

# Comparative analysis of submitted results on QTL mapping and applied methods

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# Common task

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- Describe the genetic architecture of quantitative and binary trait
- 7 groups reported QTLs for quantitative trait (QT)
- 5 groups reported QTLs for binary trait (BT)

# Methods used by participants

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- Bayesian
- BayesC
- BayesCPi
- Partial Least Squares regression (PLSR)
- GRAMMAR
- Haplotyping
- DHGLM

- A **true QTL** was considered mapped if one or more submitted positions were within 1 Mb distance from the QTL. Sometimes one submitted position maps two different QTLs.
- Number of **false positions** is the number of submitted positions with the distance to the closest true QTL exceeding 1 Mb.

# True genetic architecture

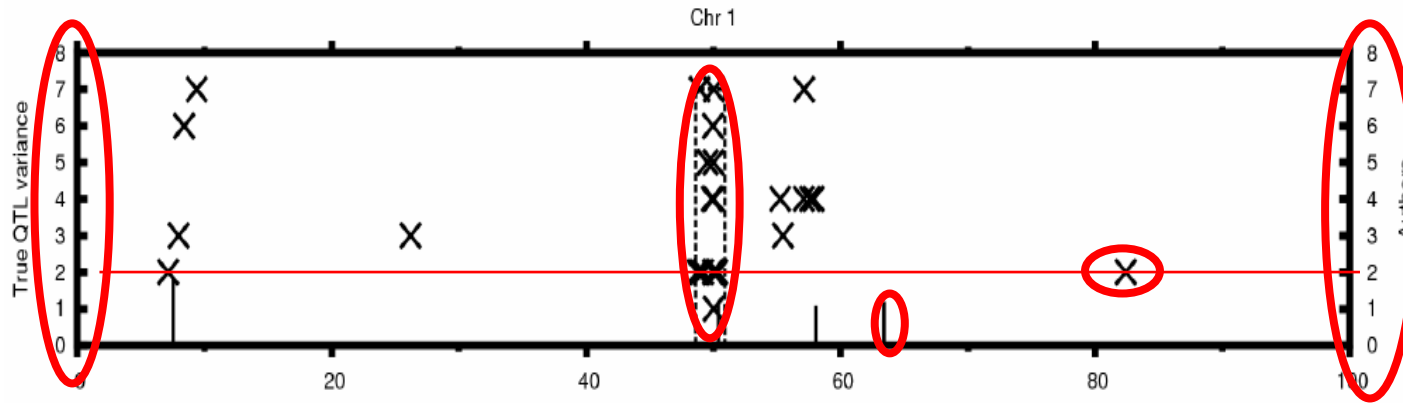
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- For quantitative trait
  - 30 additive QTLs
  - 2 pairs of epistatic QTLs
  - 3 imprinted QTLs
- For binary trait
  - 22 additive QTLs – a subset of QTLs affecting quantitative trait

- Quantitative trait:
  - QTL positions
  - % genetic variance /genetic variance
- Binary trait
  - QTL positions
  - % genetic variance /genetic variance on arbitrary scale

