



# Use of the Applied Biosystems™ Axiom™ and Eureka™ genotyping platforms to fill a gap in low to medium-density genotyping

PAG 2019  
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Classification: PUBLIC

# Key R&D centers across the world



Clinton  
US



Greensboro  
US



Research  
Triangle Park,  
US



Jealott's Hill  
UK



Ghent  
Belgium



Enkhuizen  
Netherlands



Bad  
Salzuflen  
Germany



Stein  
Switzerland



Stanton  
US



Slater  
US



Woodland  
US

Over 100 R&D sites  
around the world  
supported by many field  
locations



Beijing  
China



Goa  
India



Uberlândia  
Brazil

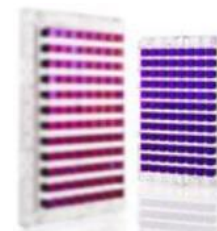
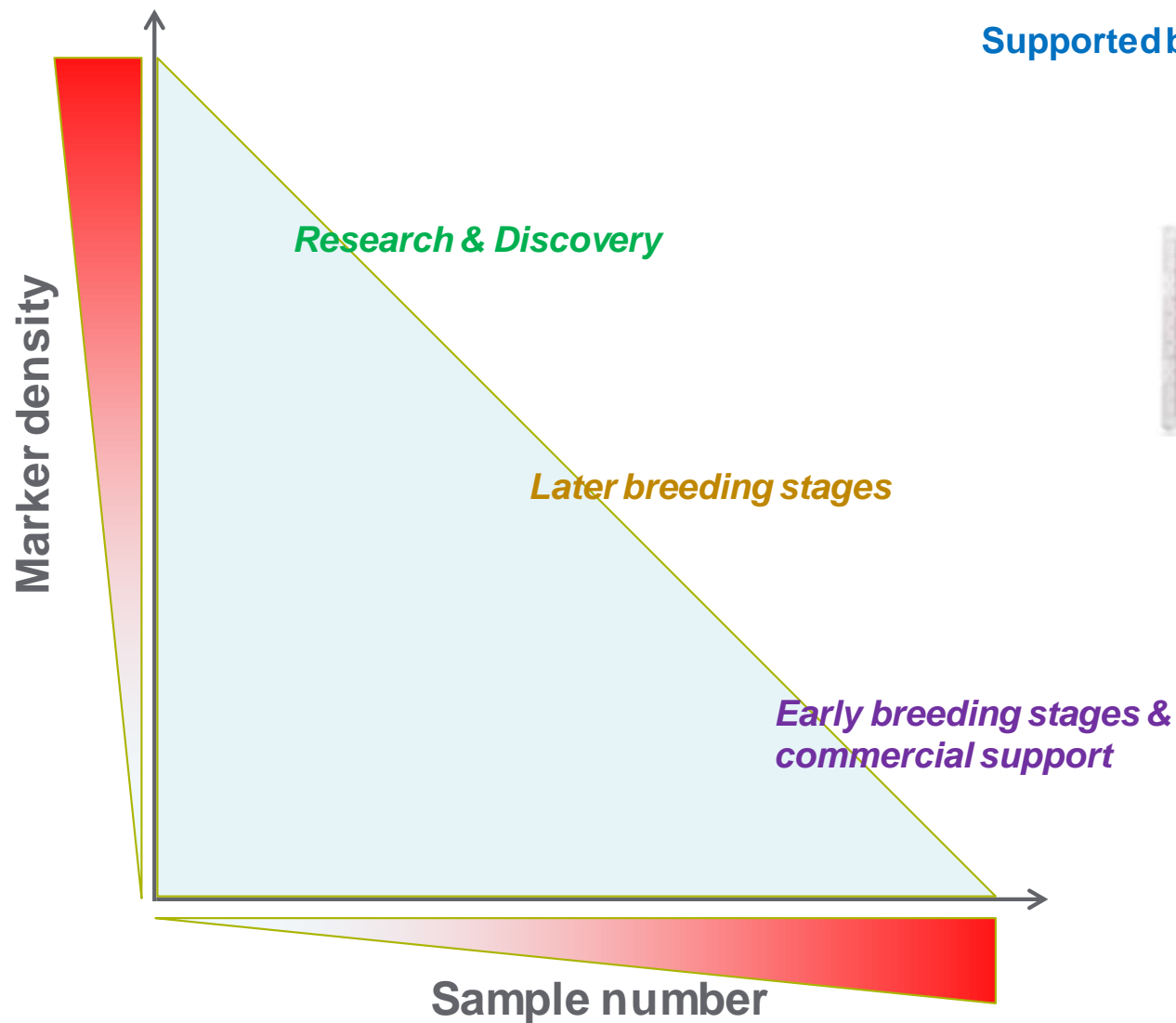


