

Making the possible practical



GWAS of meat quality traits using WGS data in a multi-breed sheep population

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Business
Cooperative Research
Centres Programme



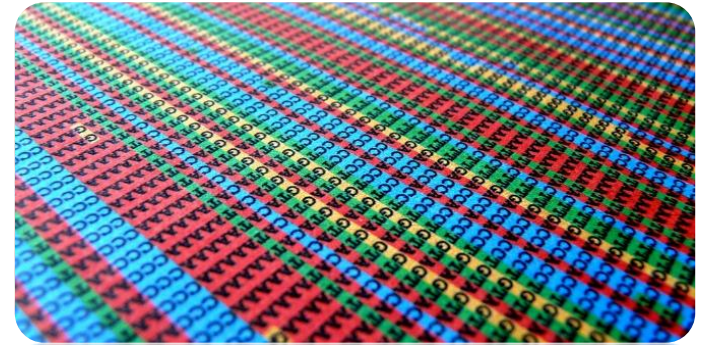
WGS data can be helpful for

- Detecting QTLs and fine-mapping of QTL
 - **More** variants
 - Variants with **low MAF**
 - **Causative** variant?
 - **Structural** variants
- Increase accuracy genomic prediction
 - Include significant SNPs from GWAS in prediction

work Moghaddar and Khansefid, presented yesterday, session Prediction 1.

What can we expect from WGS data?

- Detect more QTL, **more peaks**
- Fine map known QTL, **sharper peaks**
- **Directly compare** with functional studies such as RNA seq



What genotype data do we have?

- 726 sequenced sheep
 - 376 Australian sheep
- ~35,000 sheep with genotypes
 - 12/15K: 10,000
 - 50K: 23,000
 - HD: 2,600

→ All imputed up to sequence (*Friday presentation Bolormaa session **Imputation***)

→ 27,896,226 variants (Minimac R^2 threshold=0.4)

