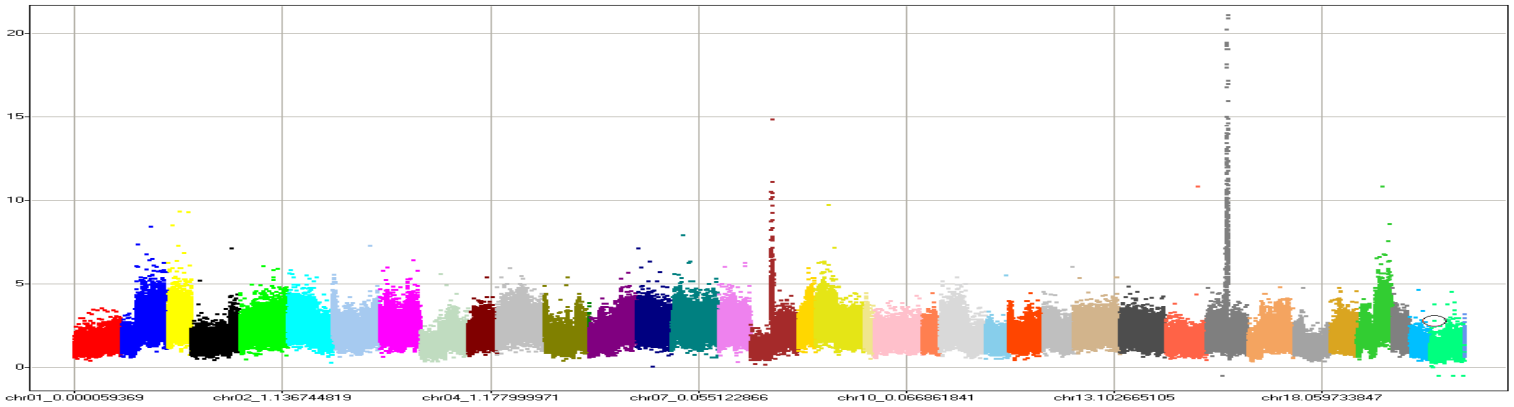
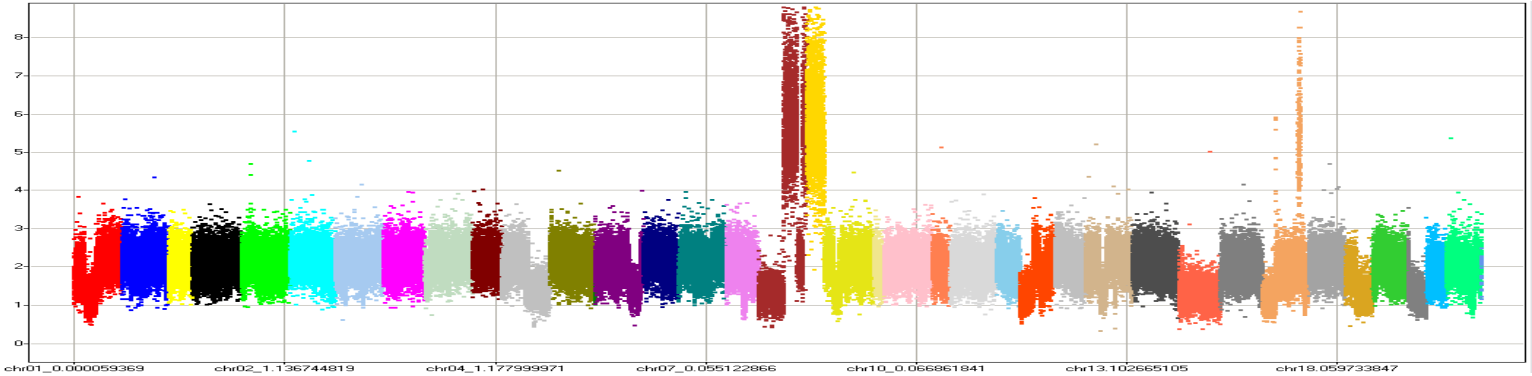
Robust copy number performance and dynamic range