Saint Sauveur  
France



# Genotypic data are used across Syngenta R&D

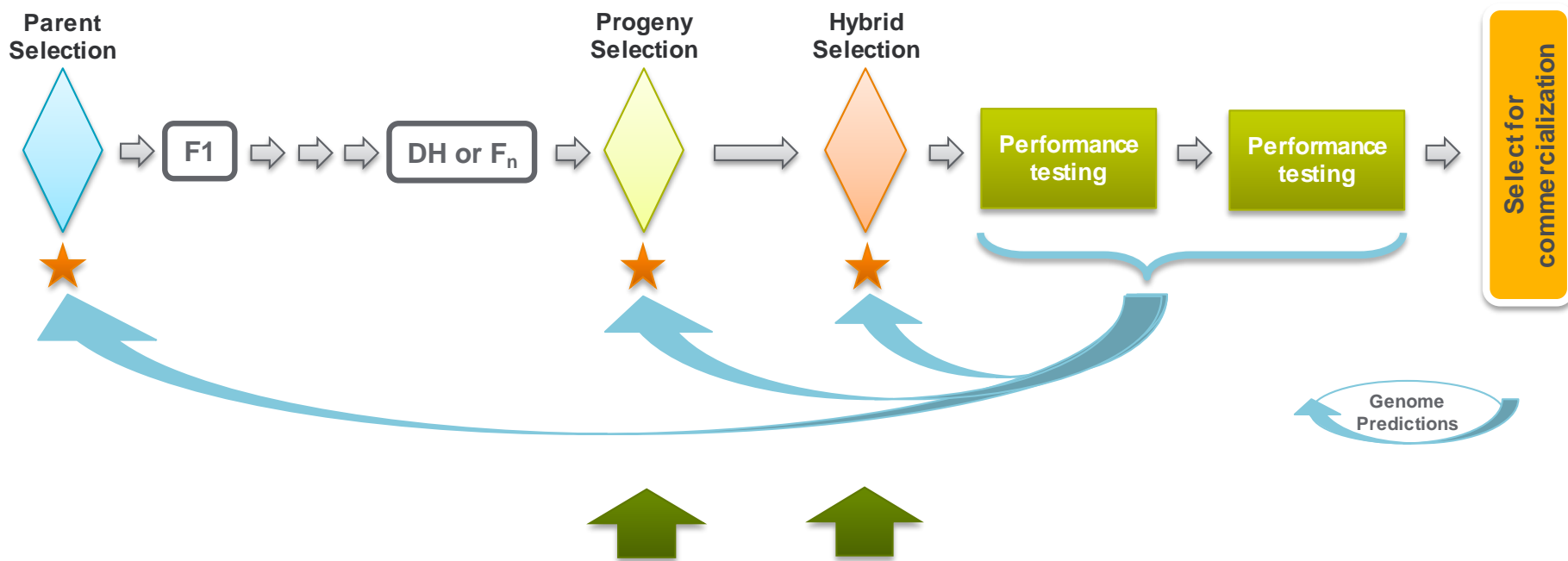
Supported by an array of technologies



# Molecular Breeding at Syngenta

Population creation and inbred *per-se* selection

Performance selection



**Need: A cost-effective, medium-density option for genome-wide fingerprinting**

# Need: a lost cost, fast-turn around option for low-density marker panels

## Rapid, low-plex genotyping of wheat and other cereals

J. D. Curry, V. Joshi, Q. Wan, H. Koshinsky  
Affymetrix, Inc., Santa Clara, CA



### Introduction

Eureka™ Genotyping Solution has utility in plant breeding and regulatory

Cluster plots of two loci produced with Eureka Genotyping Solution in *Hordeum vulgare* (barley) and a 400+-plex genotyping panel

## Application of analysis tools from Affymetrix on Eureka™ Genotyping Solution to provide accurate and automated animal and crop genotypes

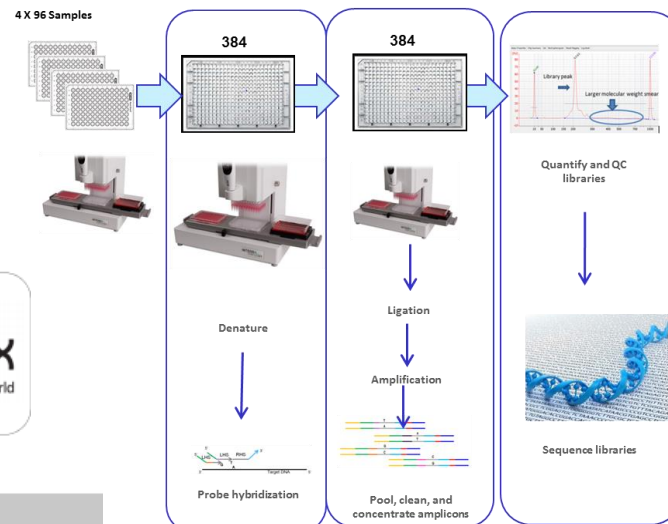
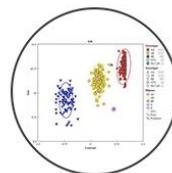
S. N. Malakshah, V. Joshi, A. Pirani  
Affymetrix, Inc., Santa Clara, CA 95051



