Fine Mapping of QTL for Mastitis Resistance on BTA11 in Three Nordic Red Cattle Breeds

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Funded partly by EC FP5 project MASTITIS RESISTANCE (QLK5-CT-2002-01186)

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Clinical mastitis

- Difficult to obtain genetic progress by traditional breeding
  - Low heritability
  - Difficult to record
  - Undesired genetic correlation with production
- Mastitis is a prime candidate for marker assisted selection (MAS)

Somatic cell score (SCS)

- SCS is an indicator trait for clinical mastitis
  - Highly correlated
  - Easy to record and routinely recorded
- QTL so far mostly reported for SCS
  - Not known if the QTL affects clinical mastitis
- Reports are mostly within family study
  - Limiting population level selection

Objective

- To fine map the QTL on BTA11 affecting clinical mastitis and SCS using combined LD/LA analysis

Populations and traits

- Animal
  - Finnish Ayrshire (8 GS)
  - Swedish Red and White (5 GS)
  - Danish Red (1 GS)
  - Total no. of sons 524 (23-83)
- Traits
  - Clinical mastitis (CM)
  - Somatic cell score (SCS)

BTA11 linkage map

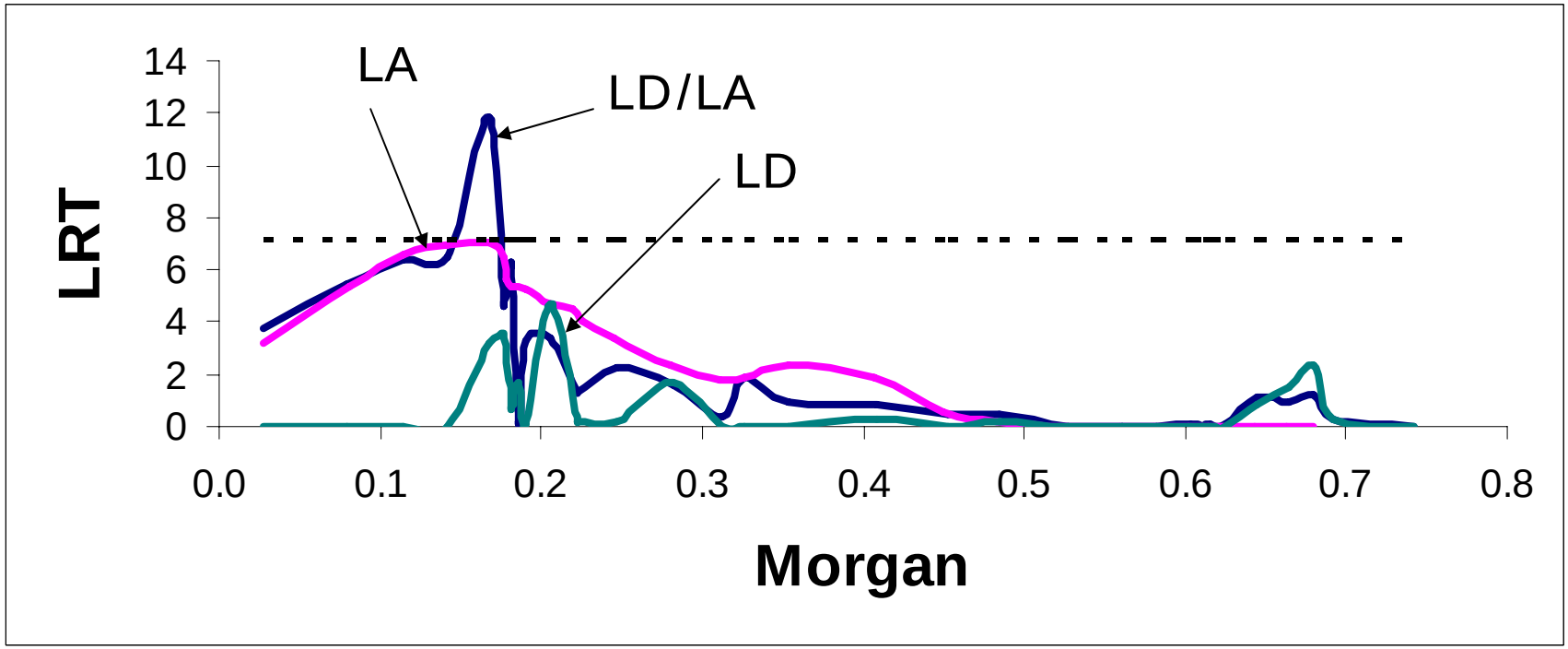
- Total 37 markers were genotyped on BTA11
  - Concentrated in 2 selected regions
- Markers order and map distances
  - CRIMAP 2.4
  - Ensembl genome sequence
  - RH map
- Linkage map
  - 85.2 cM