FFPE liver tumor: CN>20



FFPE kidney tumor: CN>10



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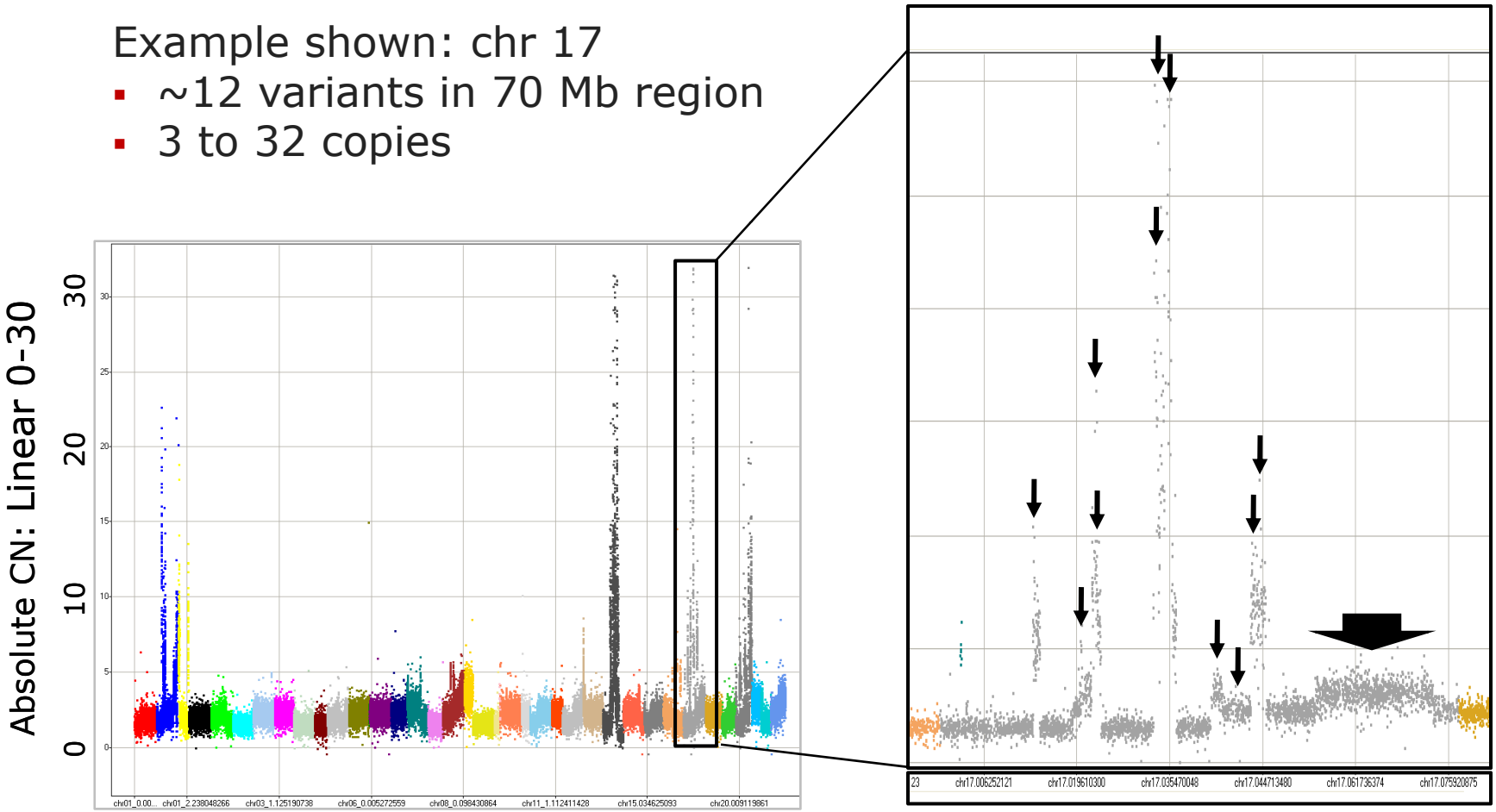
Linear dynamic range and high resolution enable deep analysis of cancer complexity

Precise breakpoint mapping – 334,000 whole-genome markers
Accurate view of gains/losses – dynamic range up to 60 copies

Example shown: chr 17

- ~12 variants in 70 Mb region
- 3 to 32 copies



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OncoScan™ FFPE Express 2.0:
Allelic ratio reveals copy-neutral loss of heterozygosity