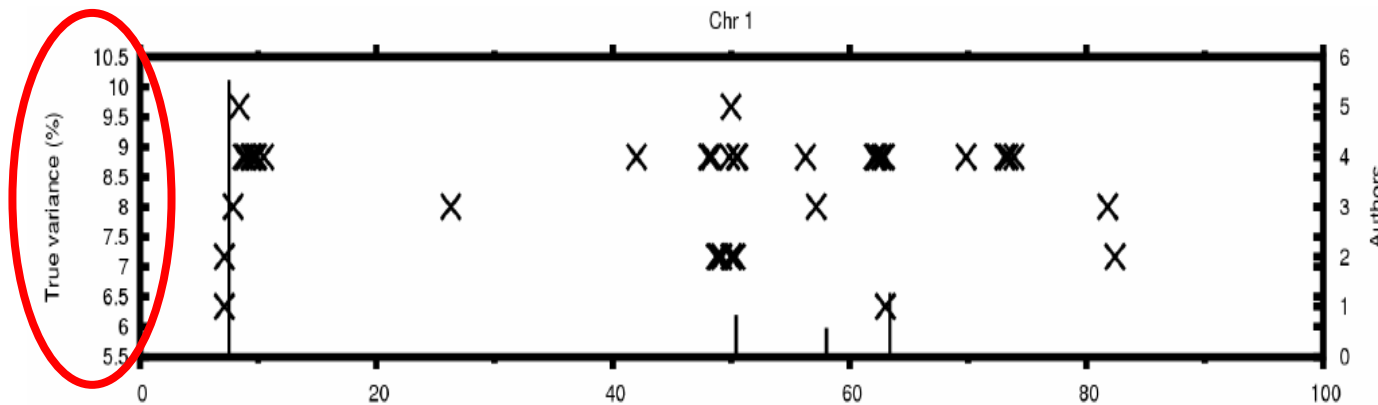
# Chromosom 1

QT



7. Sun and Dekkers
6. Shen et al.
5. Nettelblad
4. Karacaören et al.
3. Coster and Calus
2. Calus et al.
1. Bouwman et al.

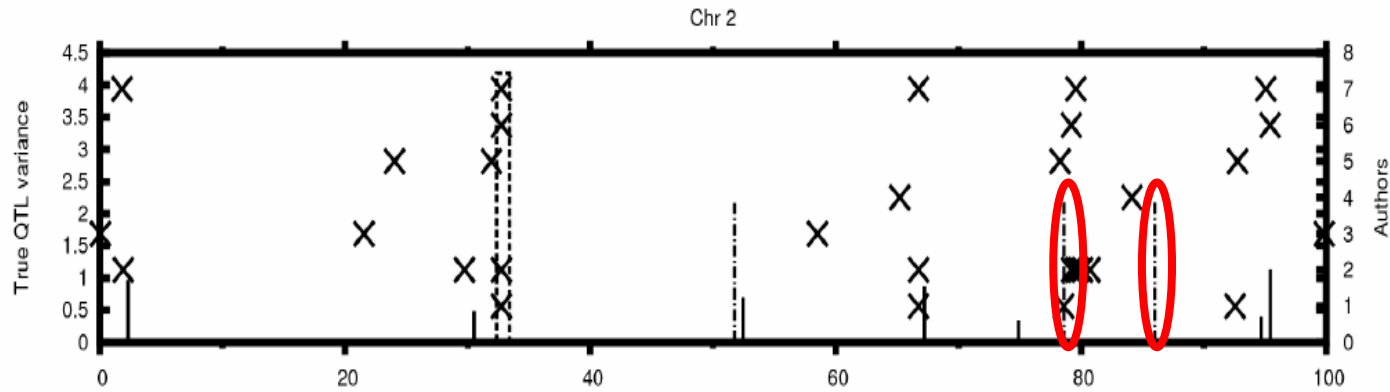
BT



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4. Karacaören et al.
3. Coster and Calus
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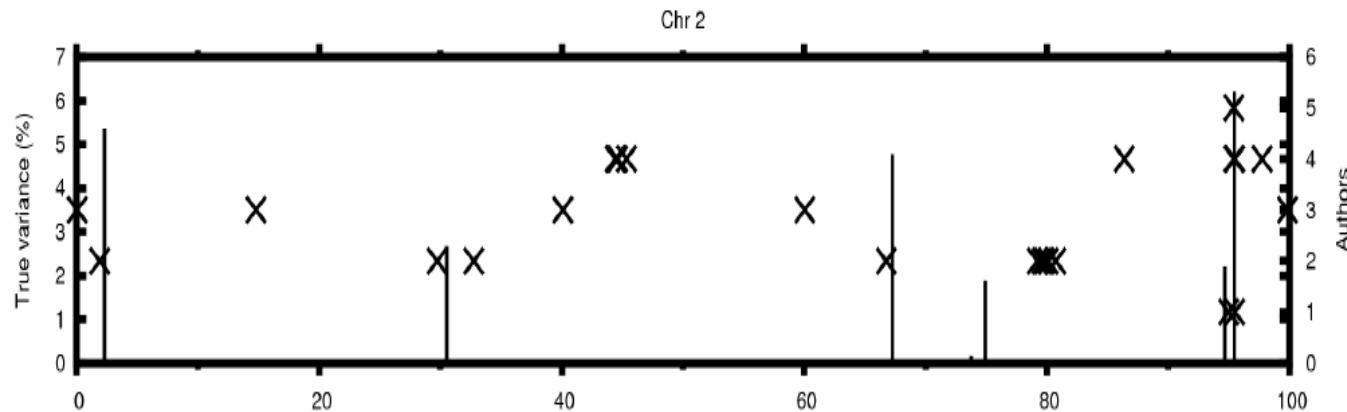