Model

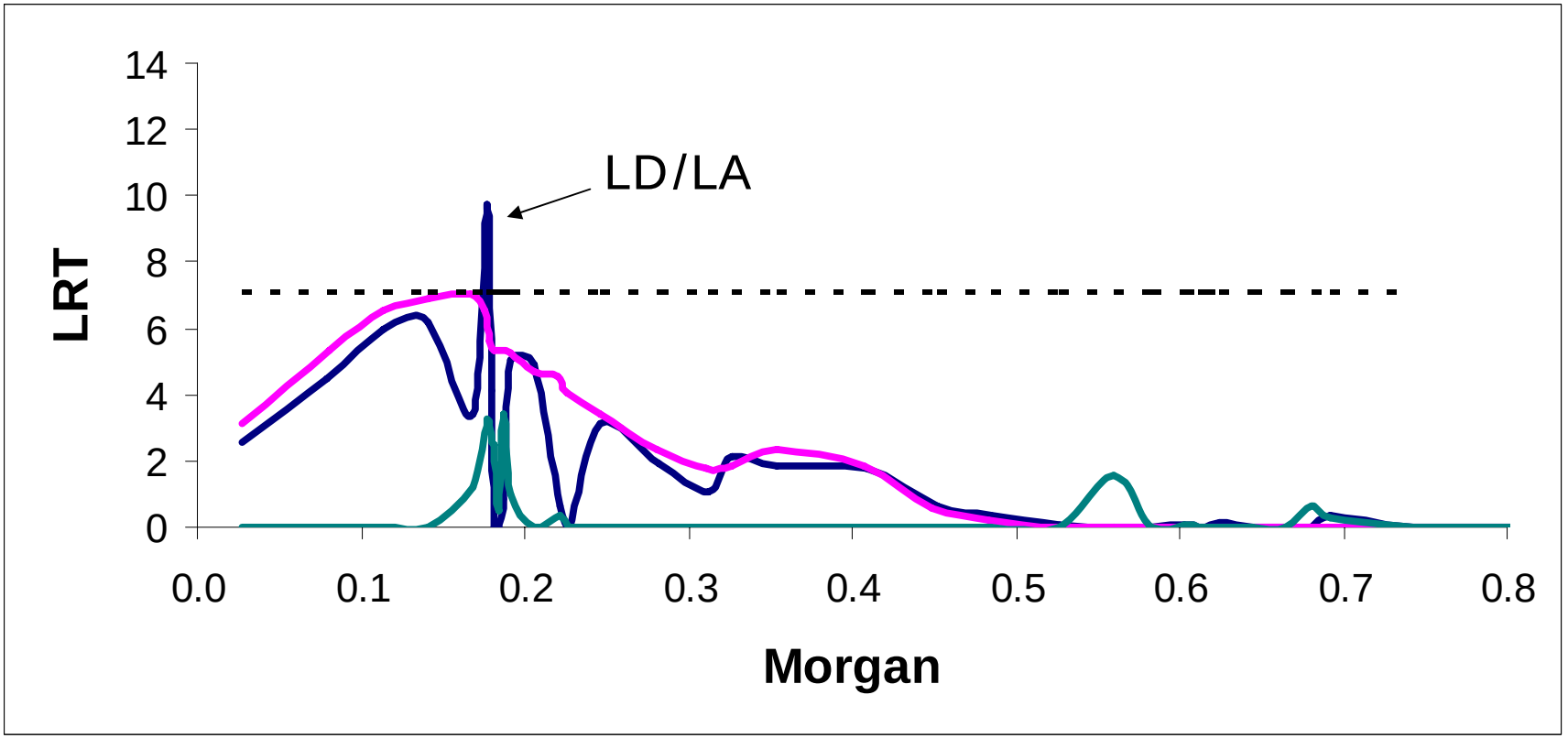
$$\mathbf{y} = \boldsymbol{\mu} + \mathbf{Zu} + \mathbf{Wh} + \mathbf{e}$$