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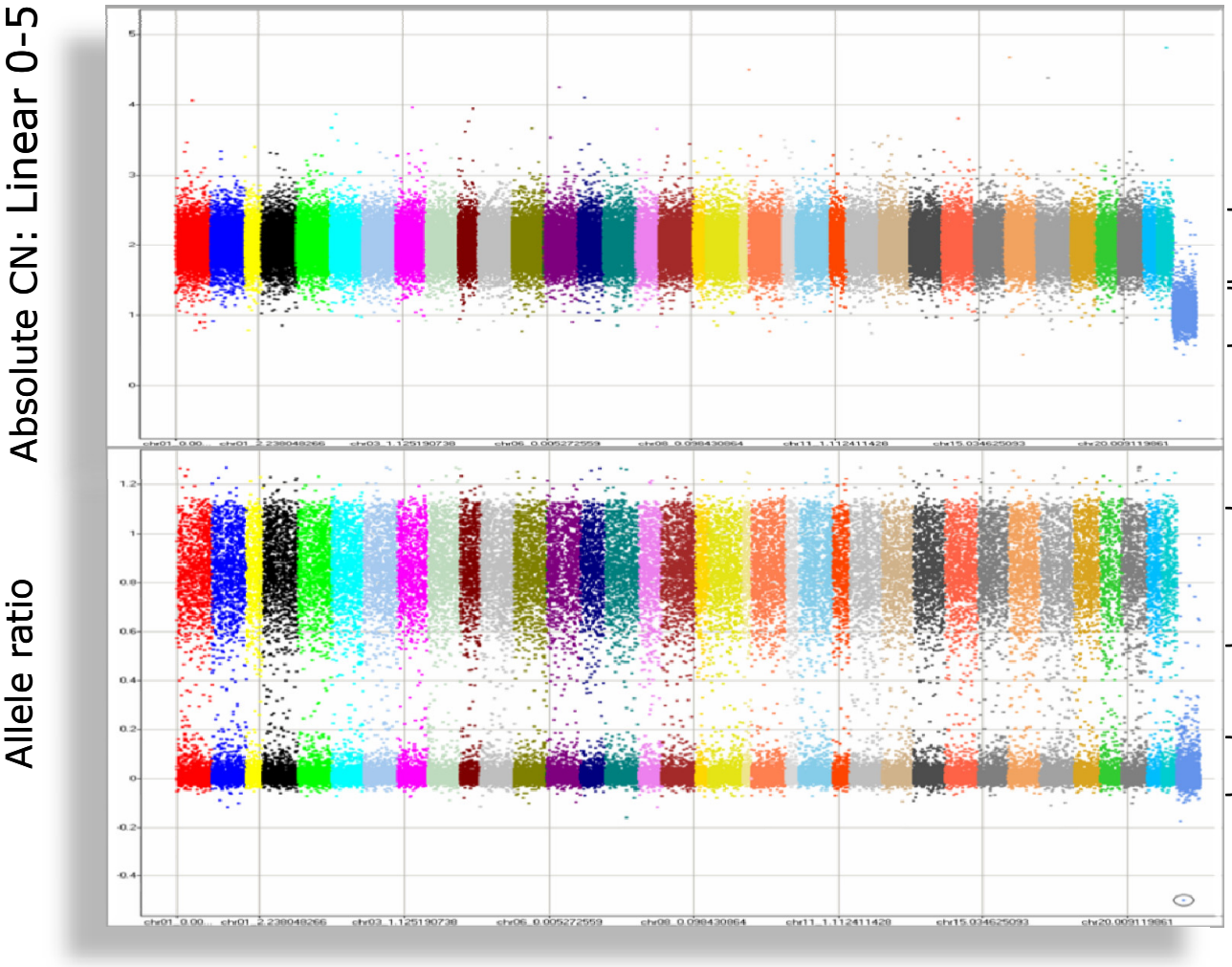
Allelic ratio data are simple to visualize

Normal diploid sample – whole-genome data across 330K markers:

Aligned data showing typical representation of allelic ratio



Copy number data

2 copies

1 copy

Allelic ratio data

Heterozygote markers (AB or BA)

Homozygote markers (AA or BB)

