

# The Interaction of Nitrogen with Yield in Wheat

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Seeding the future  
since 1856



- **WP1.1** Identification of alleles controlling Nit-UE and associated markers in **barley**
- **WP1.2** Identification of alleles controlling Nit-UE and associated markers in **wheat**
- **WP1.3** Comparison of gene and/or protein/metabolite expression profiles in **wheat** genotypes with contrasting Nit-UE under different fertilisation regimes

# Phenotyping

5 Trials: 3 Sites: 2 Seasons: 3 Nitrogen rates: 170 Genotypes



2012



2013





## WP1.2 Identification of alleles controlling Nit-UE and associated markers in **wheat**

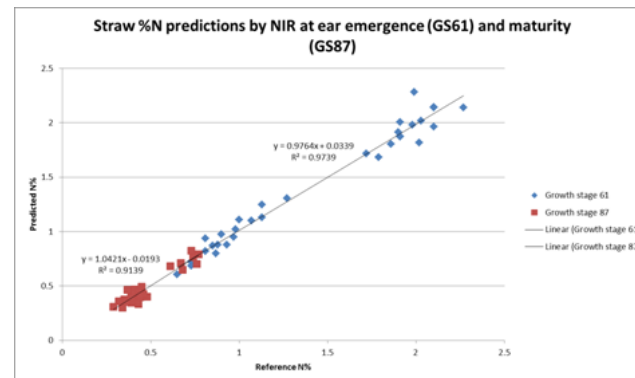
- 170 elite European wheat varieties
  - feed
  - Biscuit/cakes
  - bread making



# Phenotyping

Samples taken at Anthesis (GS61) and Harvest Ripeness (GS87)

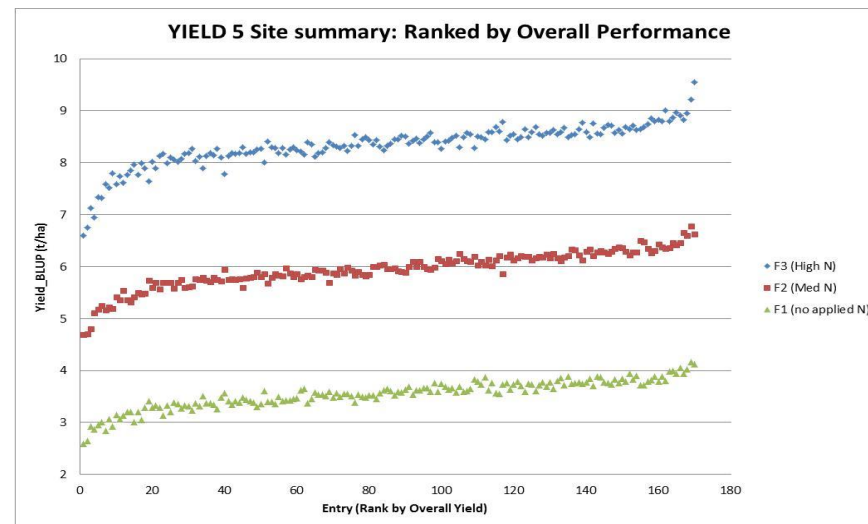
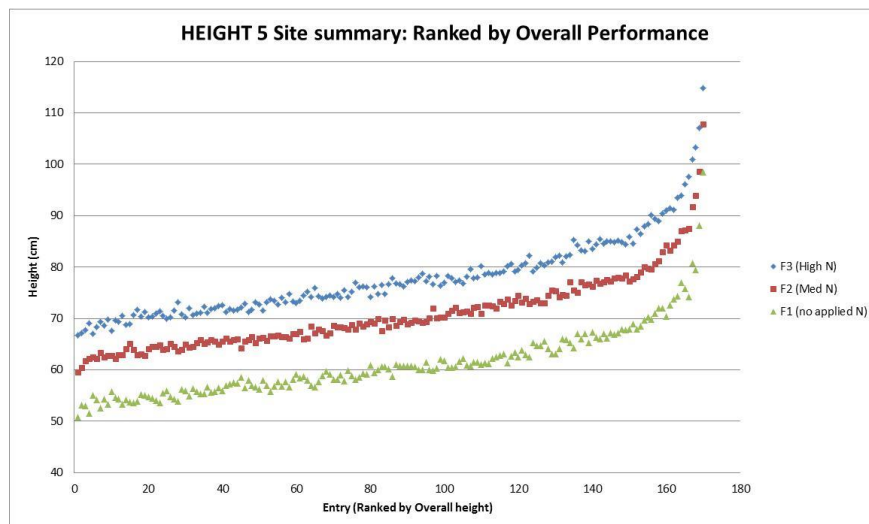
- Yield
- Grain number and grain weight
- Straw weight
- Nitrogen content