- **y -** vector of phenotypes
- **μ -** overall trait mean
- **Z** and **W -** incidence matrices
- **u -** polygenic effect
- **h -** random haplotypes effect
- **e -** random sampling error

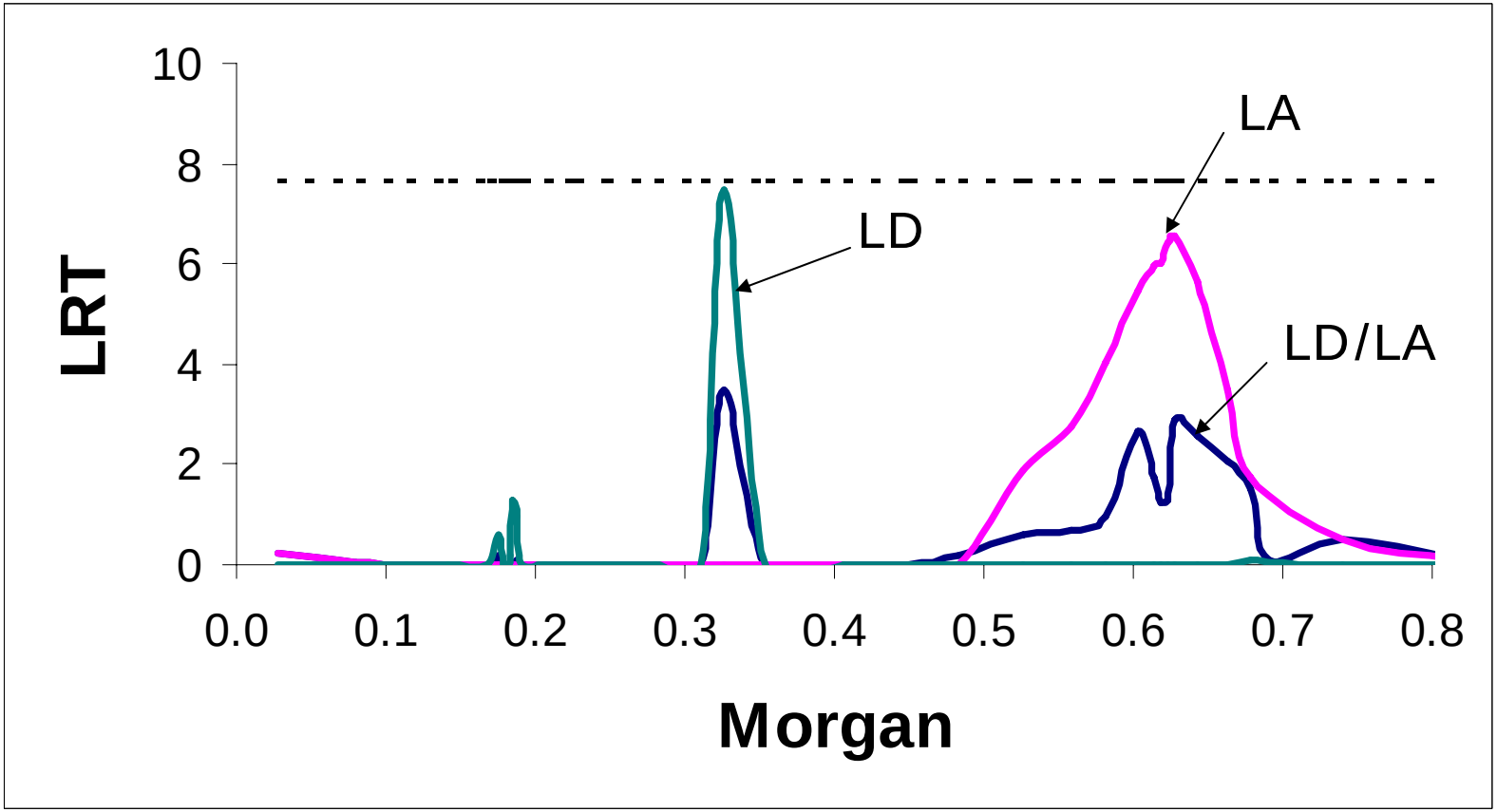
Clinical mastitis (FA)