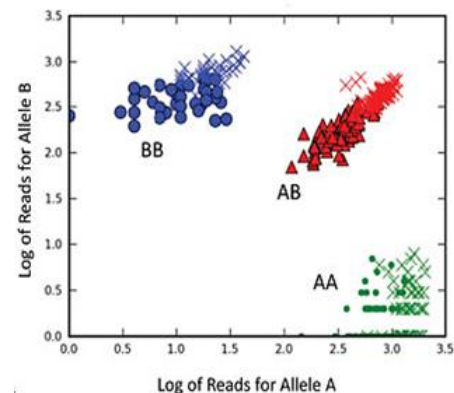
### Benefits

Genotype any species, genome size, or ploidy level with your own proprietary markers or markers from recent sequencing initiatives on the fully customizable Eureka genotyping platform.

- **Rapid:** Two-day workflow goes from extracted DNA to genotypes for thousands of samples per week.
- **Targeted:** The custom design process and assay workflow ensures that all informative loci are targeted across all samples and across all manufacturing batches.
- **Flexible:** Eureka genotyping panels can easily be updated to add or remove variants.
- **Affordable:** The low cost per base of NGS is achieved through an intelligent combination of locus and allelic barcode and sample multiplexing.

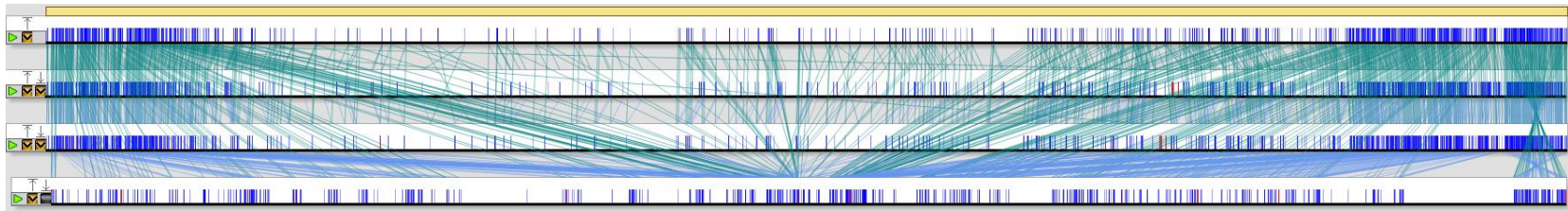


### Data scored as scatterplots



Source: Thermo Fisher

# Eureka panel development



Mostly “anonymous” markers for genome-wide selection

**S006-W5** BRAND NEW RM: 0.06

**EXCITING TOP-END YIELDS**

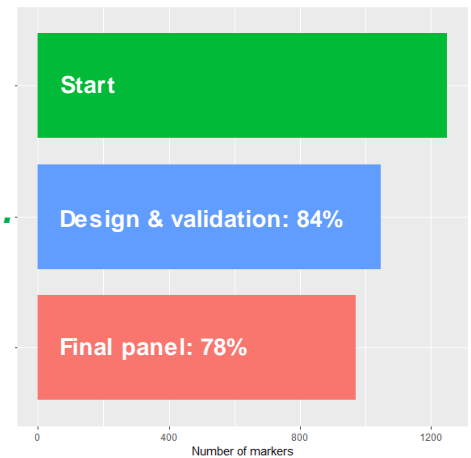
- Unique Rps gene stack for superior Phytophthora protection
- Solid standability
- Well suited for highly productive soils

Ranking	9	7	5	3	1
Emergence	[Bar]				
Standability	[Bar]				
Phytophthora Field Tolerance	[Bar]				
Stress Tolerance	[Bar]				
Iron Deficiency Chlorosis	[Bar]				
Sclerotinia White Mold	[Bar]				