BORDER LEICESTER



COOPWORTH



POLL DORSET



SUFFOLK



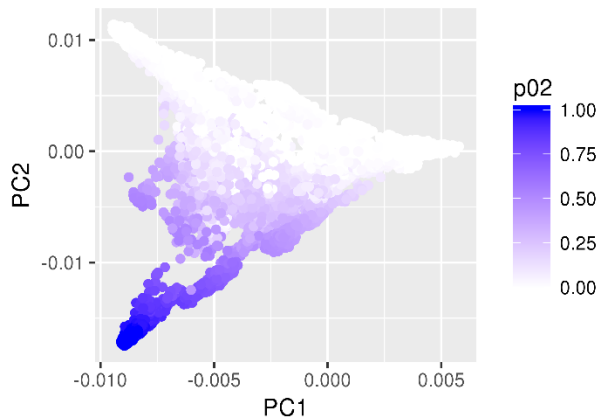
DORPER



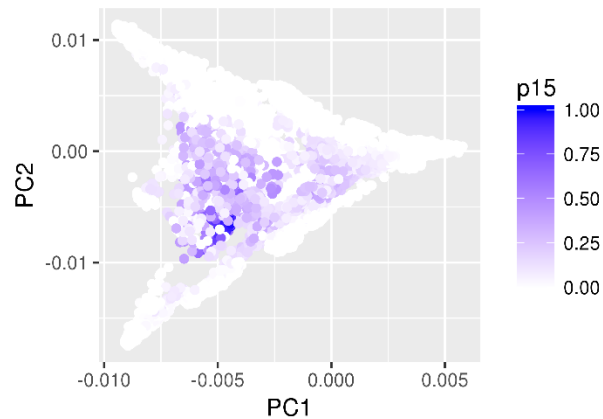
MERINO



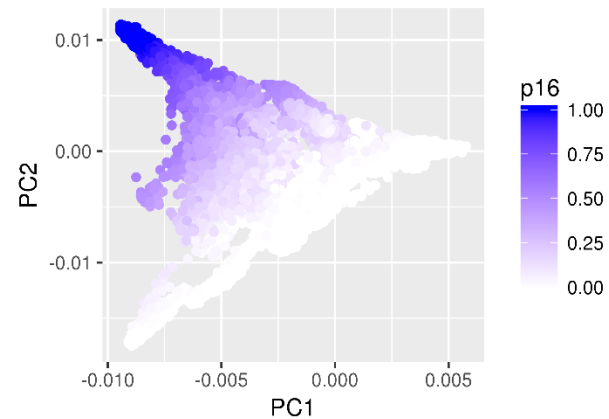
BORDER LEICESTER



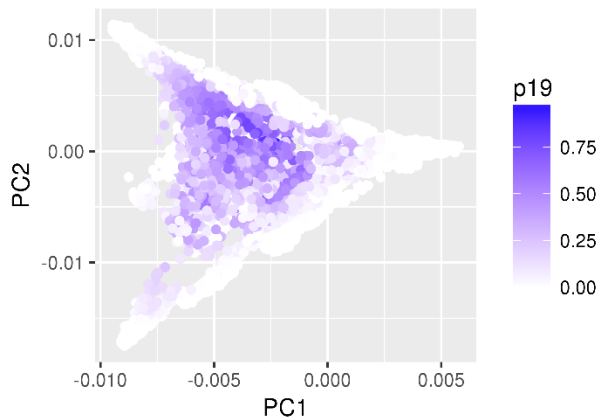
COOPWORTH



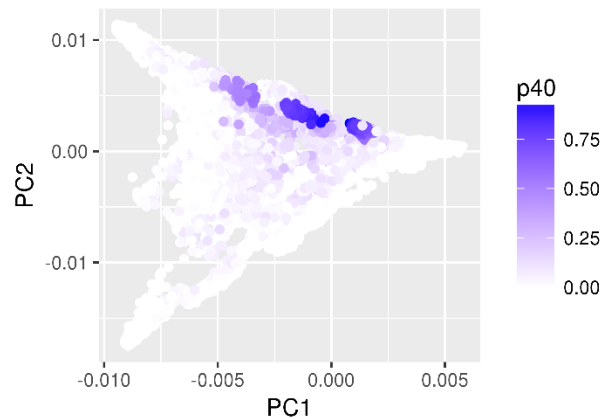
POLL DORSET



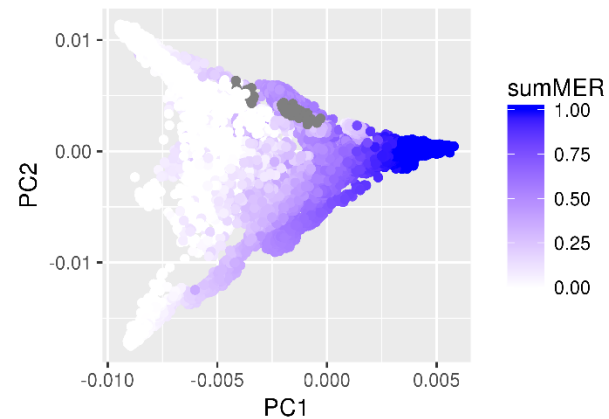
SUFFOLK



DORPER



MERINO



Traits and model

- Pre-corrected for fixed effects
- Single SNP analysis
 - SNP Snappy WOMBAT
- Simultaneously fit
 - Grm (based on HD)
 - Qmatrix (breed proportions)

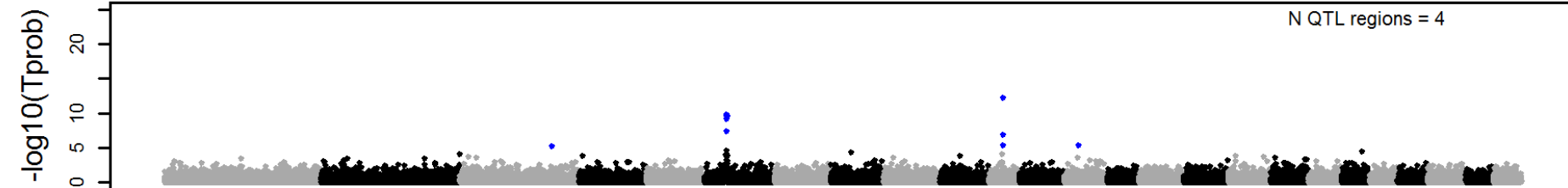
Trait	N
CCFAT	13,644
IMF	11,772
PEMD	21,412
PWT	26,769
SF5	13,363

