



# Zoetis Genetics Now and the Future

Sue DeNise  
Executive Dir.,  
VMRD Genetics  
December 2018

# STRATEGIC DRIVERS



## POPULATION GROWTH

Projected population growth and protein demand creates a productivity imperative for livestock producers



## NATURAL RESOURCES

Natural resource constraints will influence where livestock are raised and require additional production efficiencies



## HEALTHY, SUSTAINABLE FOOD

Increased socio-regulatory pressures will require novel approaches to ensuring the productivity, health and well-being of animals



## PRECISION CARE & MANAGEMENT

Emerging 'Big Data' approaches will fuel data integration as an element of diagnostic, preventative, and therapeutic decision making

# BEEF TECHNOLOGY EVOLUTION



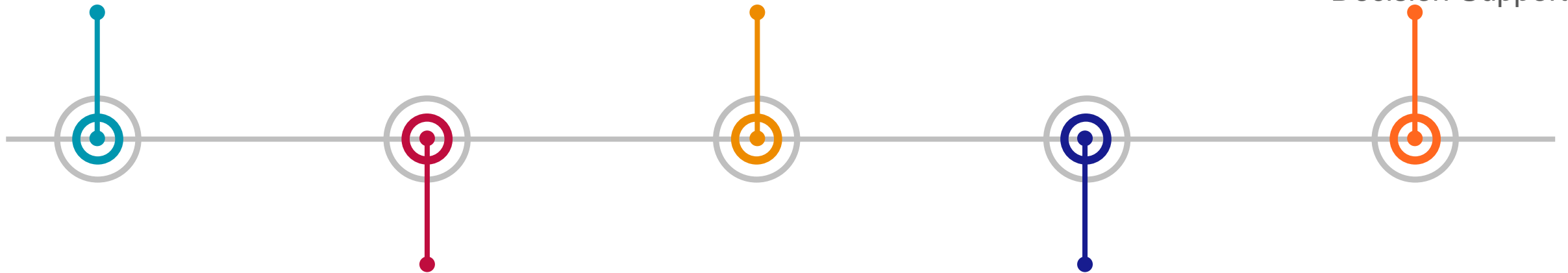
Gene Tests  
Simple Genetic Conditions



GE-EPD



ssBLUP  
Decision Support



Molecular Breeding Values



Imputation  
Commercial Derivatives



# Insights from our experiences

## Past Paradigms

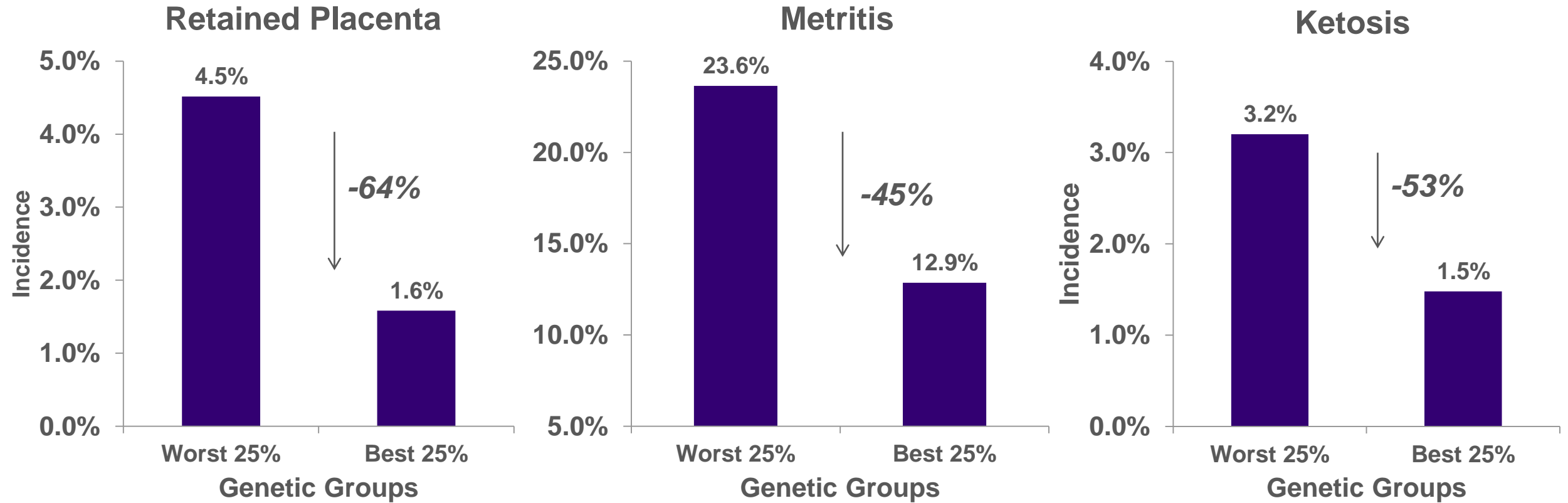
- Commercial producers benefit the most from gene flow from elite breeders
- Even if we develop predictions for lowly heritable traits, heritability will prevent us from improvement for generations
- Adding causative mutations to single step will improve accuracy of selection