Source: Syngenta

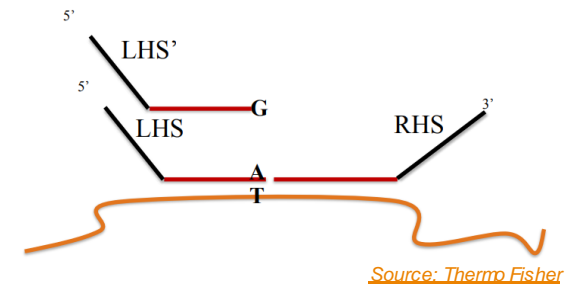
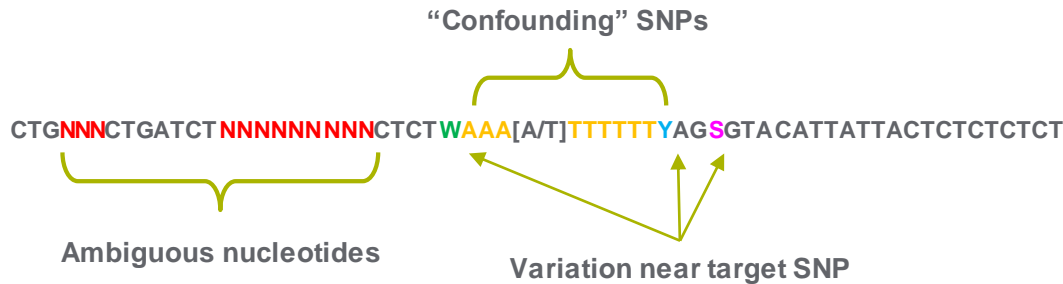
Flexibility for “must-haves”

Good designability rate...



Source: <http://www.syngenta-us.com/seed-guides/assets/nk-northern-region-2016.pdf>

... but some assays are not designable or fail during validation

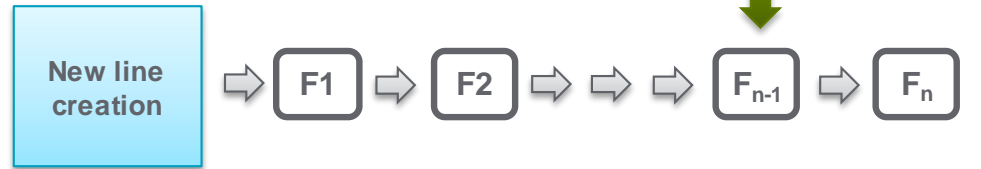


Fixed probe position limits options for challenging footprints

# Able to apply genomic selection at an earlier stage

Cost and fast data turn-around time enable progeny selection before replicated field trials

*Flexibility to add/remove assays over time is also key*



Still, some obstacles to overcome for implementation

## Adapting to a production workflow

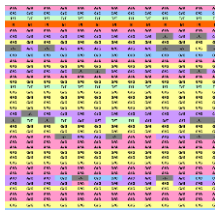
Sample management & DNA preparation



- Track and trace
- Capacity management

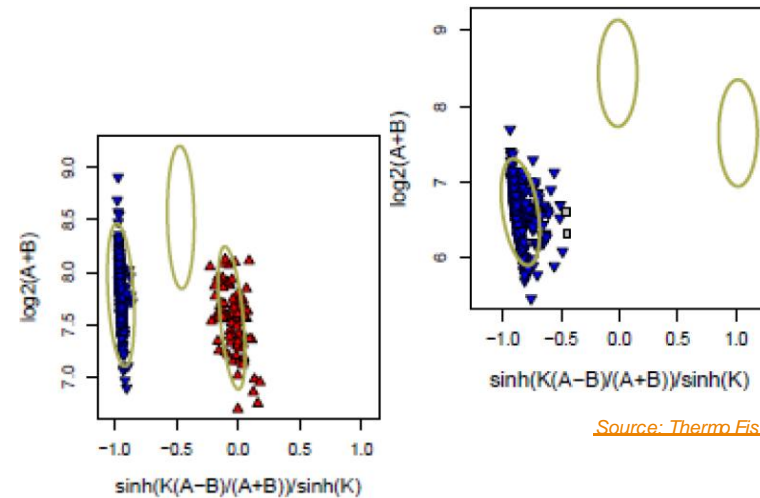


Axiom and Eureka genotyping service



Genotype QC and reporting to customer

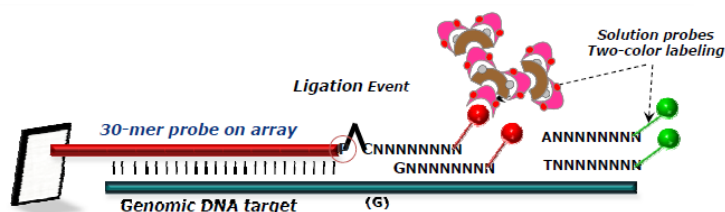
## Scoring algorithms for atypical clusters



Source: Thermo Fisher

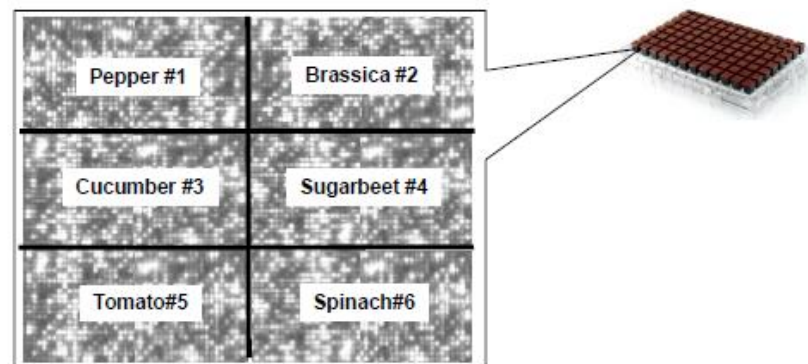
# An alternative for medium densities

- Eureka is a good fit for lower density panels, e.g., for ~1k markers
- Other crops with lower LD, higher genetic diversity, etc. require higher densities
  - Example: Corn genomic selection
- Axiom 384 HT provides an alternative for medium-density panels, e.g., 3-5k markers