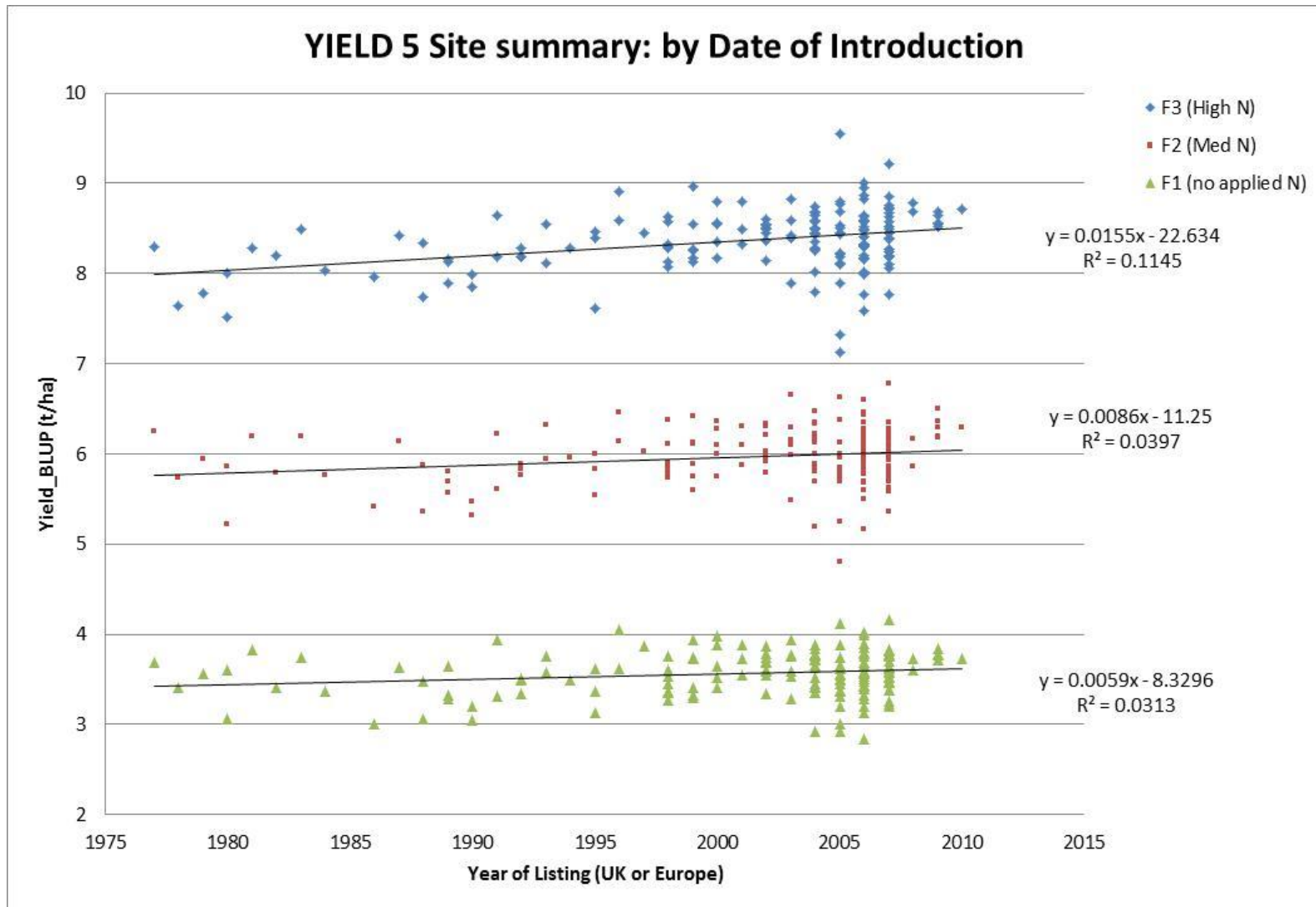


## Experimental Design

- 5 trials of 576 plots
- 3 Fertiliser (Nitrogen) nutrition levels
- Unbalanced replication
- Spatial analysis at each site
- BLUPs formed for each Fertiliser level