## Our current approach

- Commercial producers can benefit from big data approaches and from direct genomic benefits
- Single step technologies genomic selection benefit all technologies
- With potential exceptions, causative mutations benefit small, uniform populations with intermediate allele frequencies for the causative; but data overwhelms the benefit of adding causative mutations.

# CLARIFIDE PLUS DAIRY WELLNESS TRAITS FIELD TRIAL: PERCENT DIFFERENCE IN DISEASE YEAR 1

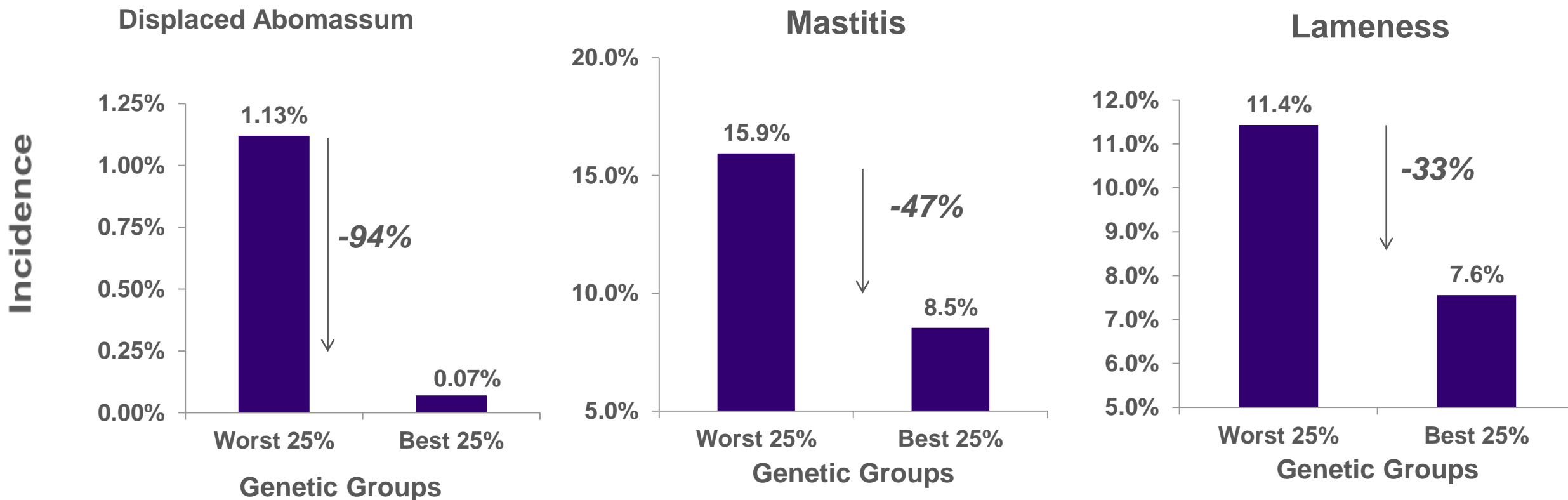
## Difference Between Best and Worst Quartile



McNeel AK, Reiter BC, Weigel D, Osterstock J, Di Croce FA. Validation of genomic predictions for wellness traits in US Holstein cows. *J Dairy Sci.* 2017;100:9115–9124.