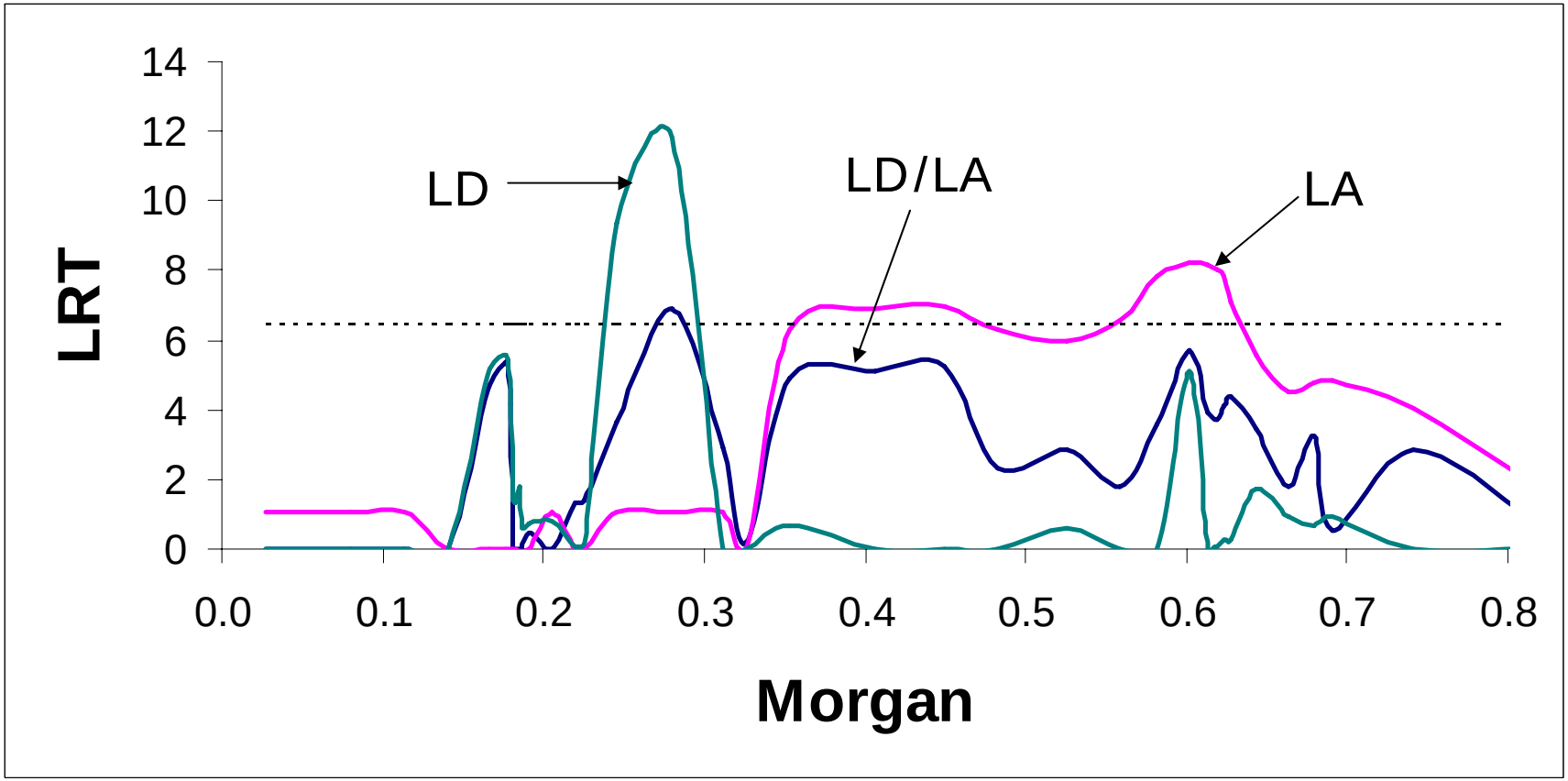
Clinical mastitis with 4-marker haplotype (FA)