Source: Thermo Fisher

## Ability to multiplex crops





# Flexibility in array design

Typically 1 probeset per variant

Forward strand  
ProbeSet

CAACATCATATGCAGGAGGTGCTCTGACAA[G/T]AAAAATAAGCAACTGGATCTCCCCAGT  
GTTGTAGTATACGTCCTCCACGAGACTGTT[C/A]TTTTTATTCGTTGAACCTAGAGGGGGTCA

Reverse strand  
ProbeSet

SNP Site

Source: Thermo Fisher

For more complex or “Must-have”, both directions are used

Left side requires 1 probe

GGTGGCCCTAAGTCCCTAACAAATGACATTAAAGTT[A/G]TTYAGWGGTGTCTAAAKKGAGATAGGAACTTGCCA

Right side requires 16 probes

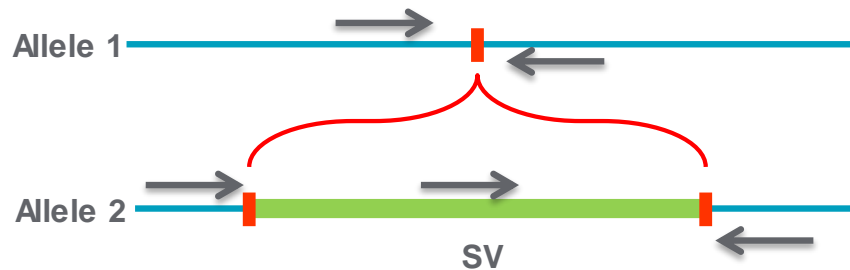
Left side requires only 2 probes but not recommended

GGAAGTTTTTTTTTTTTTTKTGTGTGTGTGAA[A/C]GAAGCAATTAGAACGTAAGCCCGATGATGCTAATC

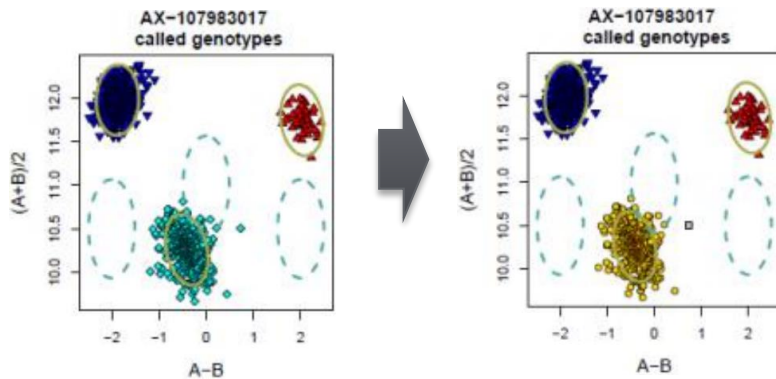
Right side requires 1 probe

**Best probeset can vary**

## Different handling for larger SVs

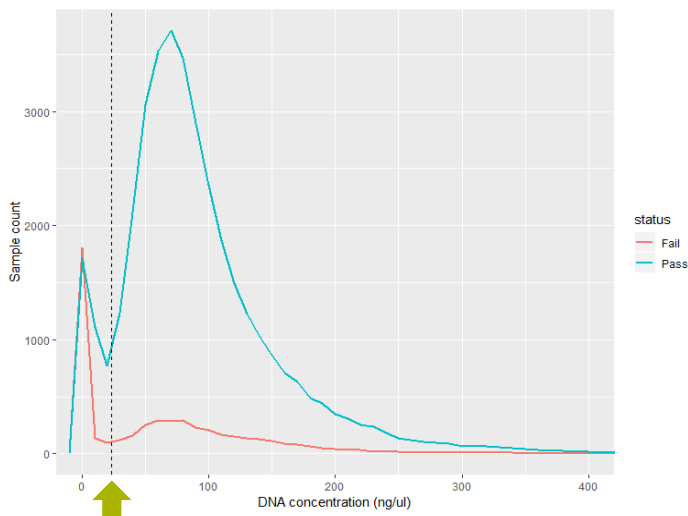


# Many factors contribute to results quality & consistency



Credit: Thermo Fisher

## DNA quantity is important...



... but doesn't always correlate with success/failure

## Footprint quality matters!

E.g., variation closely flanking the SNP of interest

GGTATTTTTT**G**ACCATTASGGCT**TNN**CTCTKA[A/G]TTYAGWGGTGTCTAAAKKGAGATAGGAACCT

Didion et al. *BMC Genomics* 2012, 13:34  
<http://www.biomedcentral.com/1471-2164/13/34>