# CLARIFIDE PLUS DAIRY WELLNESS TRAITS FIELD TRIAL: PERCENT DIFFERENCE IN DISEASE YEAR 1

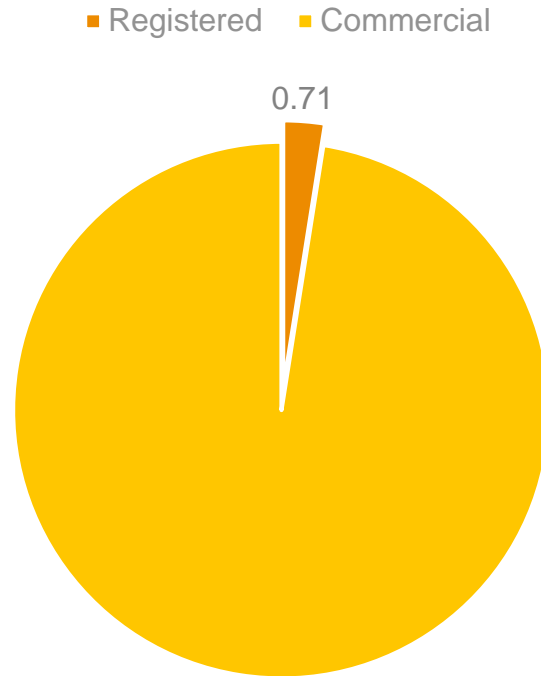
## Difference Between Best and Worst Quartile



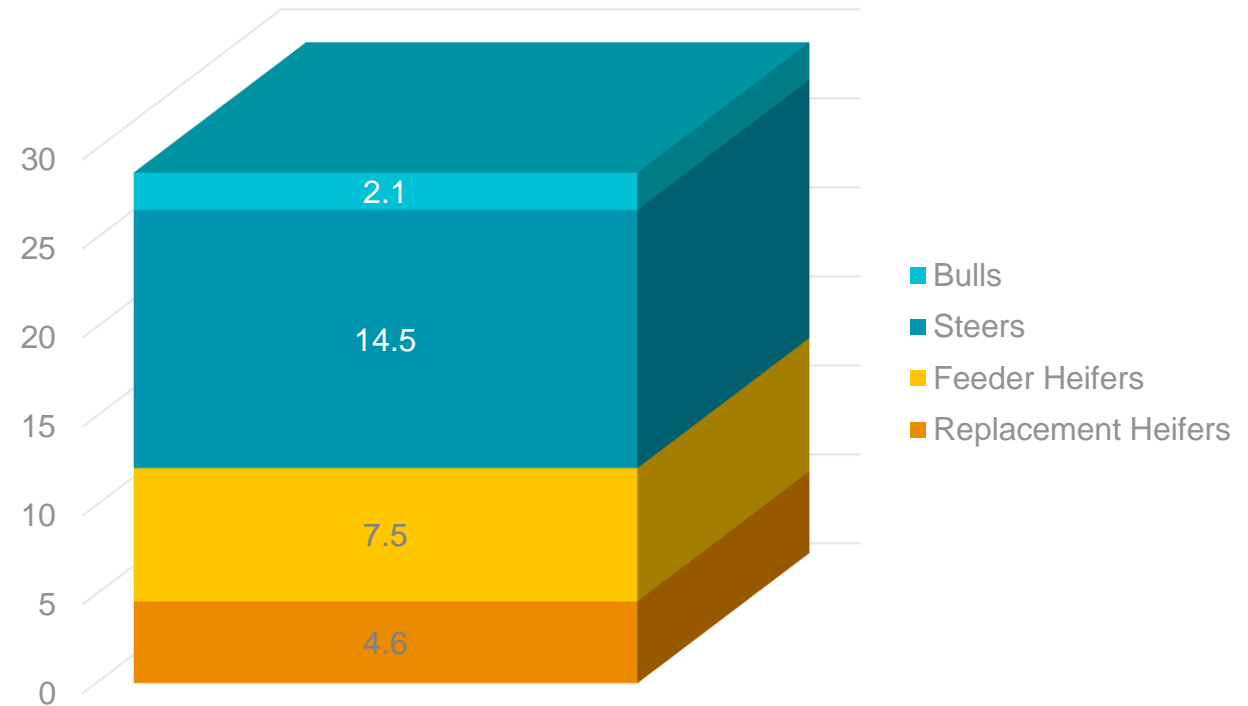
McNeel AK, Reiter BC, Weigel D, Osterstock J, Di Croce FA. Validation of genomic predictions for wellness traits in US Holstein cows. *J Dairy Sci.* 2017;100:9115–9124.