SCS (FA)



SCS (SRB)



Across breed analyses

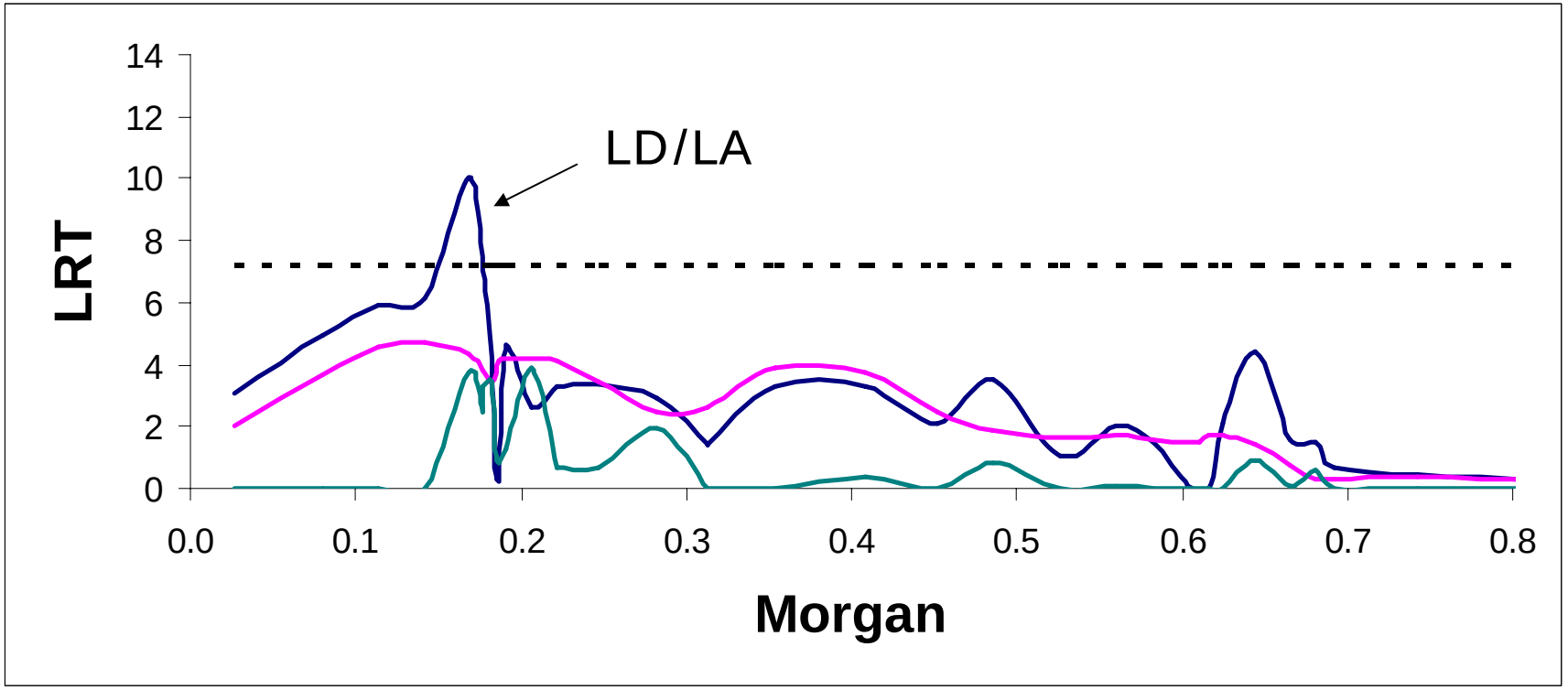
Finnish Ayrshire

Swedish Red and White