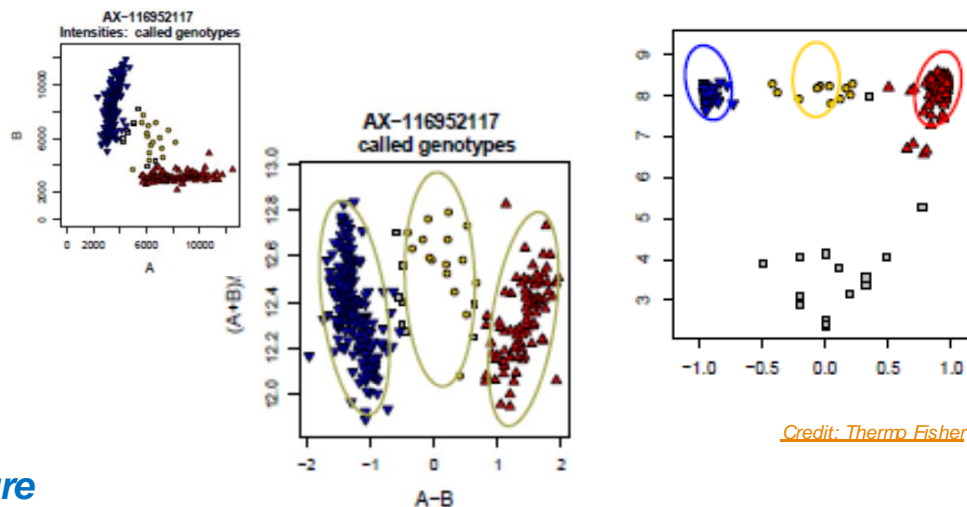
METHODOLOGY ARTICLE

Open Access

Discovery of novel variants in genotyping arrays improves genotype retention and reduces ascertainment bias

John P Didion<sup>1,2,3†</sup>, Hyuna Yang<sup>4†</sup>, Keith Sheppard<sup>5</sup>, Chen-Ping Fu<sup>6</sup>, Leonard McMillan<sup>6</sup>, Fernando Pardo-Manuel de Villena<sup>1,2,3\*</sup> and Gary A Churchill<sup>5\*</sup>