# BEEF CATTLE POPULATION - US

Annual Calf Crop<sup>1,2</sup> (M Hd)



Calves >500 lbs<sup>2</sup>



***Opportunity exists to provide genomic solutions directly to the commercial segment instead of the trickle down from seedstock***

<sup>1</sup>National Pedigreed Livestock Council, 2016 Beef Breed Registry Statistics, <http://www.nplc.net/aws/NPLC/pt/fli/62000/false> accessed 10/30/2018

<sup>2</sup>USDA NASS, 2018 <http://usda.mannlib.cornell.edu/usda/current/Catt/Catt-07-20-2018.pdf> Accessed 10/30/2018

# Zoetis Future for Beef Producers

**Goal:** To increase the value of genetic information in beef cattle production by providing relevant information, in the right place, at the right time, with the resources necessary to capture the value of genomic insights

## Customer Focused Solutions

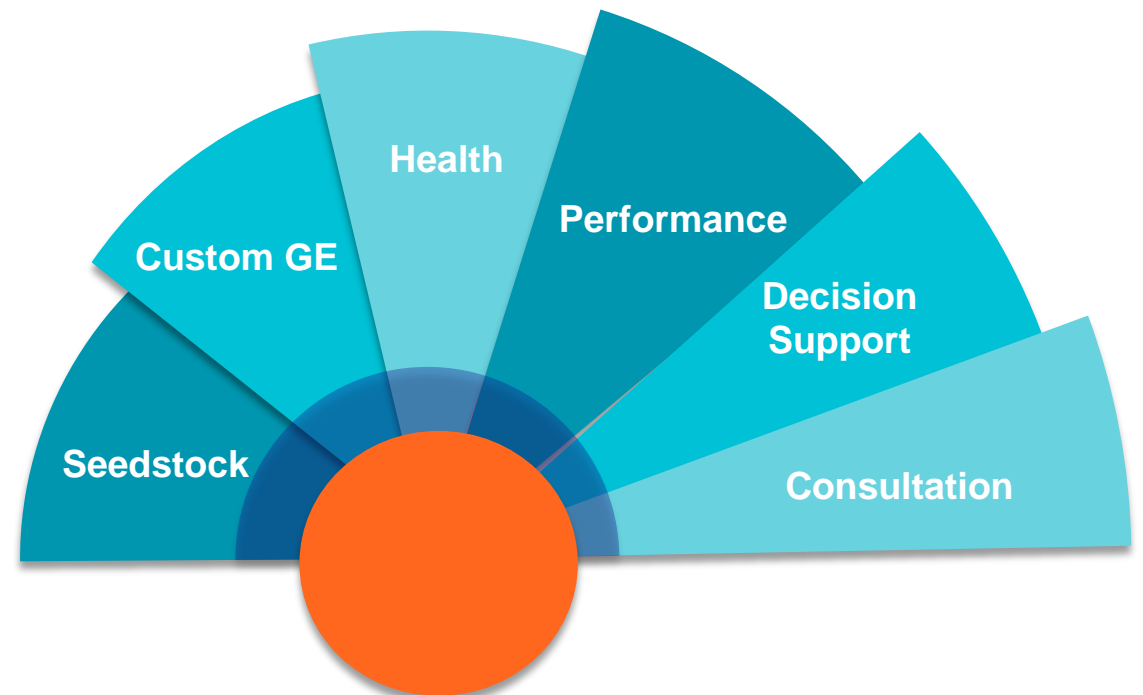
**Valued Genomic Solutions with Demonstrated Efficacy**

