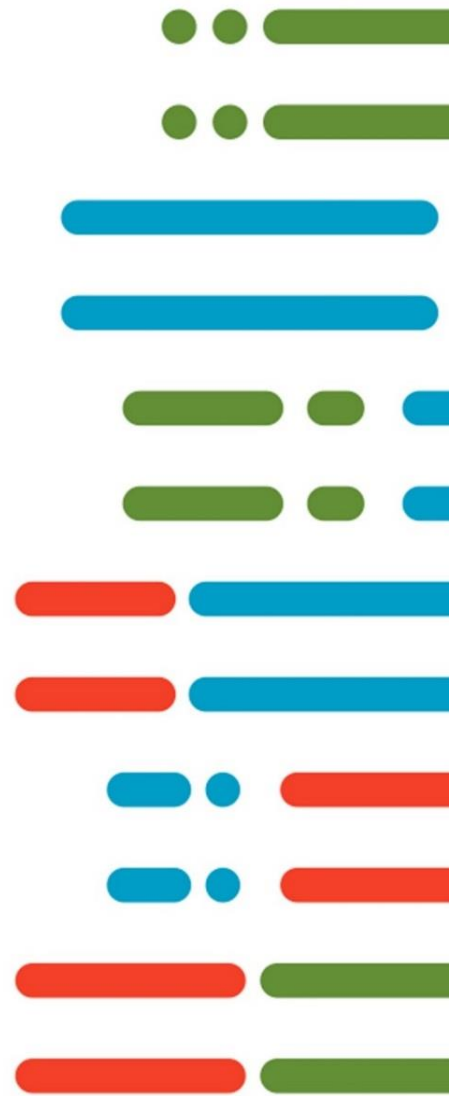


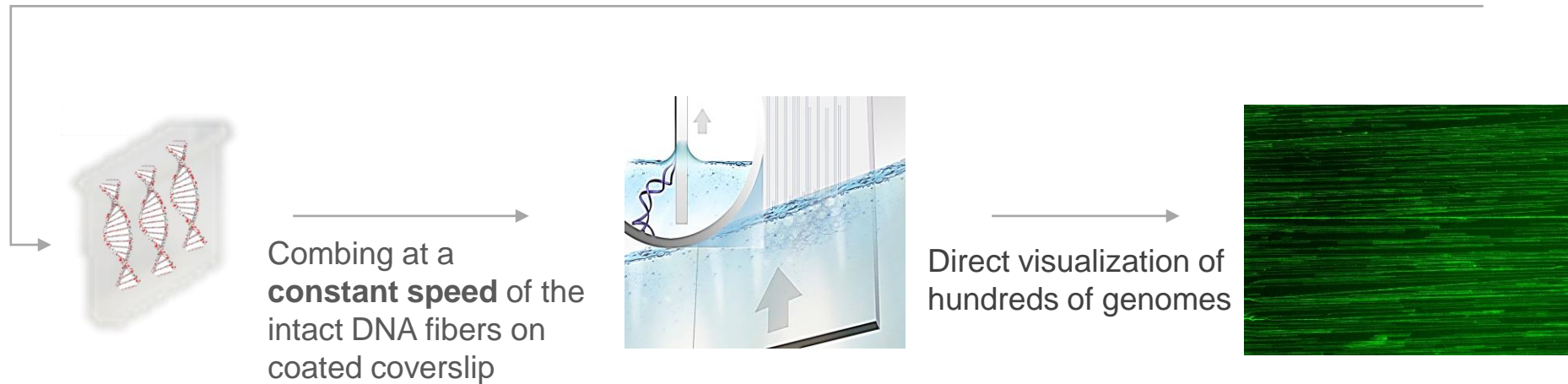
# Molecular Combing Technology: digital and unbiased quantification of rearrangements resulting from targeted genome editing