## Complex or bulked samples can have poor clusters



Credit: Thermo Fisher

# The use of priors can improve scoring

*Especially with 1 or 2 clusters*

Previous performance

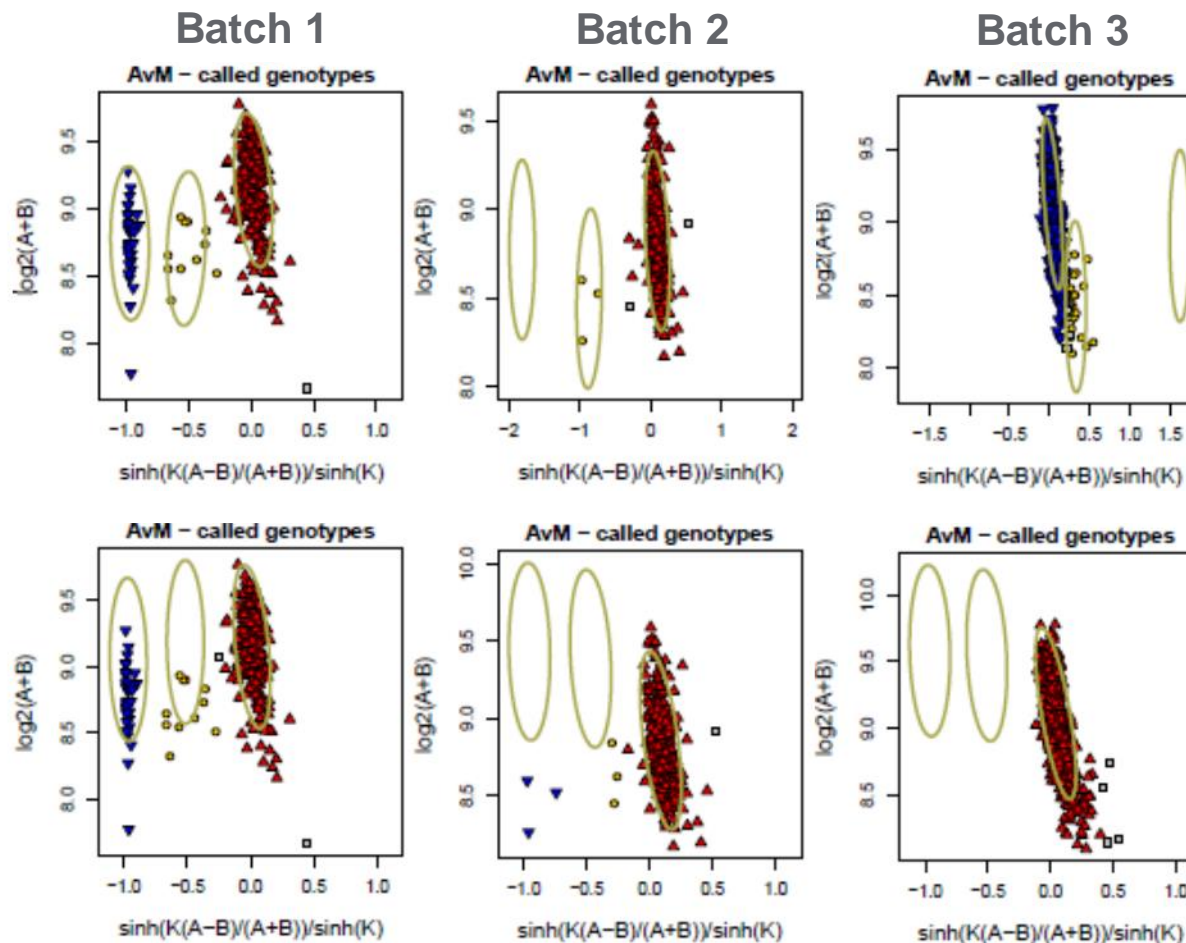
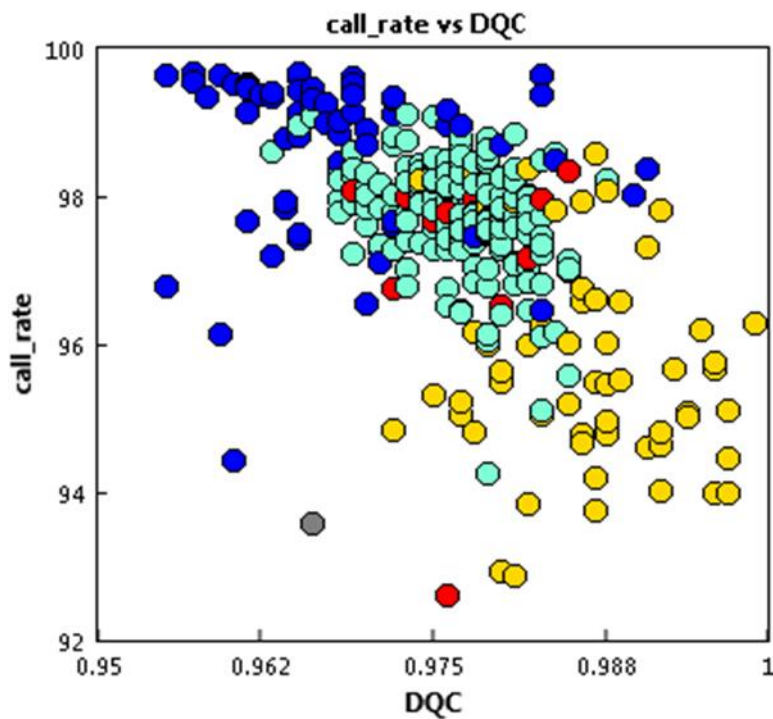


Figure credit: Thermo Fisher

# Accounting for population structure can also improve scoring

## Example crop 1

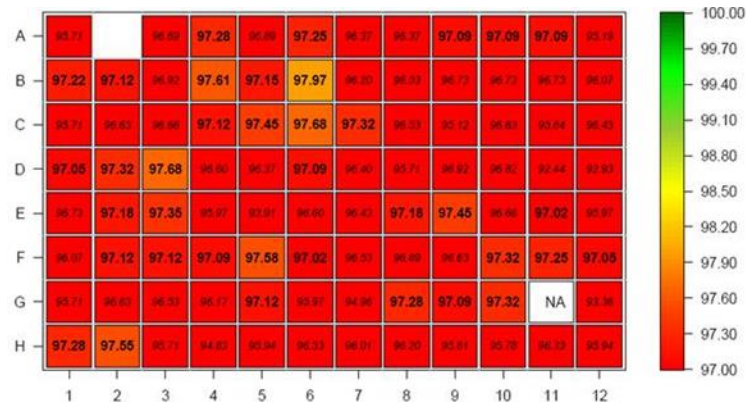


*Probesets selected for QC during validation may not be optimal for divergent populations*