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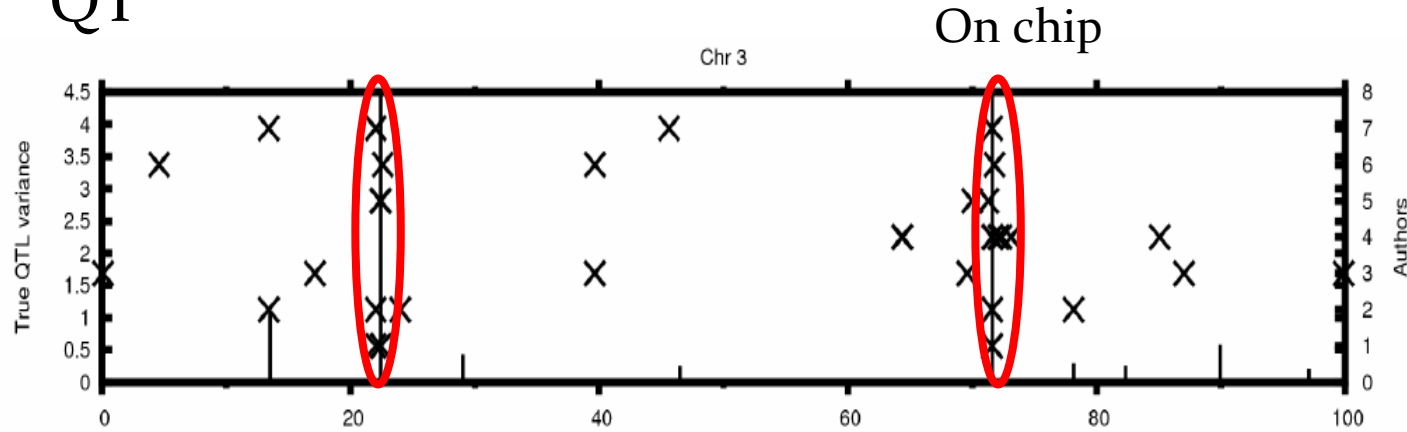
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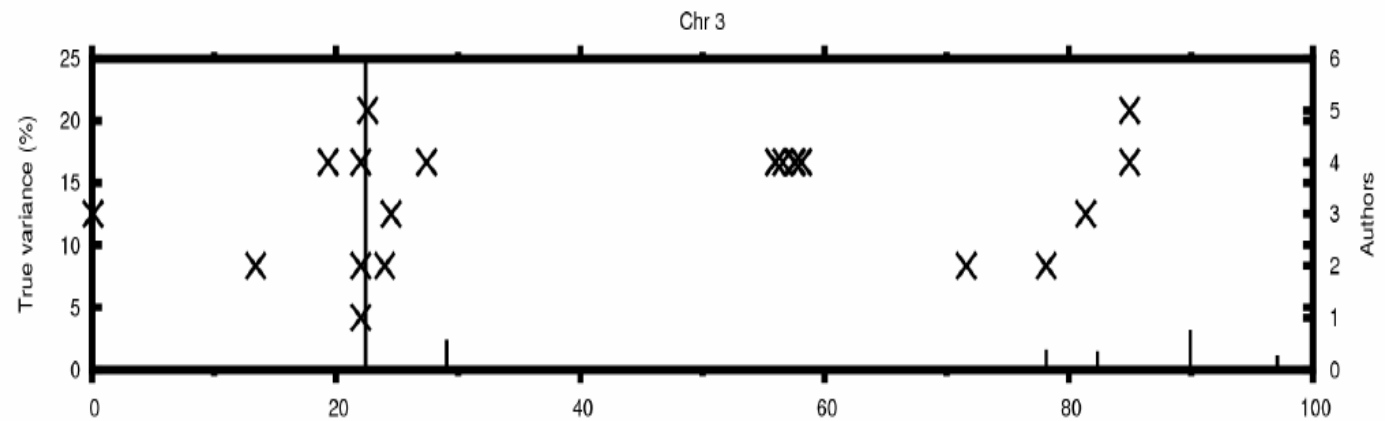