Alex Simon  
April 24<sup>th</sup>, 2018  
NIST-FDA Genome Editing Workshop

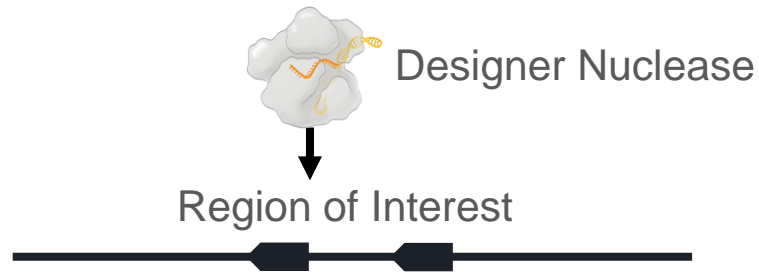


# The Molecular Combing Technique



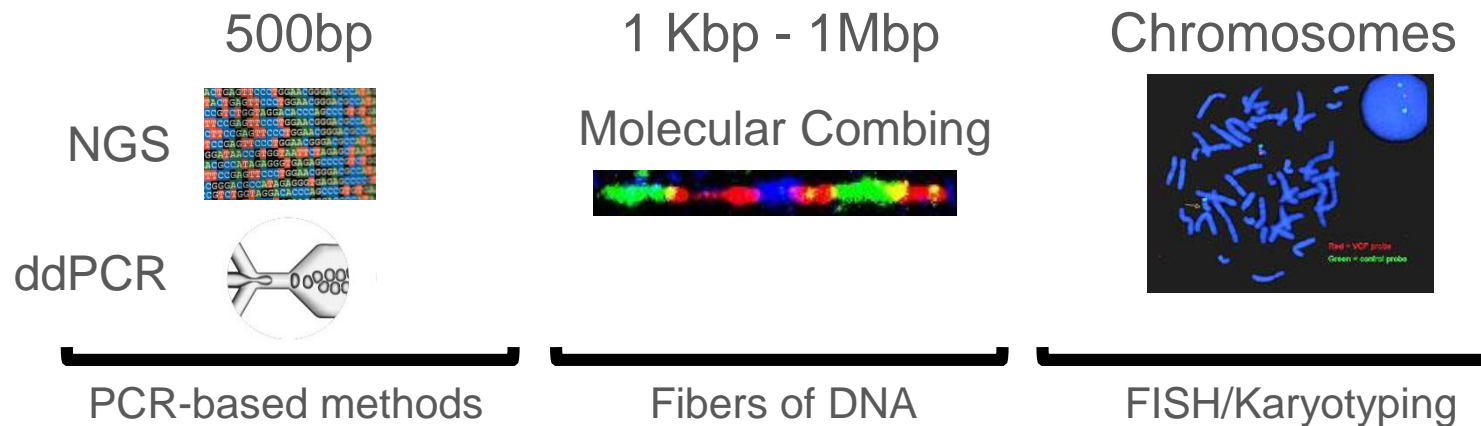
- ⇒ **Direct visualization** and analysis of single DNA molecules, without amplification
- ⇒ **150-200 human genomes** stretched on each coverslip
- ⇒ **Accurate measurement** of distances with a constant stretching factor ( $1\mu\text{m} = 2\text{kbp}$ )

# Molecular Combing: Range of Use



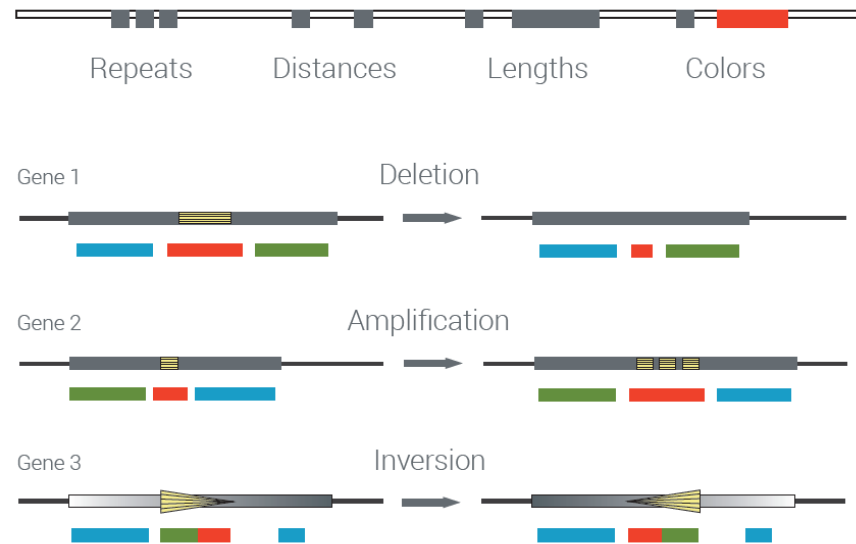
## Detection and Quantitation of Modifications