Compare SNP density

FDR of 5%

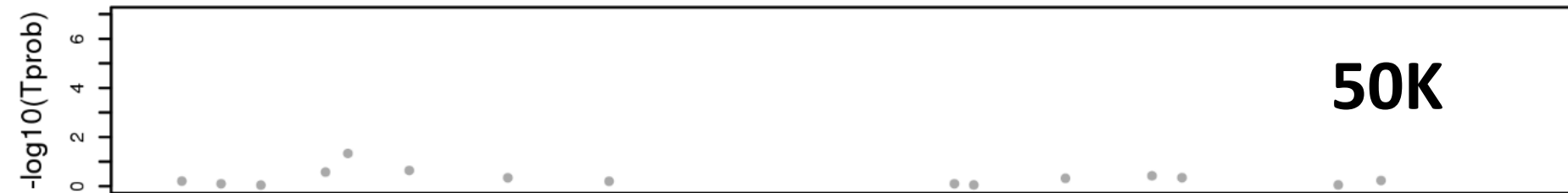
A GWAS pemd 50K

N QTL regions = 4

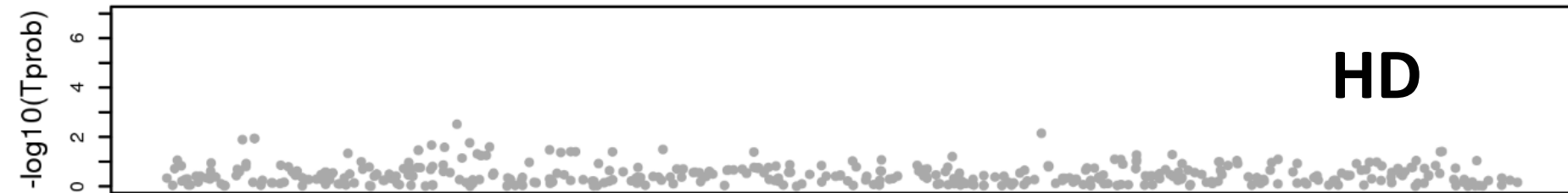


Zoom of a region

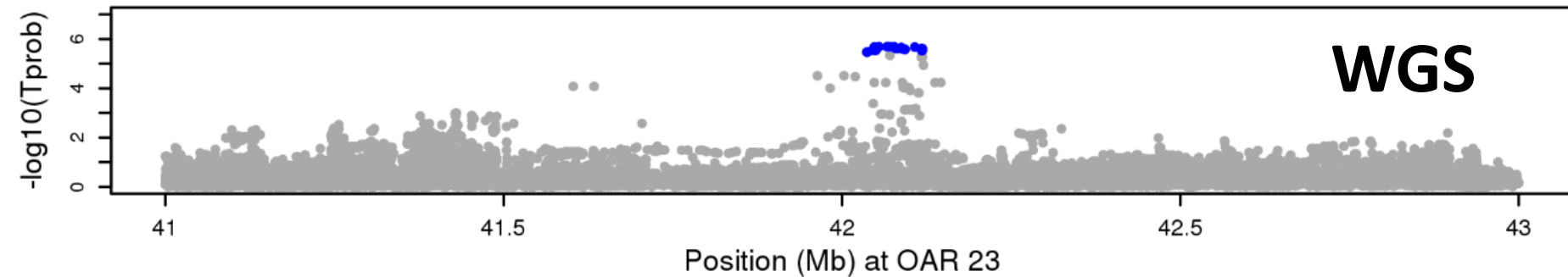
GWAS imf 50K



GWAS imf HD



GWAS imf SEQ



N QTL per trait

Trait	50K	HD	WGS
CCFAT	4	9	41
IMF	2	8	38
PEMD	4	15	49
PWT	5	13	88
SF5	3	7	34
Total	20	52	250

Significance SNPs

(min and max $-\log_{10}(\text{Pval})$)