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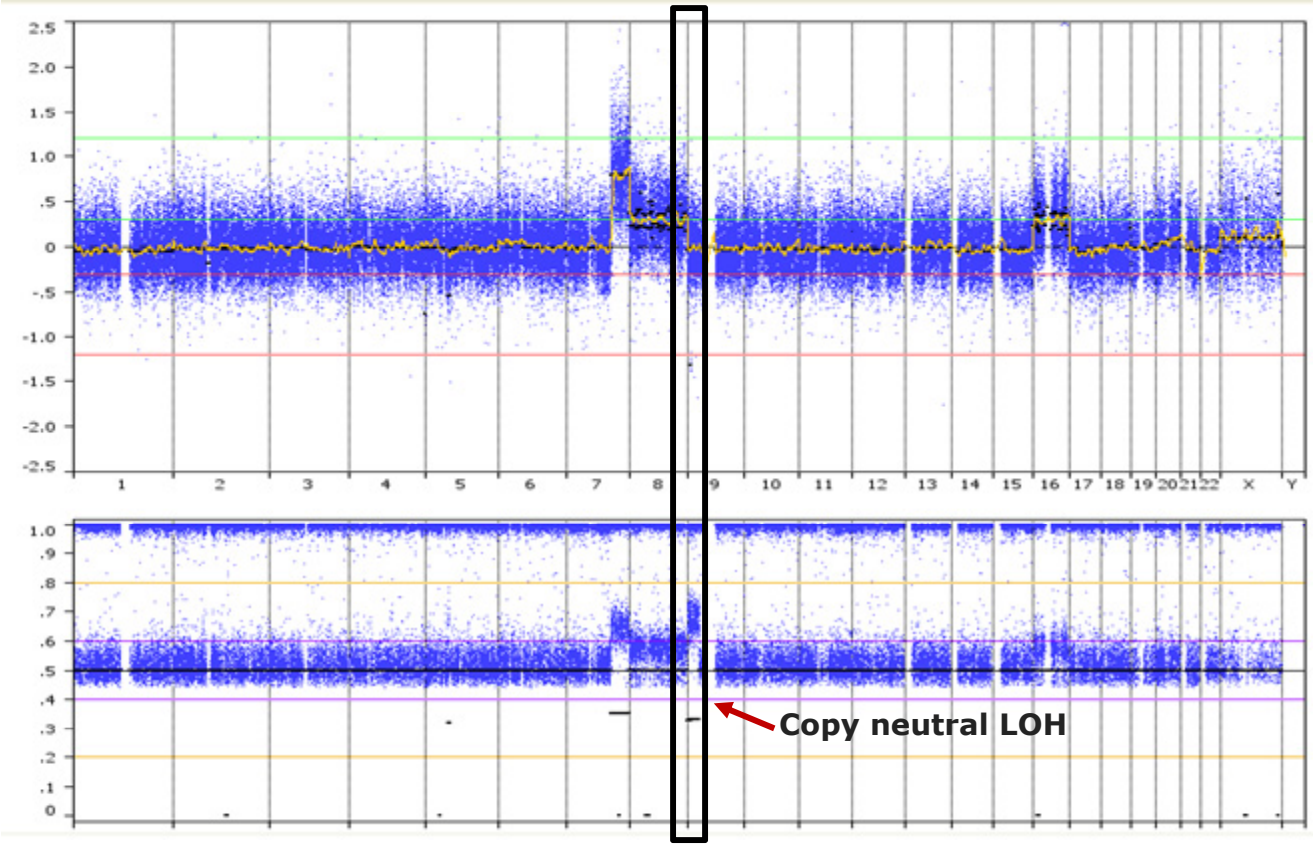
Allelic ratio reveals copy-neutral aberrations

Importance of allelic ratio information

- Allelic ratio information shows that both copies are from the same allele, leading to an increase in mutation susceptibility
- SNP information identifies which allele (and haplotype) is deleted or amplified

Stromal contamination: copy number measurements along with allelic information can help identify levels of stromal cell contamination and lead to a better interpretation of copy number information



Detection of loss of heterozygosity

Copy number data indicate a diploid genome, which looks identical to a normal sample.

Allelic ratio reveals copy-neutral **loss of heterozygosity** on chr 9.

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OncoScan™ FFPE Express 2.0
Somatic mutations