Resolution



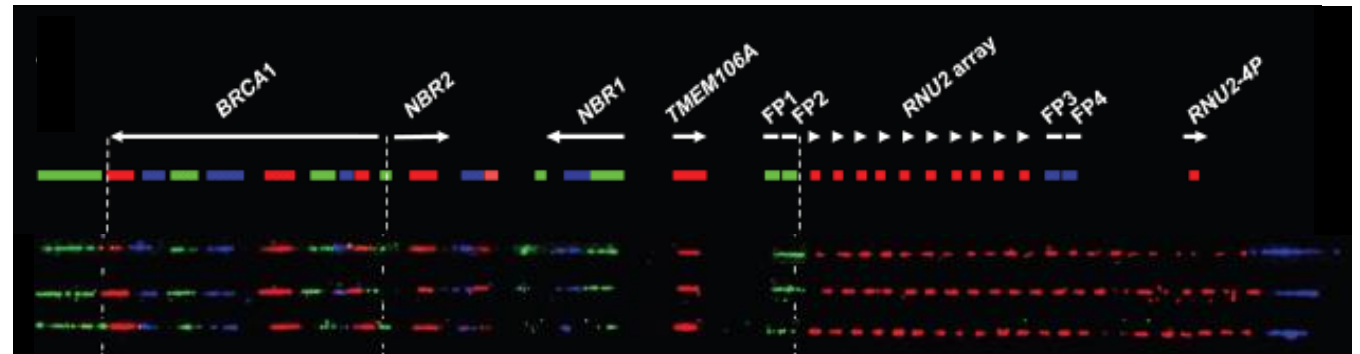
# The Genomic Morse Code (GMC)

## FiberProbes

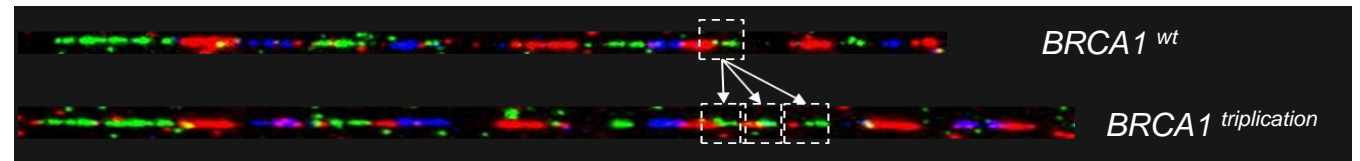


Changes in GMC pattern directly indicate structural variations with no ambiguity

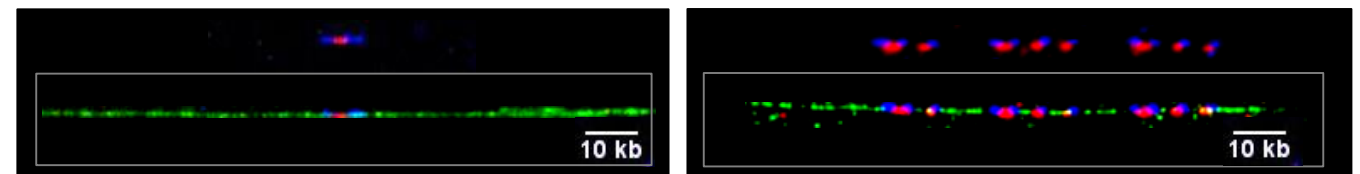
- Probes: 1 kb to 1000+ kb
- **Precision ~3 kb**
- Possible multiplexing



