Session 1
Use of full sequence data

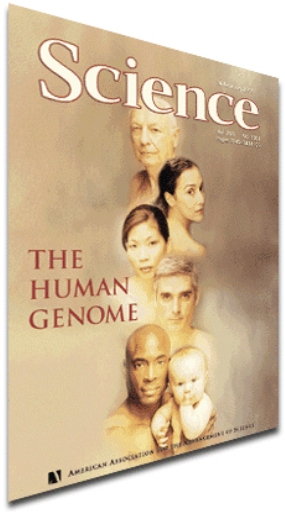
5th GenSAP Annual Meeting
15-16 November 2017
Billund, Denmark

Sequencing genome

"... [A] knowledge of sequences could contribute much to our understanding of living matter."

Frederick Sanger (1980)

- Understanding the structure of the genomes
- Understanding the biology of genomes
- Understanding the biology of the phenotype
  - Advancing the science of phenotype prediction & improving the effectiveness of breeding



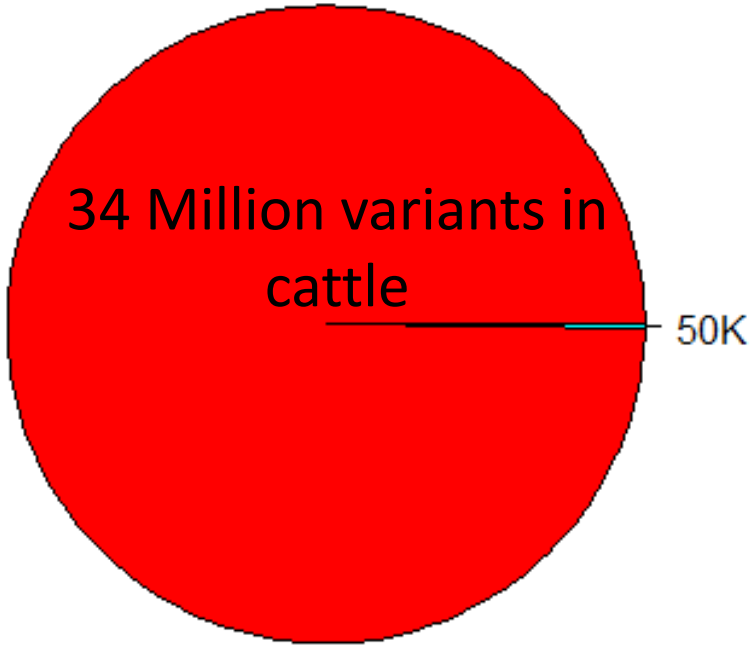
Advantages of whole-genome sequencing

1. Provides a high-resolution, base-by-base view of the genome
2. Captures both large and small variants that might otherwise be missed
3. Identifies potential causative variants for further follow-on studies of gene expression and regulation mechanisms
4. Delivers large volumes of data in a short amount of time to support assembly of novel genomes