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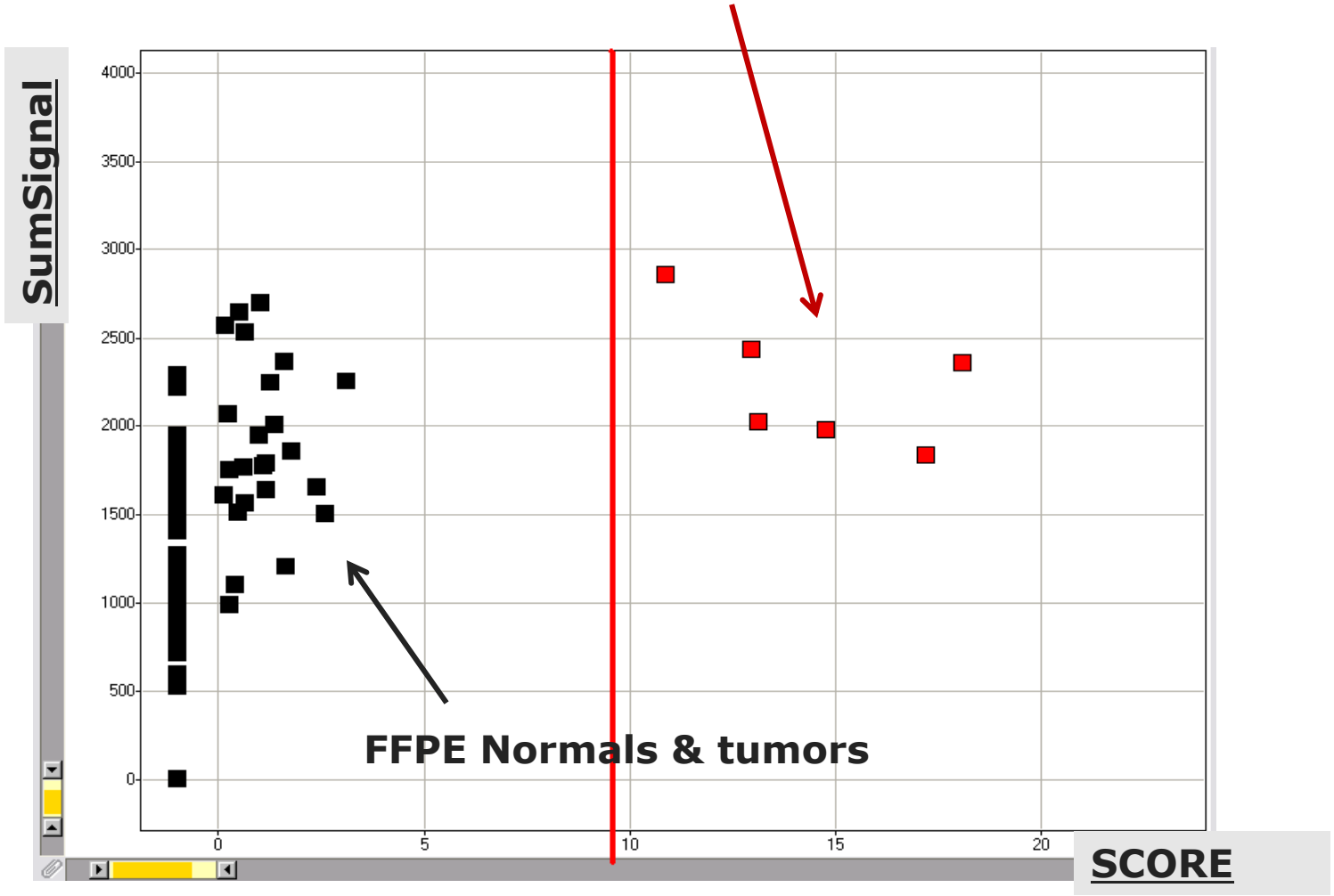
Somatic mutations

- Probes for more than 400 somatic mutations have been shown to give tight clusters for the wild type allele, including:
  - KRAS, PIK3CA, TP53, APC, BRAF, CDH1, CTNNB1, MLH1, MSH2, SMAD4, TGFBR2

- Validation of somatic mutation is ongoing
  - Assess in cell lines when available
  - Enabling a mutation spike-in method that will allow us to demonstrate appropriate signal from mutant allele and also assess lower limit of detection of mutant allele in heterogeneous mixtures

TP 53 somatic mutation highly reproducible in a FFPE kidney tumor sample



TP53_pR273H_c818G_A, mutation called in 6/6 samples
Score: 11 - 18

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OncoScan™ FFPE Express somatic mutation probe performance

- Genotyping accuracy: **99.0%**
  - Comparison with >200K HapMap SNPs
- Copy number reproducibility: **>98.0%**
  - As measured by allelic copy number
- Call rate in FFPE samples: **96.6%**
- Extensive copy number probe coverage in approximately 180 oncogenes and tumor suppressor genes

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OncoScan™ FFPE Express 2.0

Unlock the potential inside your FFPE samples

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OncoScan™ FFPE Express 2.0

- OncoScan FFPE Express
  - Proven best-in-class performance in small archived FFPE samples (up to 28 years)
  - A single test that measures copy number, genotypes, and somatic mutation data in integrated analysis
- An important tool in clinical research that will aid treatment selection
  - Enables statistically powered discovery using large retrospective data sets
  - Prospective trials begin with a clear understanding of a target population
- Developed in conjunction with leading cancer centers:
  - M.D. Anderson Cancer Center, UCSF, Huntsman Cancer Institute

For research use only.
Not for use in diagnostic procedures.

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To maximize cancer discoveries from your FFPE collections

- Email or phone your local account manager
- Contact your local Affymetrix office
  - Select "Contact Us" in the "About Affymetrix" menu at www.affymetrix.com
- Complete the form at www.affymetrix.com/oncoscan
  - Click on "Download Performance Data"

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