Sizing of RNU2 array CNV associated to BRCA1 gene



Triplication of 16kbp within the BRCA1 gene – ambiguous detection with CGH & MLPA



HPV16 genome integration (red and blue probes) into human host DNA (green line)

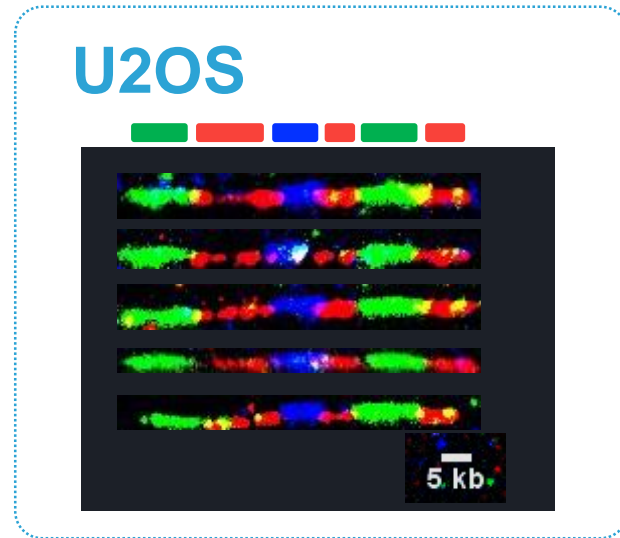
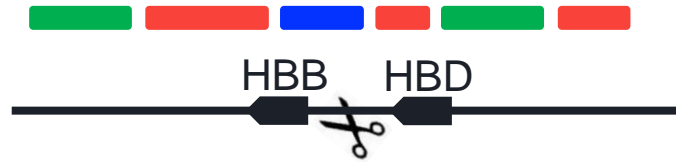
# The FiberVision<sup>®</sup> Molecular Combing Platform

From DNA purification to Data Output  
The platform offers a complete and flexible workflow

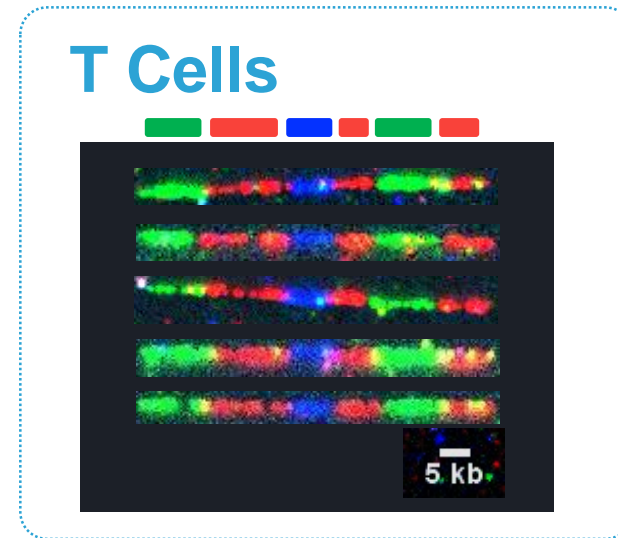


# Quantitation of Non-Canonical Signals After Editing\*

High frequency editing with a RNP (RiboNucleoProtein) in U2OS and T cells:



**96.5% of canonical signal**



**98.7 % of canonical signal**

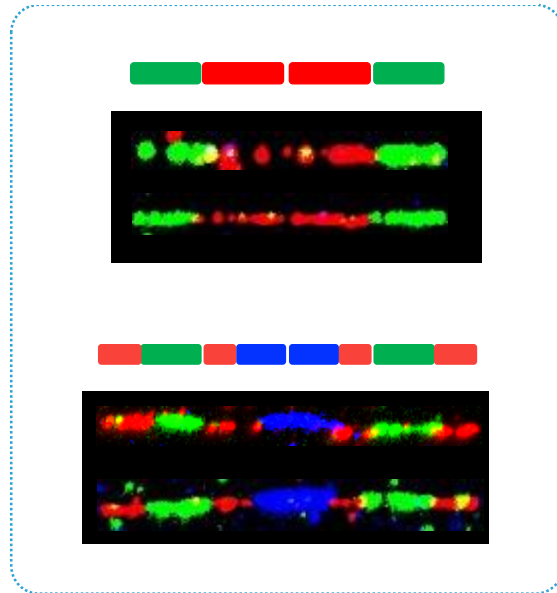
- Vast majority of signals are canonical, suggesting no large scale rearrangements
- Small percentage of signals are non-canonical