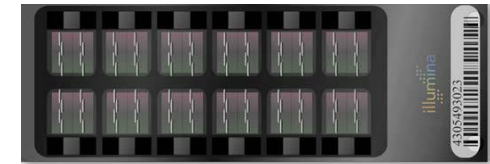
Item	GS61		Height		Yield	
	Variance Component	Sig.	Variance Component	Sig.	Variance Component	Sig.
Genotypes	4.904	***	51.987	***	0.100	***
Fertiliser x Genotype	0.026	ns	1.867	***	0.018	***
Genotypes x Sites	1.760	***	5.193	***	0.081	***
Fertiliser x Genotype x Site	0.133	**	1.376	***	0.049	***
Error	6.888		25.890		0.316	
Heritability (of BLUP)	94.1%		97.8%		87.6%	







- 90K iSelect chip
- Have genotype data for all 170 lines except one where the number of missing data was too high

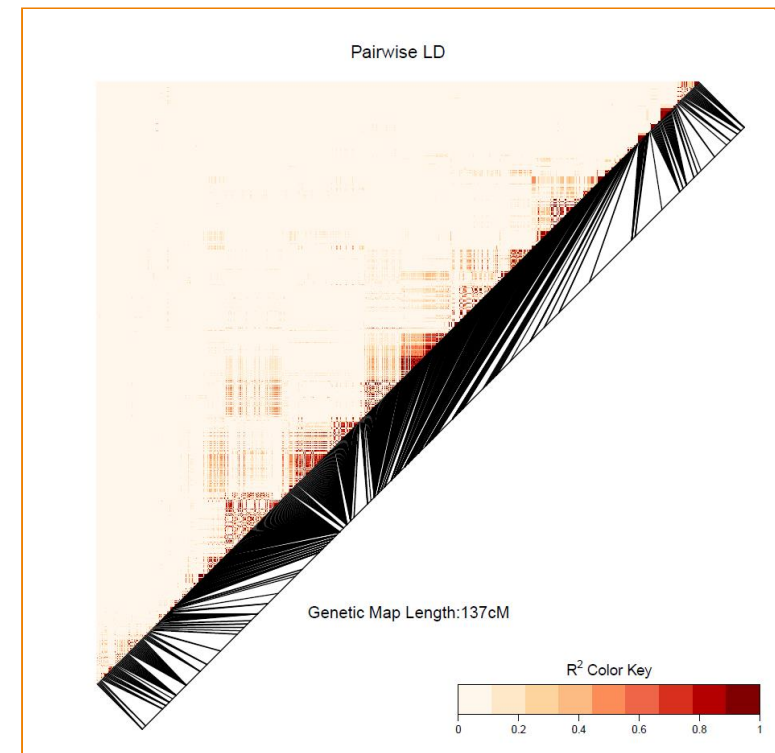


Source: www. Illumina.com

Markers available on the 90K chip	81587
Markers with scored data reported	31438
Monomorphic in this germplasm	6055
Minor Allele Frequency < 1%	2172
<b>Markers used in the Association Mapping</b>	<b>21950</b>

Marker coverage		genome		
		A	B	D
Linkage group	1	1615	1735	362
	2	1531	1708	381
	3	1175	1446	188
	4	833	703	142
	5	1322	1716	242
	6	1488	1108	172
	7	1449	948	181
Unknown				1505
Total	9413	9364	1668	21950

Note: at present 53% have been genetically mapped within the chromosome (Edwards et al.)