QT



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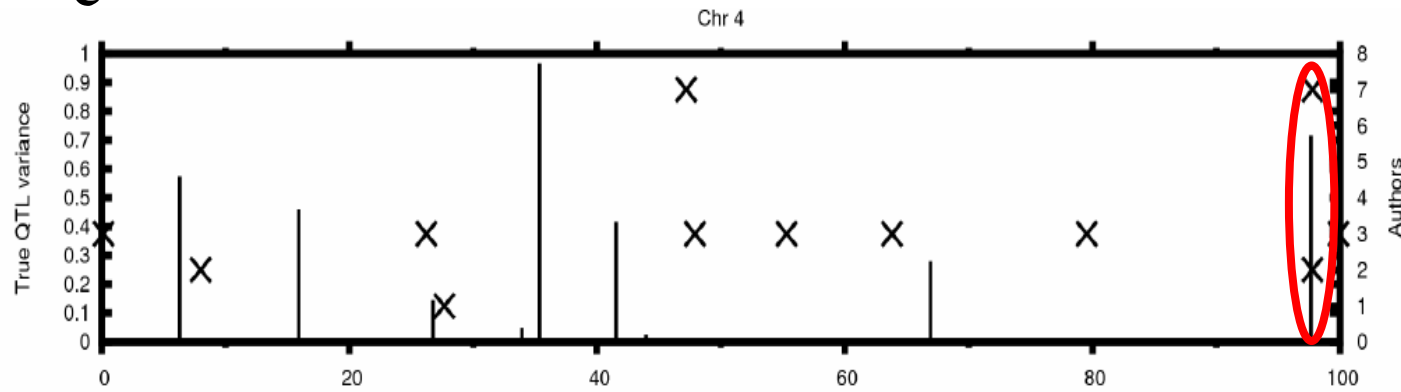
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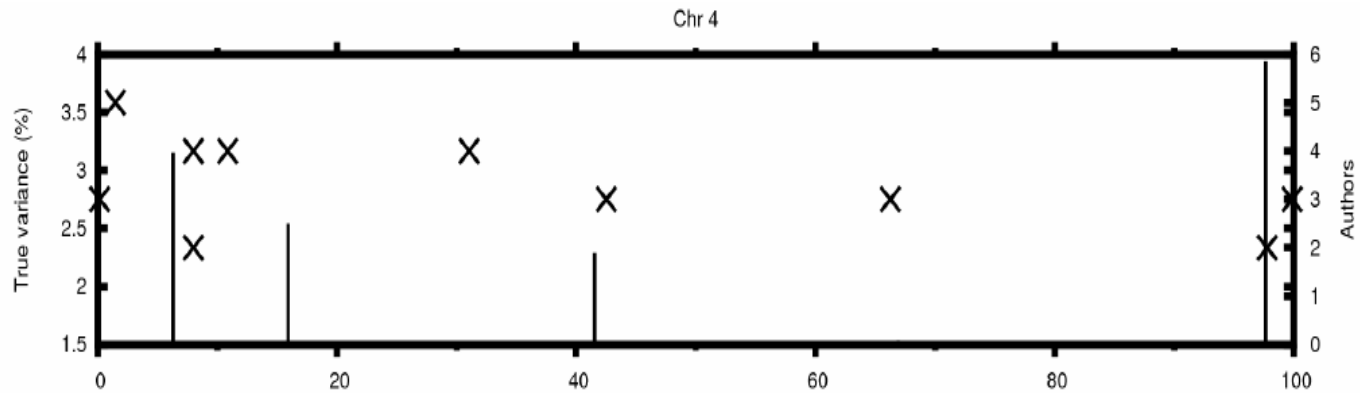