# Quantitation of Non-Canonical Signals After Editing\*



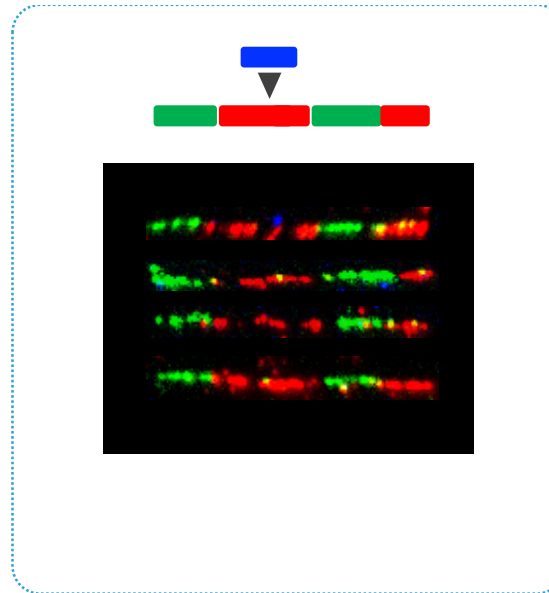
Canonical signal

**Symmetrical:  
Same chromosome  
translocations**



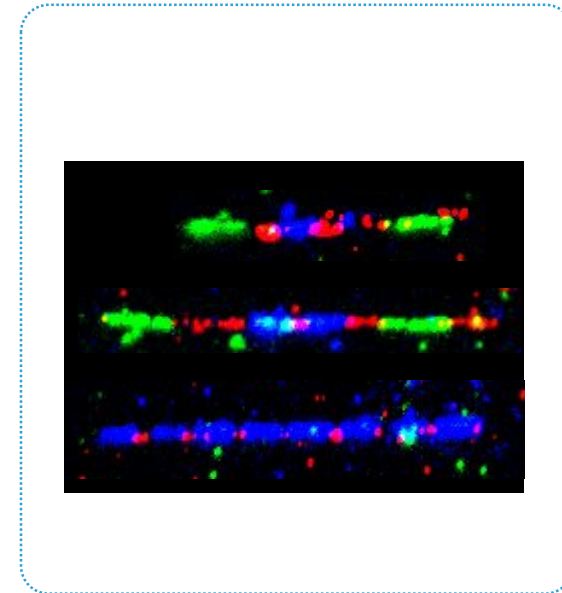
Challenging to detect by  
NGS/PCR-based strategy  
due to structural complexity

**Loss of Blue Probe:  
Single Strand  
Annealing**



Challenging to detect by  
NGS/PCR-based strategy  
due to size and unknown  
extent of rearrangement