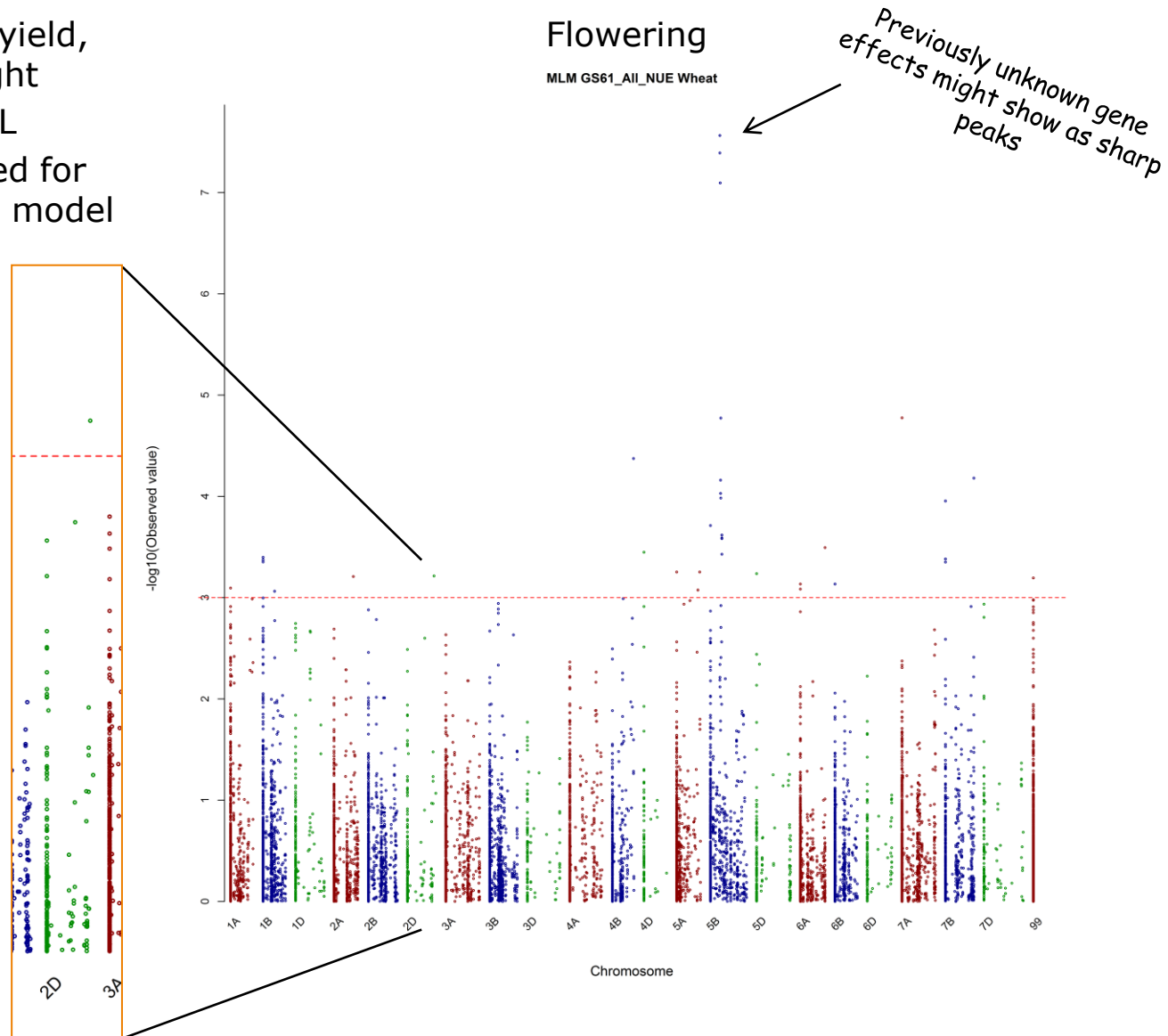


# Association Mapping

- Preliminary analysis of yield, flowering time and height
- Processed using TASSEL
  - Structure accounted for using the KINSHIP model