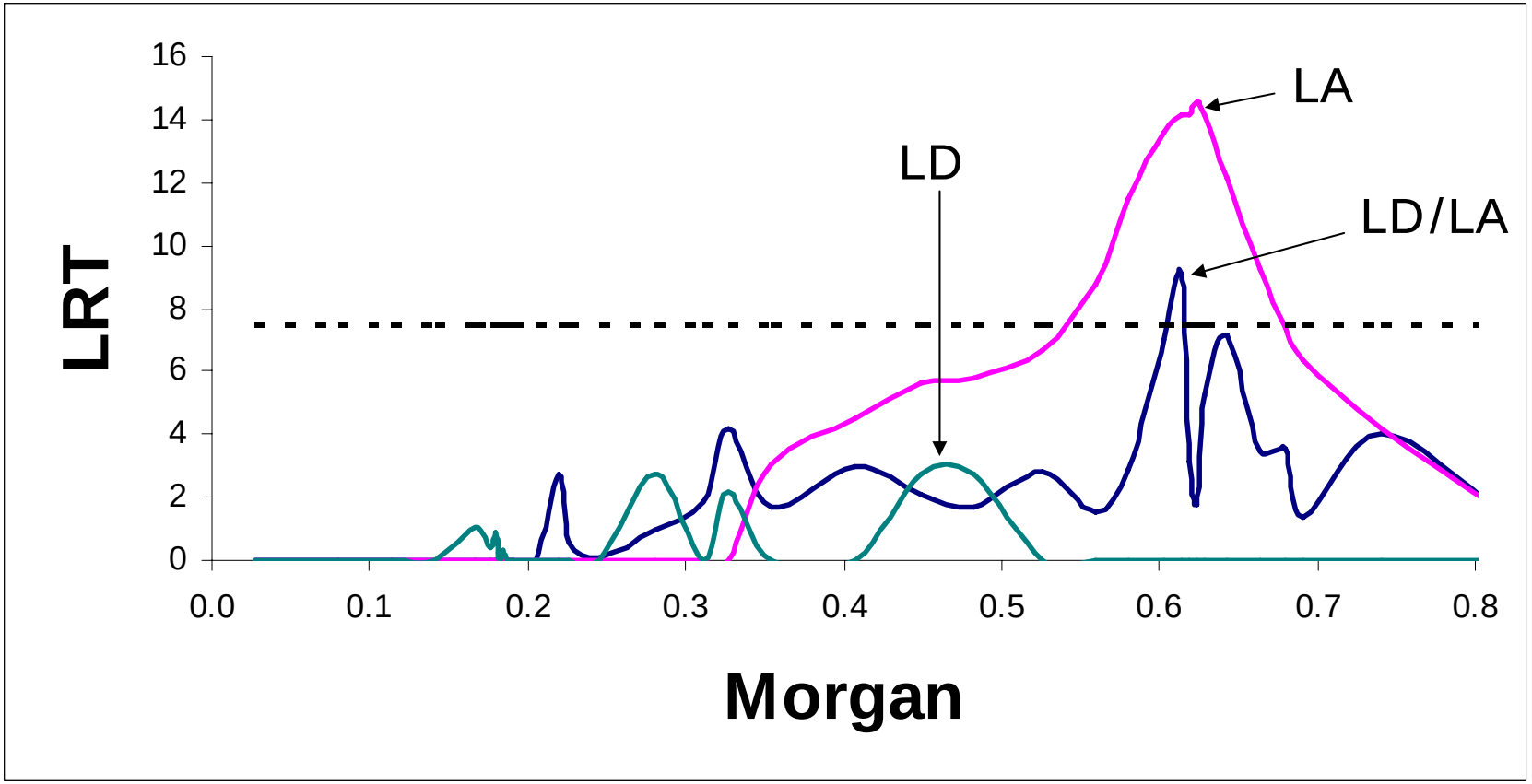
Danish Red

- FA, SRB and DR are distinct breeds but have historic and recent genetic connection