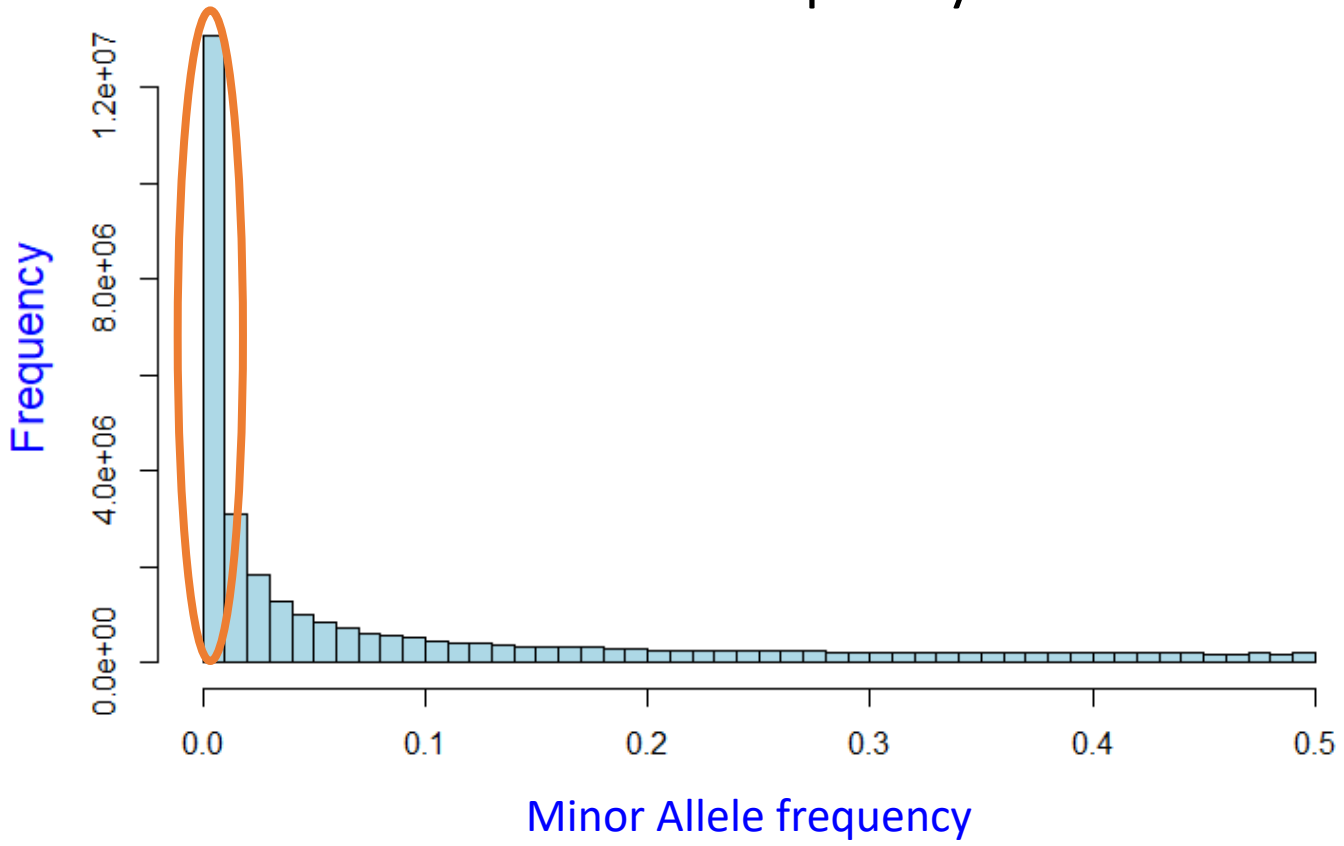
"Illumina promises to sequence human genome for $100 -- But not quite yet"

Matthew Herper , FORBES Staff, Jan 9, 2017

Are we fully exploiting the genome data?



Rare and low frequency variants



Are we fully exploiting the genome data?

Common sequence variant types

1. Single nucleotide polymorphism (SNP)
2. Insertion/Deletion (Indel)
3. Structural variants

Across species/ populations information

1. Annotations / gene functions
2. QTL across populations / breeds
3. Learning from model organisms

Species without genome assembly / SNP array

Session 1: Use of full sequence data

Time	Title	Speaker
10:30	*Next generation sequence data in gene mapping and genomic prediction: opportunities and challenges.*	Didier Boichard
11:00	*Detection of large chromosomal deletions in cattle and their phenotypic consequences.*	Md Mesbah Uddin
11:15	*Using model organisms to study complex diseases across species.*	Palle Duun Rohde
11:30	*Allelic imbalance in sequence-based genotyping data*	Prof. Torben Asp
11:45	*Validation of SNPs from a Nordic WGS based GWAS using independent French populations*	Andrew Marete
	Imputation to whole sequence variants in pigs	Pernille Merete Sarup
	Role of rare variants in genomic prediction	Qianqian Zhang
	Using expression data to detect small QTL in dairy cattle	Irene van den Berg