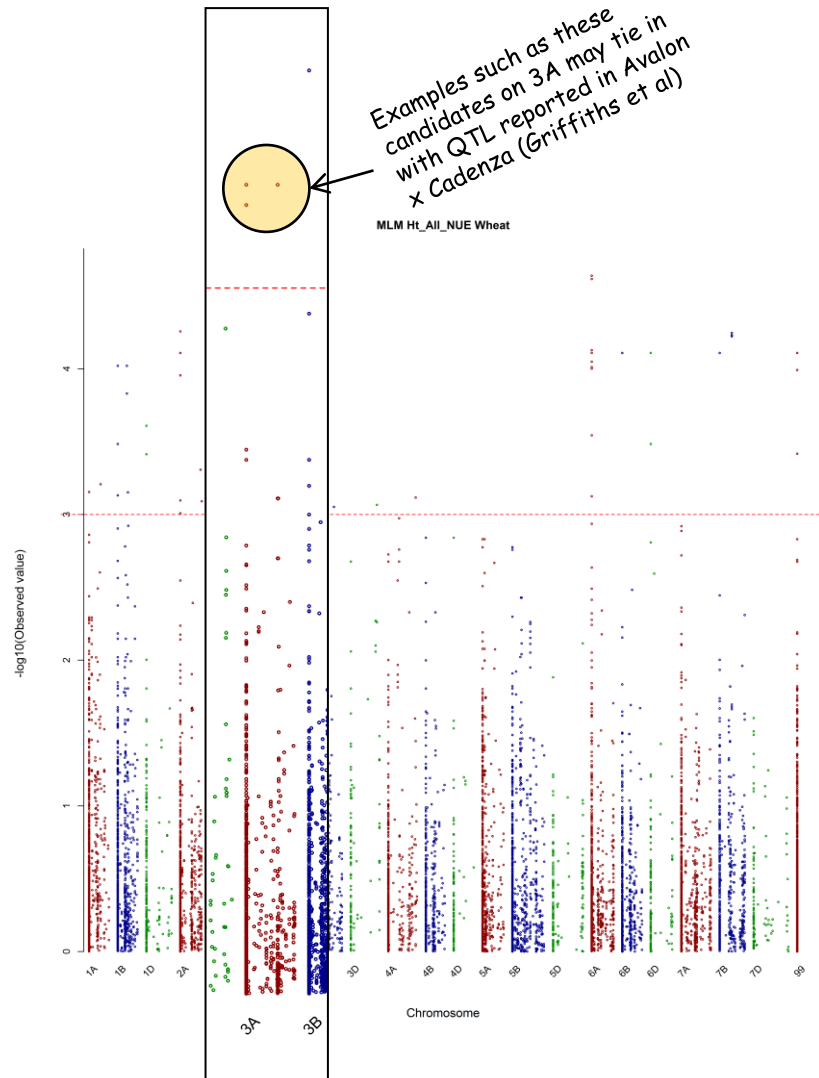
We can look for expected gene effects

- such as Ppd-D1a (Ppd1) on 2D
- Where the known genes are not already in the SNP set we will run them on the genotypes
- Analysing several 'known' genes will validate the resolving power of the genotype/marker panel