**Best in Class Customer Experience**

**On-farm Technical and Decision Support Resources**

**Genomic Tools that Complement Existing Data**

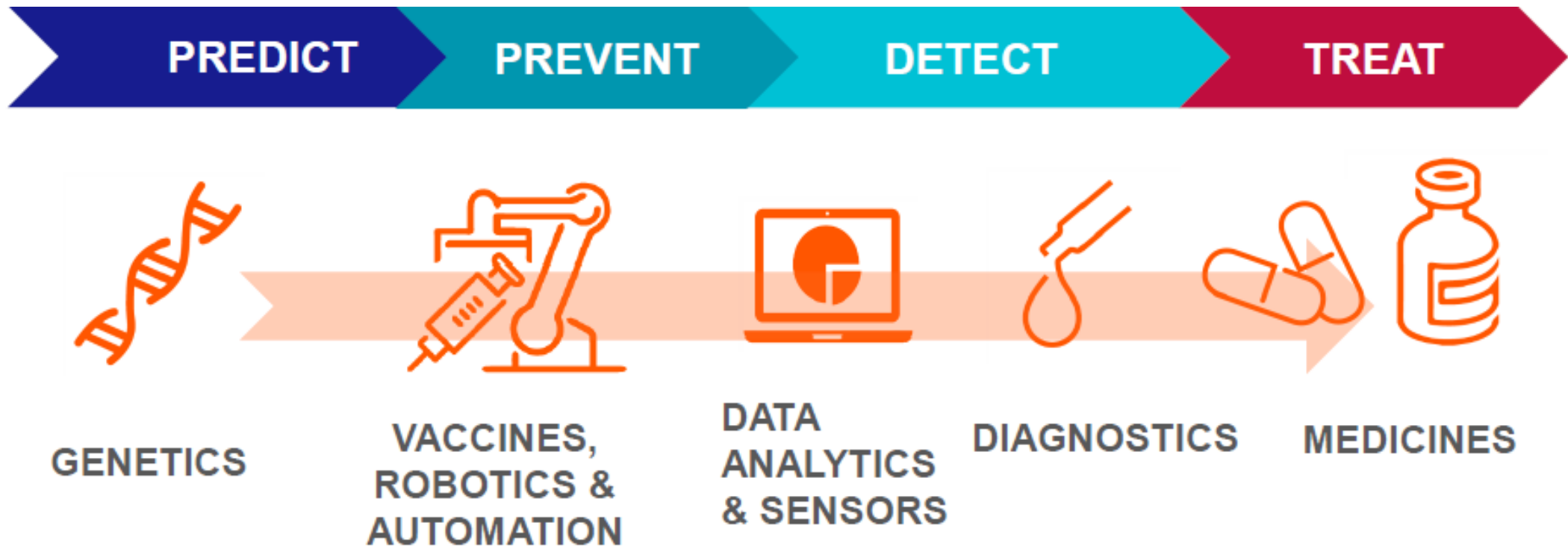
**Genomic Insights that Inform End-to-end Management**





# Genomics Works Across the Animal Health Portfolio

Integrating genetic understanding into our products



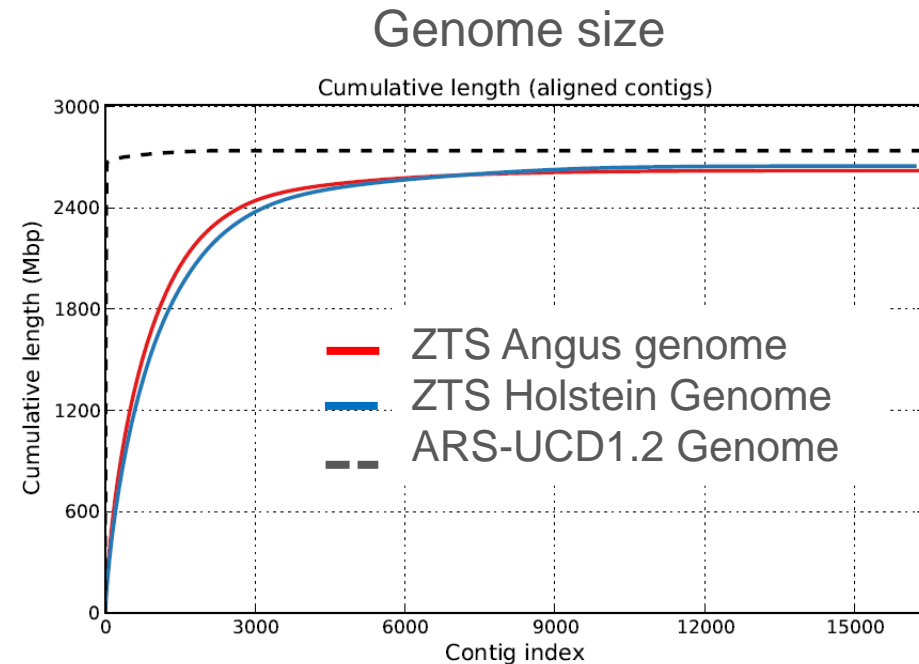
Innovation is core to our mission. We support research internally and externally.