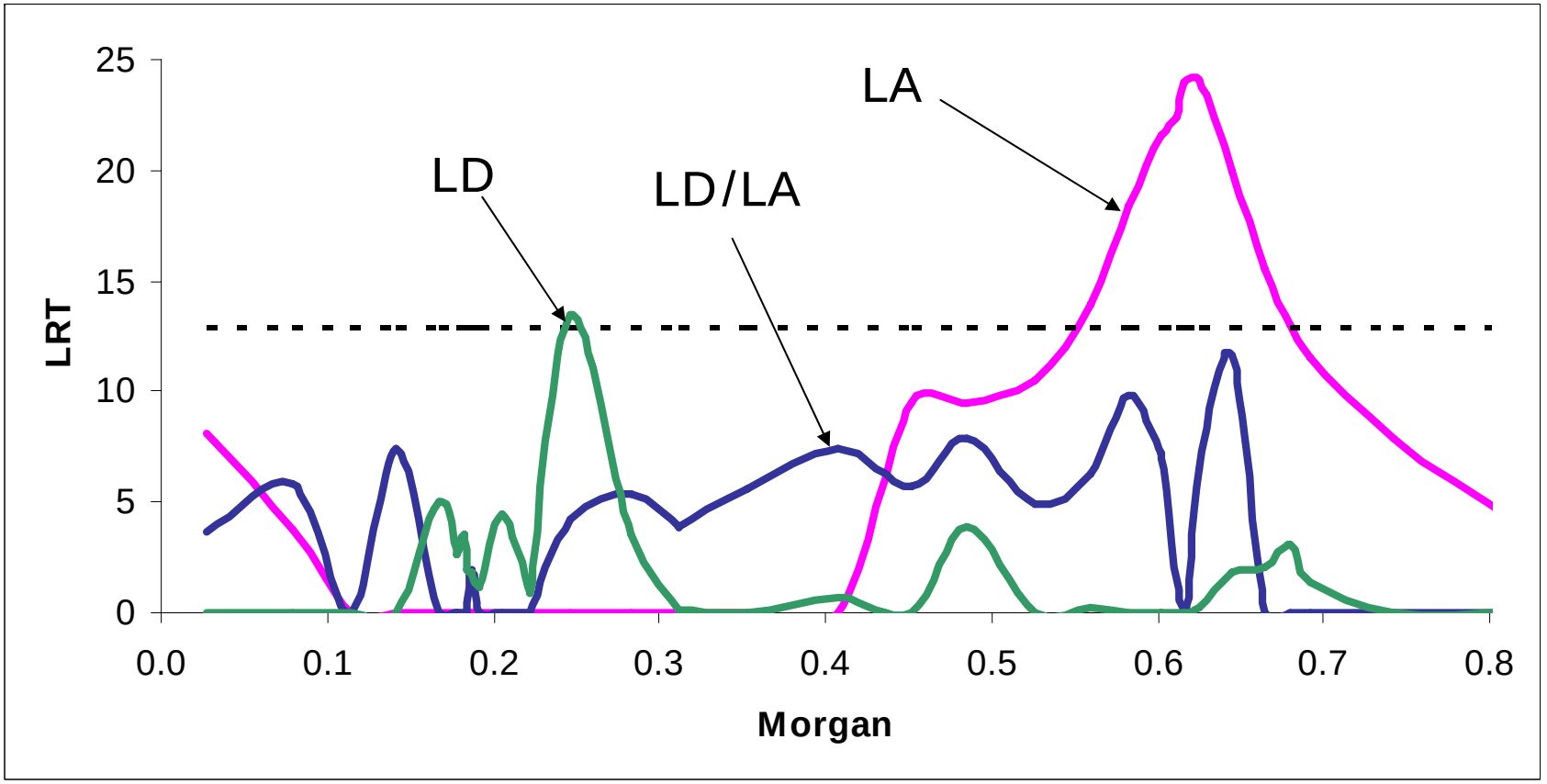
Clinical mastitis (combined)