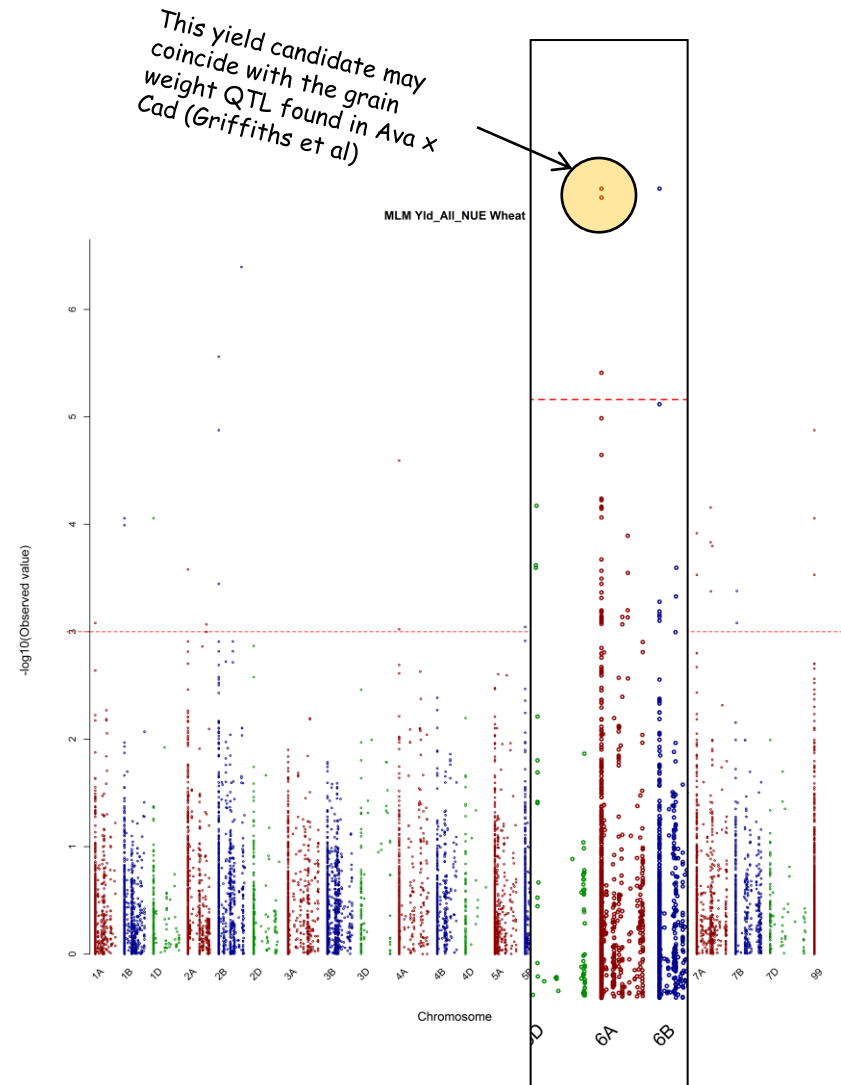


# Association Mapping

- Height

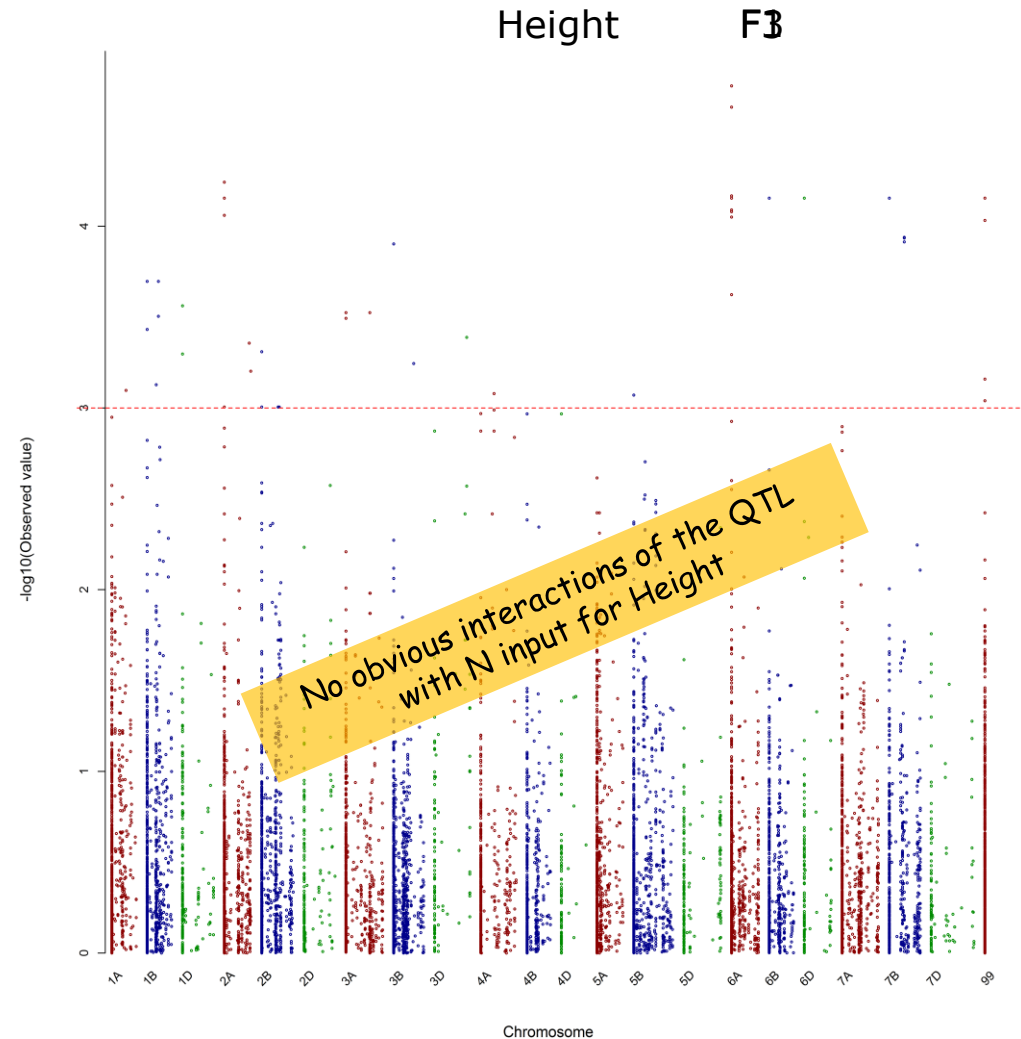


## Yield



# Association Mapping and NUE

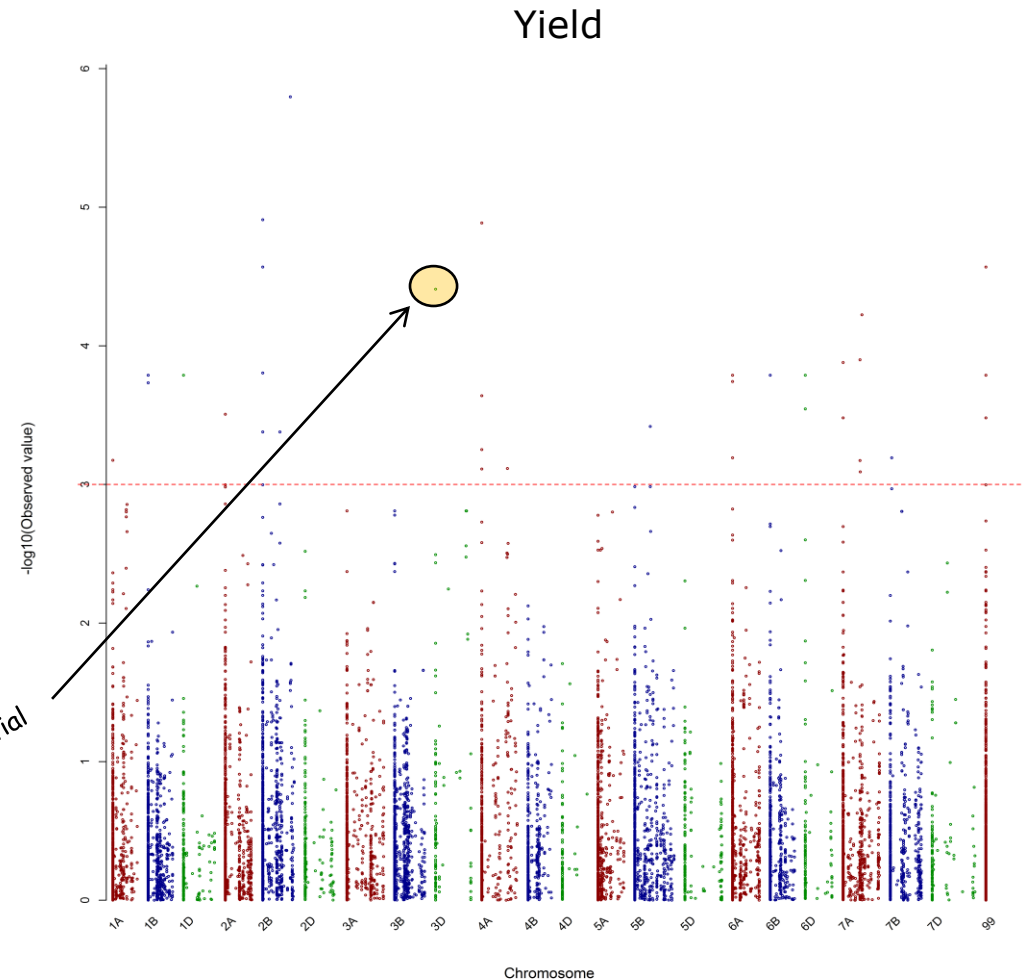
- Most interesting QTL may be those that differ between high and low input
- At least two approaches are possible
  - Derived a statistic to summarise the relative differences at the high and low N rates
  - Simply compare the QTL analysis from the high and low N rates



# Association Mapping and NUE

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This association only appears to be substantial in F3





# Further Work

- There is a lot of detailed analysis to be completed
- Many candidate QTL will be identified
- Validation will be key and will work on more than one level
  - Cross-referencing to previously published wheat QTL
  - Study of the inter-species synteny between barley and wheat
  - Use of bi-parental populations to look at yield components