# Angus “de novo” Reference Genome Assembly

Zoetis Angus Assembly	Statistics
Number of scaffolds	3,962
Total size of scaffolds	2,646,922,564
Longest scaffold	74,707,193

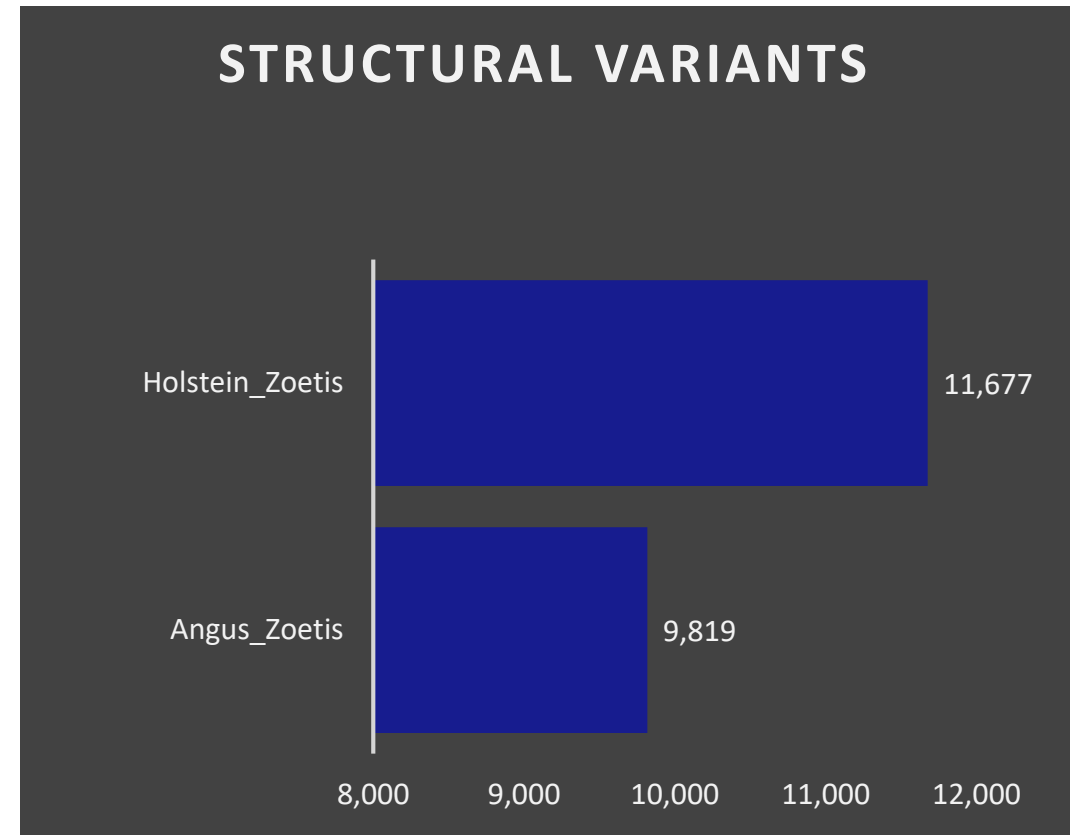
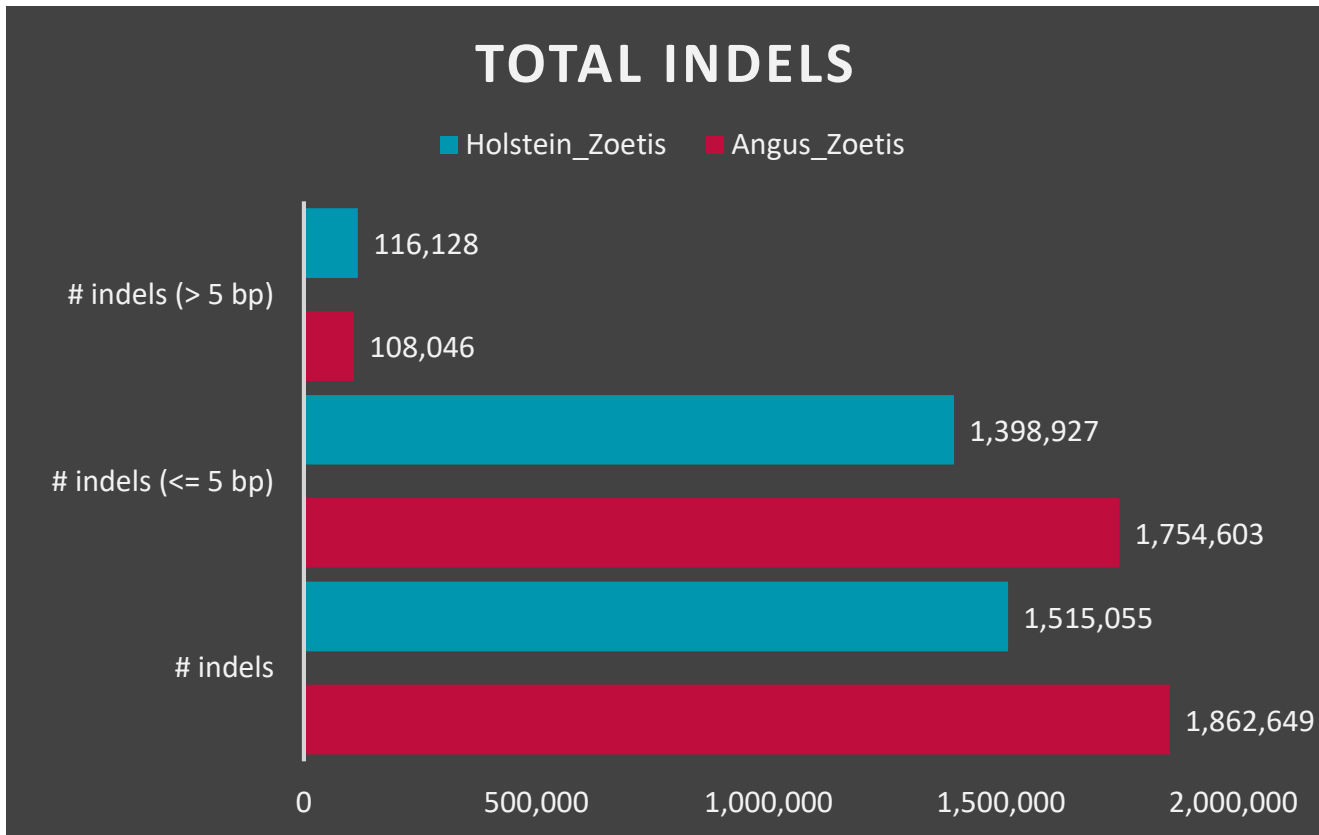
## State of the Art Technologies

- Long reads: PacBio 55x coverage
- Physical Mapping: DoveTail 225x
- Short reads: Illumina Pair End 100x



**Genome Assembly Quality:** Genome size, N50 scaffolds and scaffold length are very similar to the new ARS-UCD1.2 Hereford Genome and ZTS Holstein assemblies

# Differences between reference genomes



Structural differences between Zoetis Angus and Holstein reference genomes and the Hereford ARS-UCD<sub>1.2</sub> assembly

# INNOVATION TO IMPROVE OUTCOMES FOR OUR CUSTOMERS

**Transcriptomics**

**Single Cell Sequencing**

**Epigenetics**

**Data Lake to support decision support and big data analytics**

**Precision Livestock Management**

*zoetis*