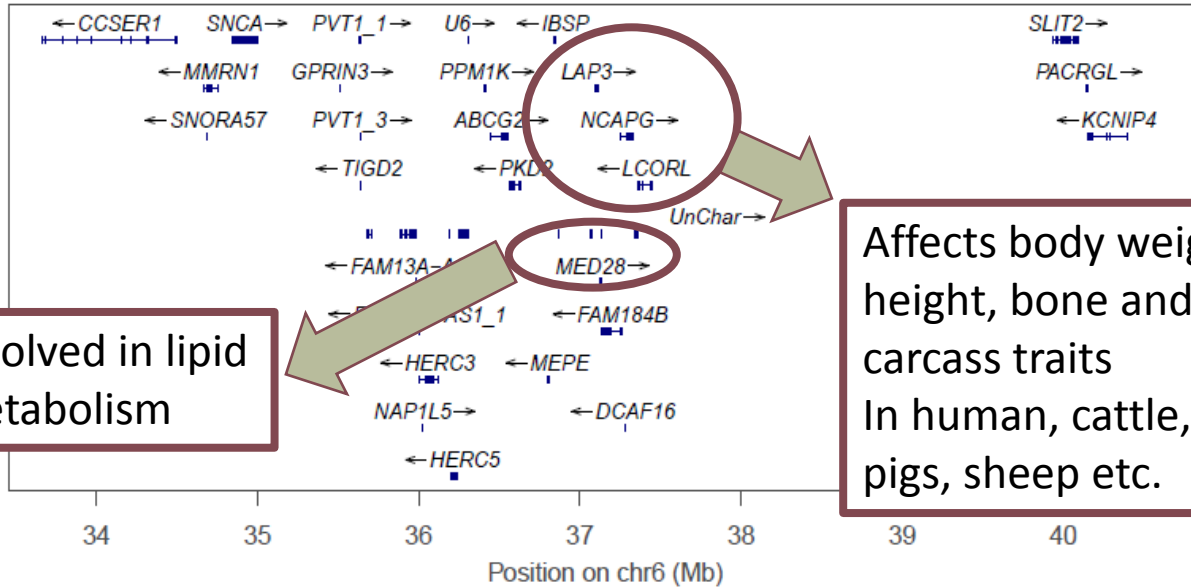
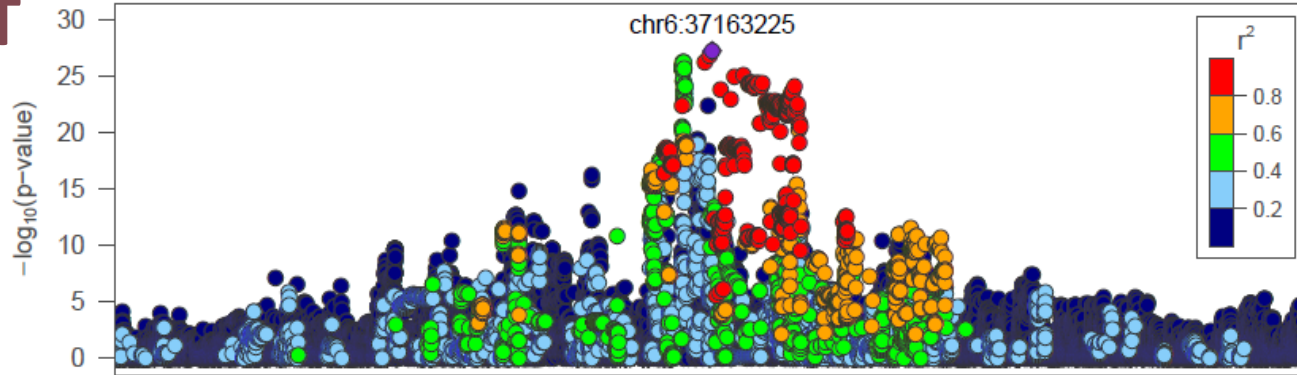
■ 50K : 5-15

■ HD : 5-22

■ WGS : 5-29

→ More and higher peaks!