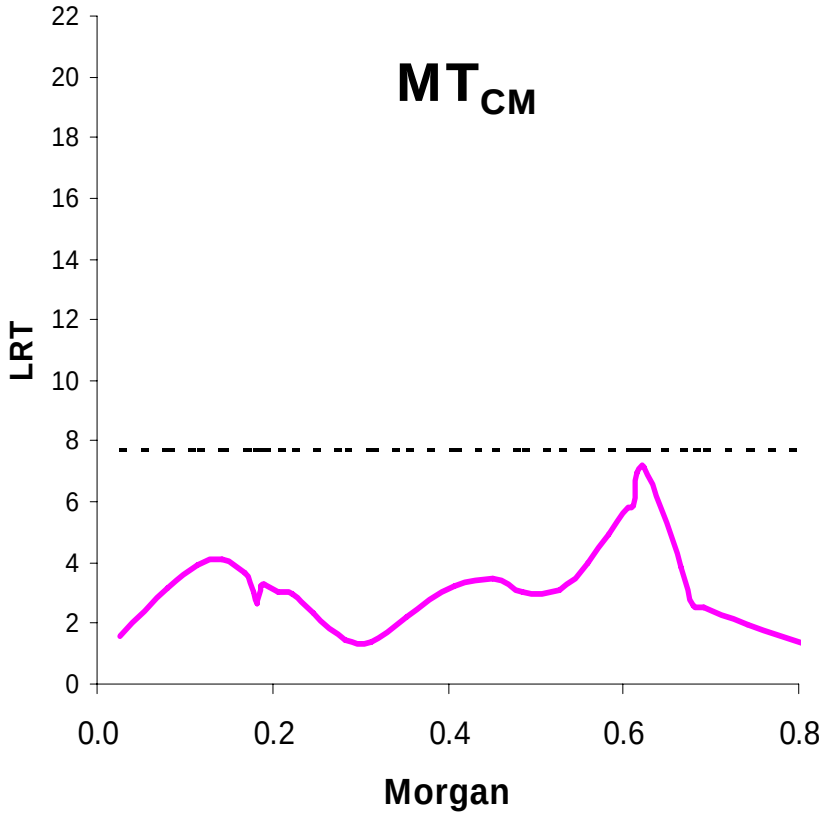
SCS (combined)

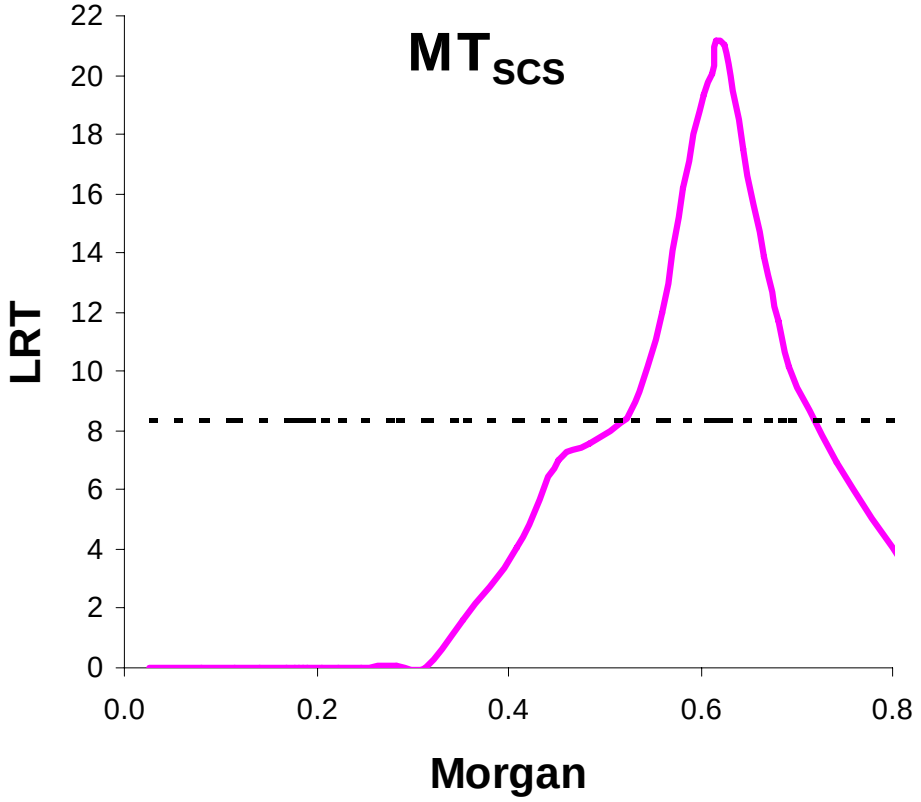


Multi trait – pleiotropic QTL



Multi trait analyses





Multi trait analyses (combined)

Model	LRT	QTL_{CM} (cM)	QTL_{SCS} (cM)
MT_L	26.1	14.2	61.6
MT_P	24.1	62.5	62.5
MT_{CM}	7.1	62.5	
MT_{SCS}	21.2		61.6

Conclusions

- QTL affecting clinical mastitis is segregating on BTA11 in FA
  - The LD/LA analysis fine mapped the QTL
- QTL affecting SCS is segregating in both FA and SRB
  - But could not be fine map due to lack of LD between markers and QTL