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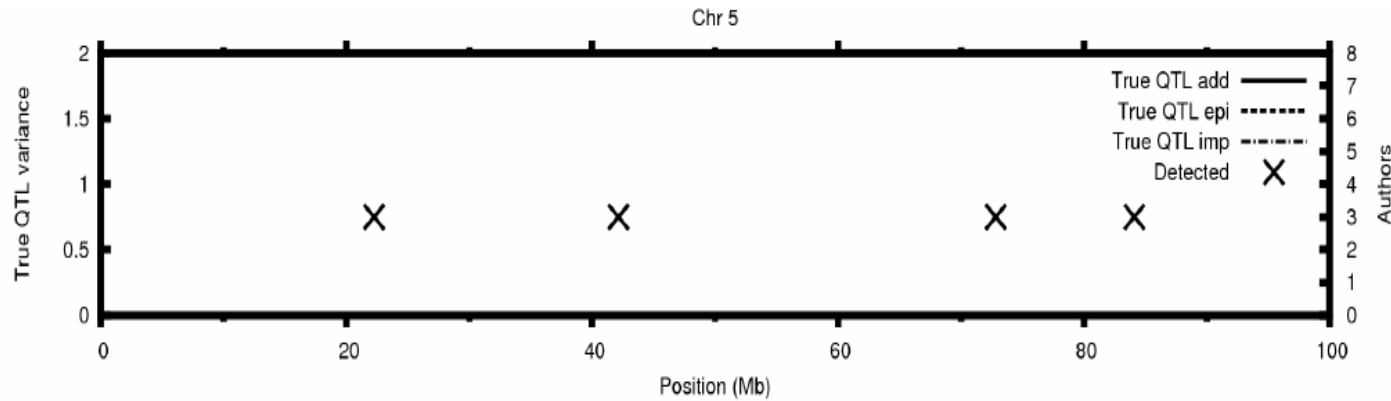
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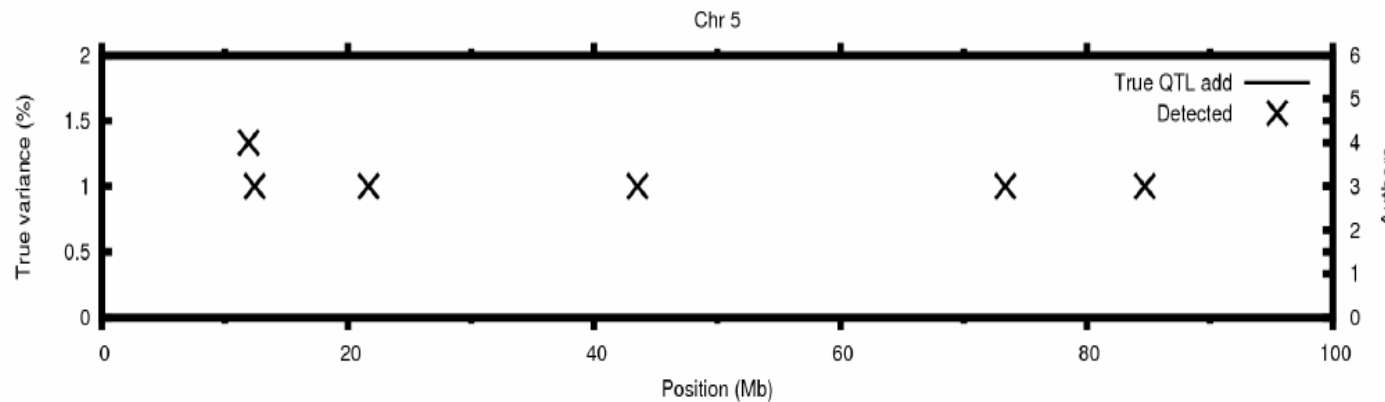