**Others:  
Unknown  
Mechanism**



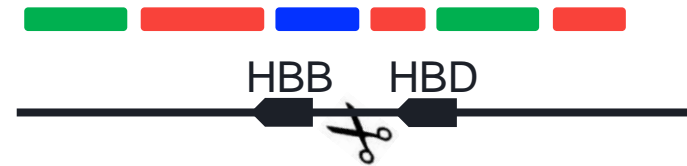
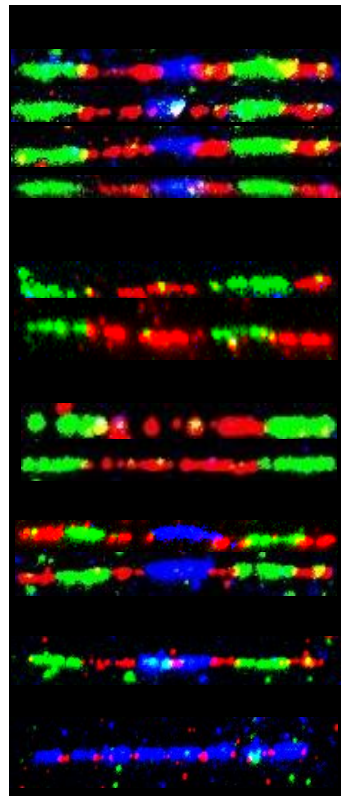
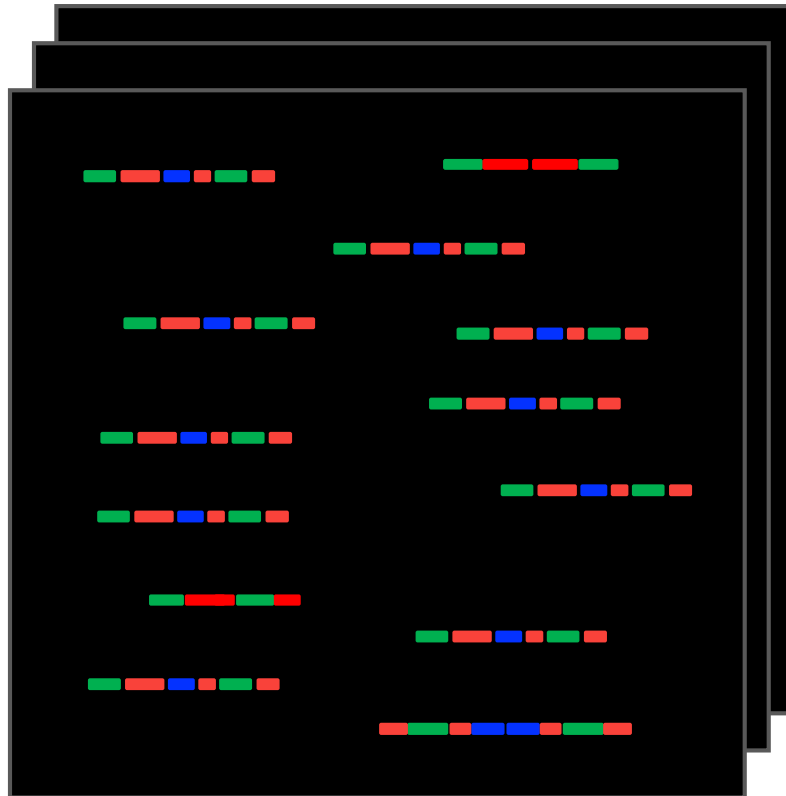
Not detectable by  
NGS/PCR-based strategy  
due to unexpected nature of  
events

\*Cecilia Cotta-Ramusino et al., CSHL Meeting: Genome Engineering: The CRISPR-Cas9 Revolution, July 21-23, 2017.

# Quantitation of Non-Canonical Signals After Editing\*

High frequency editing with RNP in T cells:  
Comprehensive detection and quantitation of rearrangements

> 150x HG equivalents per slide  
10 slides per sample



Classification	Frequency	Interpretation
	98.7%	Canonical Signal
	0.3%	Single Strand Annealing
	0.2%	Same Chr Translocation
	0.2%	Same Chr Translocation
	0.4%	Unknown
	0.2%	Unknown

\*Cecilia Cotta-Ramusino et al., CSHL Meeting: Genome Engineering: The CRISPR-Cas9 Revolution, July 21-23, 2017.



# Concluding Remarks

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## Molecular Combing's Value for Specificity Measurements:

- ⇒ **Sensitive** : >150x coverage per slide; 1500x per sample (~0.25% sensitivity); can be increased
- ⇒ **Digital Quantitation** : single-molecule counting of ROI signals
- ⇒ **Unbiased by Complex Patterns & Translocations** : visual, direct detection
  
- ⇒ **Technical Advantages:**
  - Multiple cell input types
  - No amplification bias
  - Highly complementary to NGS/PCR based assays
  
- ⇒ **Currently working with Genome Editing Biopharmas**
- ⇒ **Platform ready for translation in Process Development**
- ⇒ **Future potential as a QC assay in Manufacturing**