# Acknowledgements

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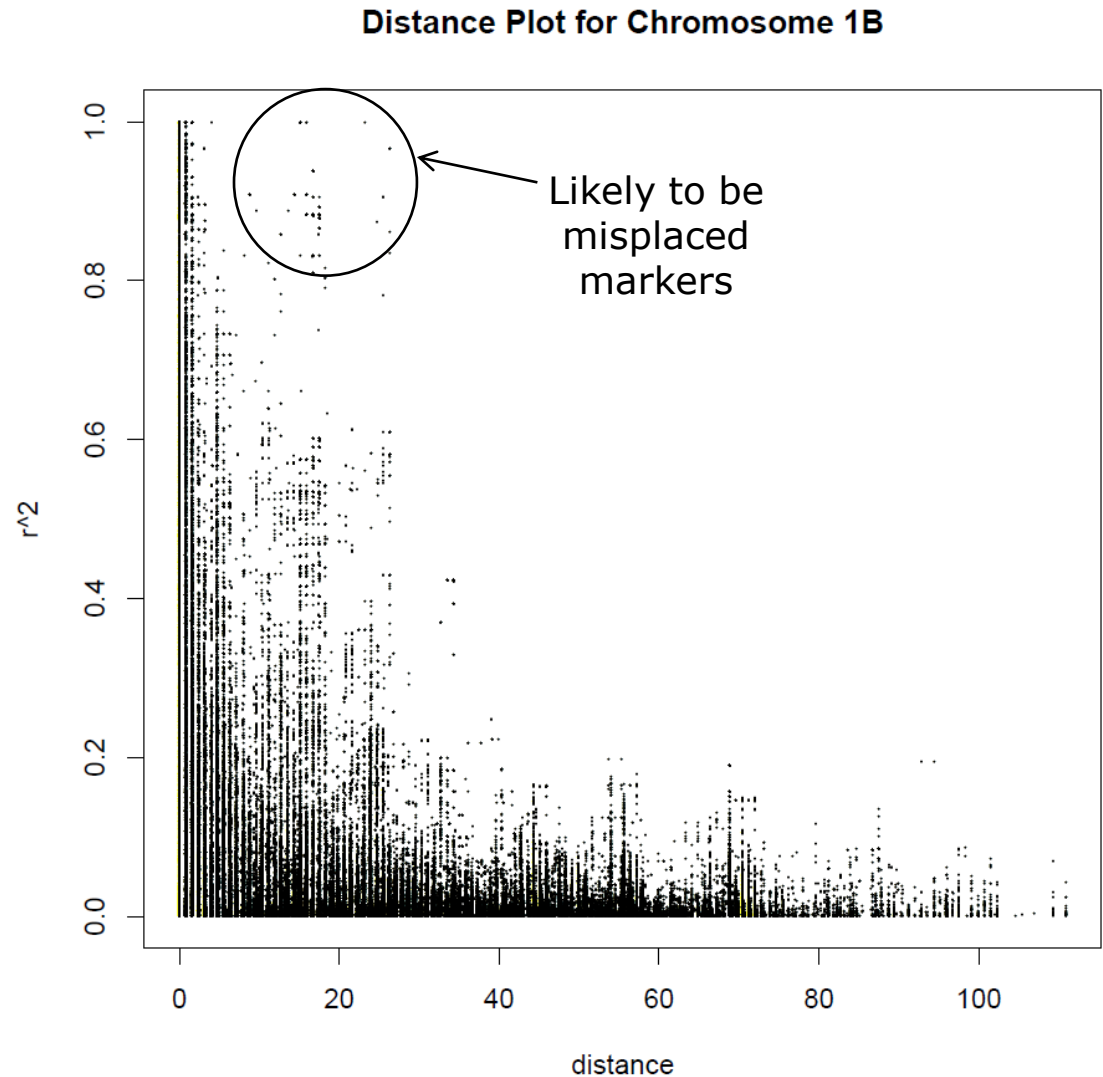
*Thank you for your  
attention*



<http://research.ncl.ac.uk/nefg/nuecrops/page.php?page=1>

# Supplementary slides

- Several of the chromosomes show on the LD plots clear issues regarding the current map



# LD on Chromosome 1B

Many centromeric markers are co-mapped and are in fact closely associated

A large minority of the markers look misplaced