Figure credit: Thermo Fisher

## Example crop 2

Original: pass rate = 39%



Re-processed with new QC controls

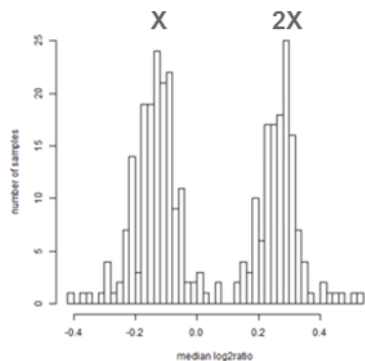
New: pass rate = 95%



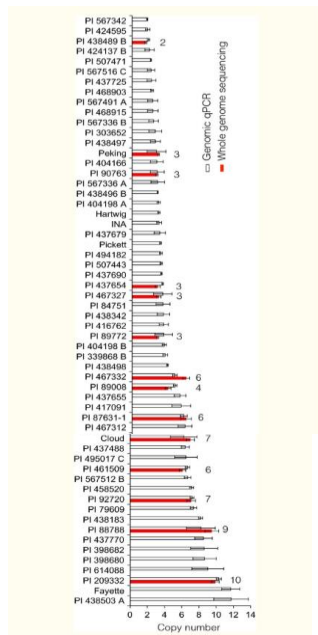
# Opportunities

## Structural variants

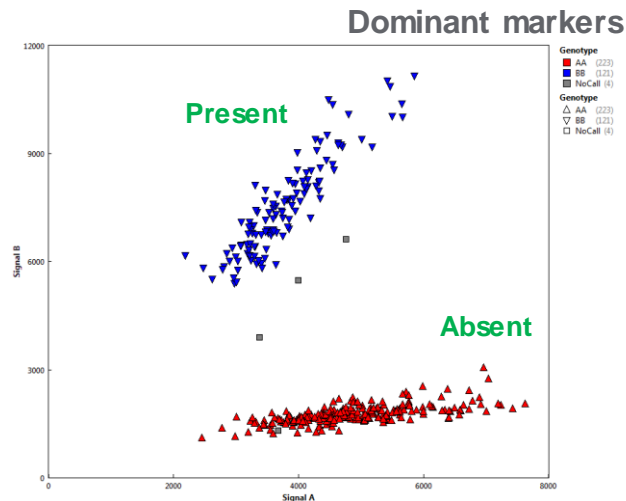
E.g., quantifying copy # variation



Credit: Thermo Fisher



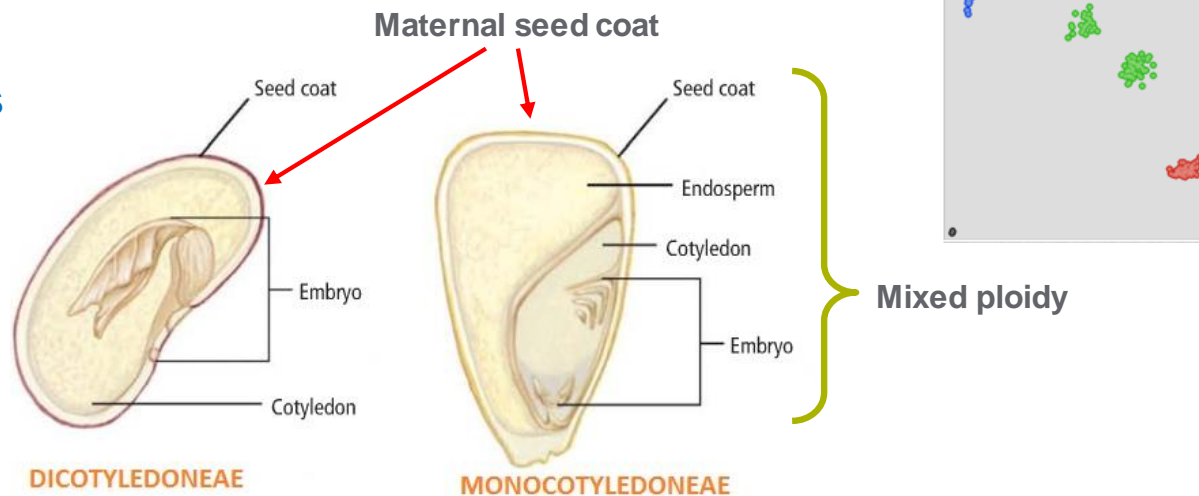
<https://onlinelibrary.wiley.com/doi/full/10.1111/mec.13138>



## Seeds and other tissues

Composition complexity:

- Starch
- Oils
- Polyphenols
- Etc



<https://biologigonz.blogspot.com/2010/01/angiospermae-gymnospermae.html>

## Summary

- Eureka and Axiom are in use for production-scale genotyping for most crops for early genomic selection.
- Invested significant effort to properly adapt to and integrate with Syngenta's existing infrastructure for production workflows.
- Ability to handle high sample volumes with short turn-around times offers the possibility to extend Eureka to other, more demanding applications.

# *Bringing plant potential to life*

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