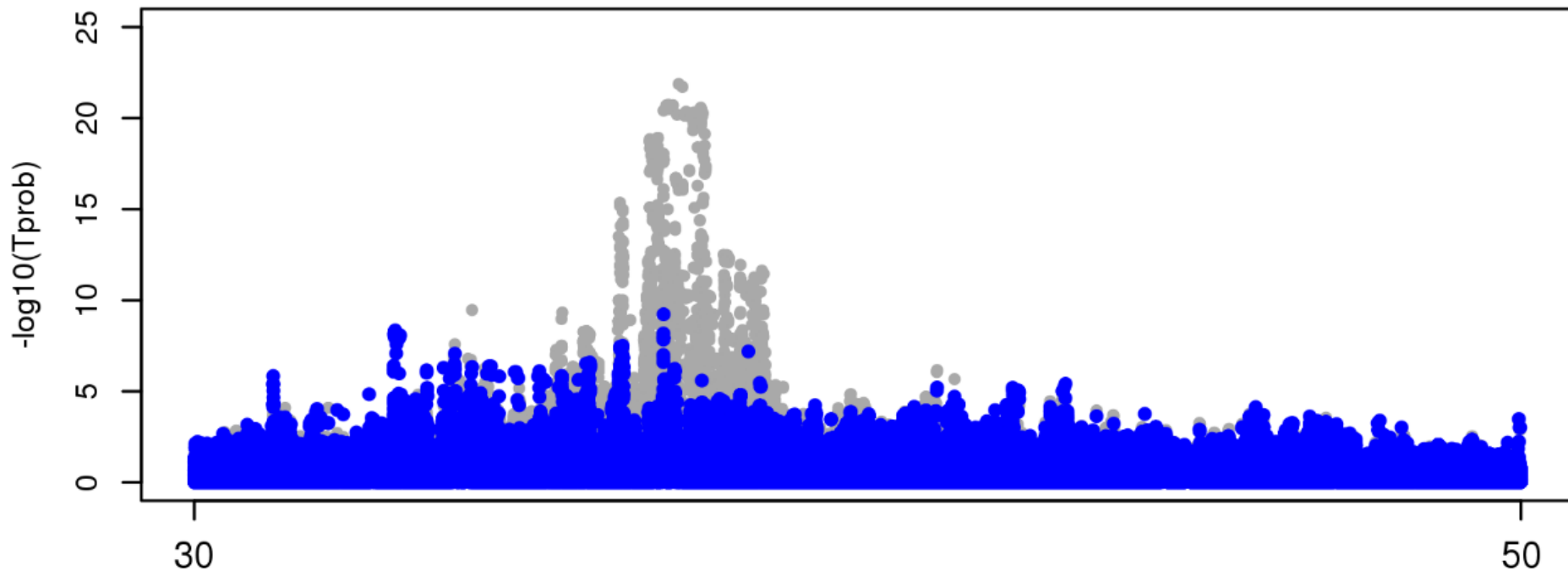
PWT

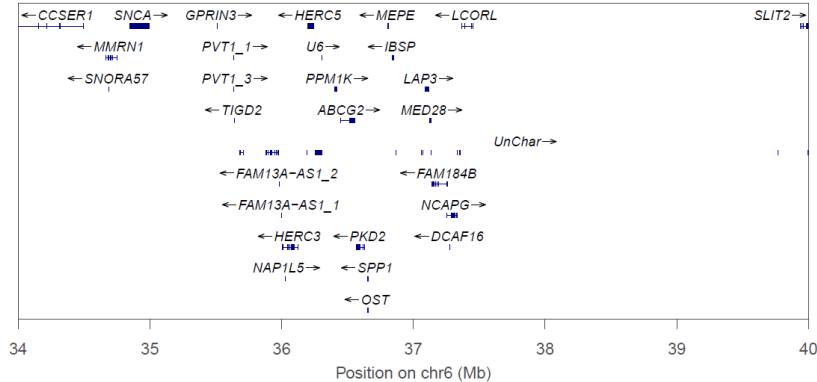
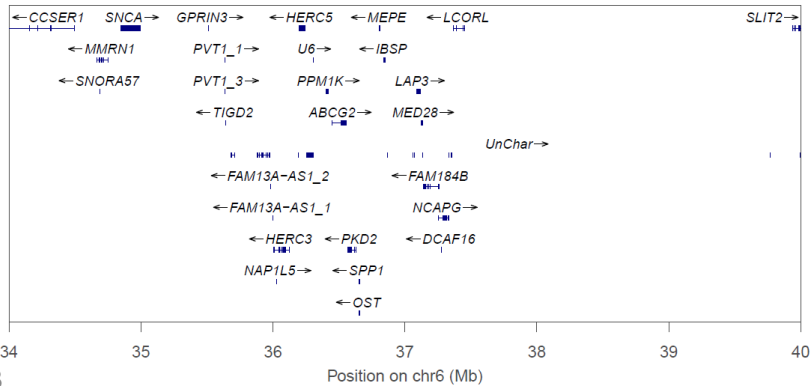
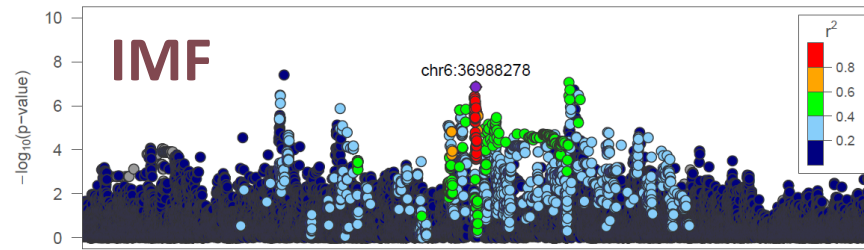
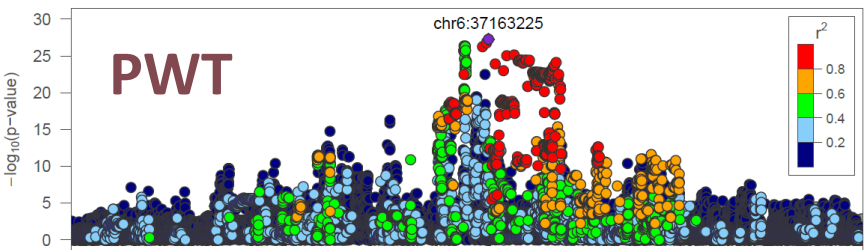
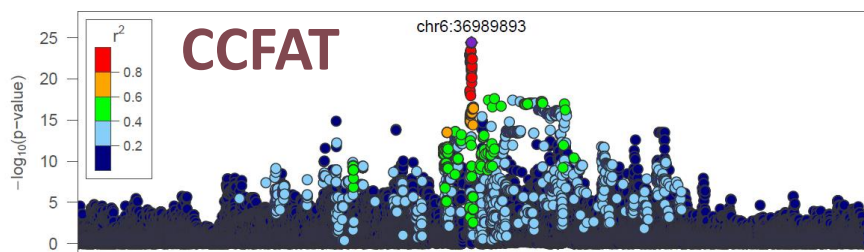
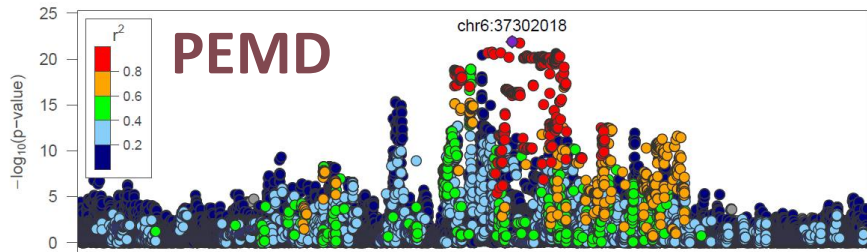


Involved in lipid metabolism

Affects body weight, height, bone and carcass traits
In human, cattle, pigs, sheep etc.

GWAS trait PEMD for OAR 6 corrected for sign. SNP





WGS gives us

- **More** peaks
- More **significant** peaks
 - Use more data
 - And / or multi-breed pop. **LD** exists over **shorter distances**
- The basis for companion studies on **functional studies** to validate candidate genes and mutations



Acknowledgements

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Questions?