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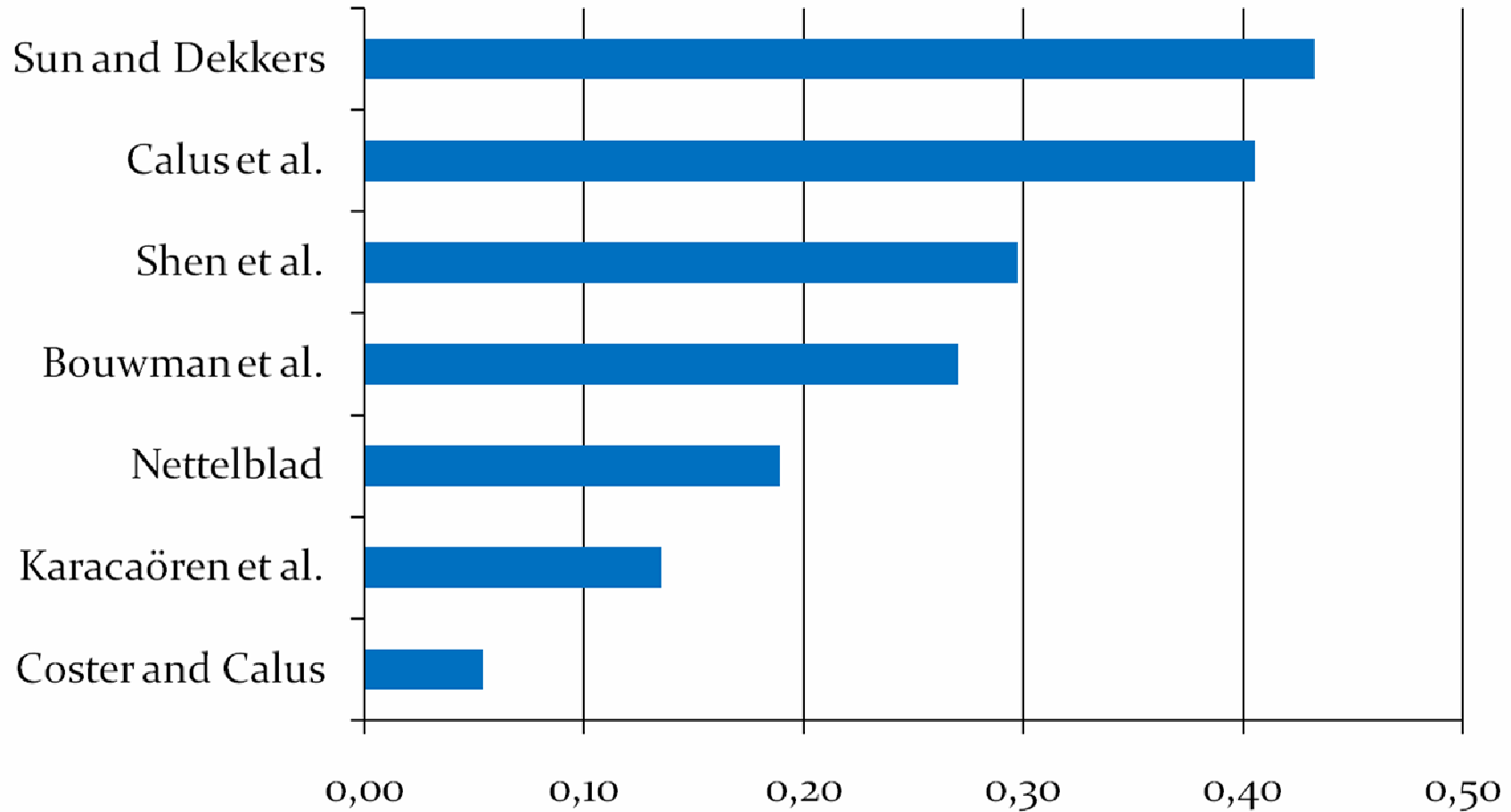
Authors	Method	Reported positions	Mapped QTLs	Mean dist.	False
1. Bouwman et al.	Bayesian	9	10	0.34 Mb	1
2. Calus et al.	BayesC	24	15	0.26 Mb	6
3. Coster and Calus	PLSR	25	2	0.62 Mb	20
4. Karacaören et al.	GRAMMAR	16	5	0.31 Mb	7
5. Nettelblad	Haplotyping	10	7	0.34 Mb	3
6. Shen et al.	DHGLM	9	11	0.42 Mb	2
7. Sun and Dekkers	BayesCPi	15	16	0.41 Mb	2



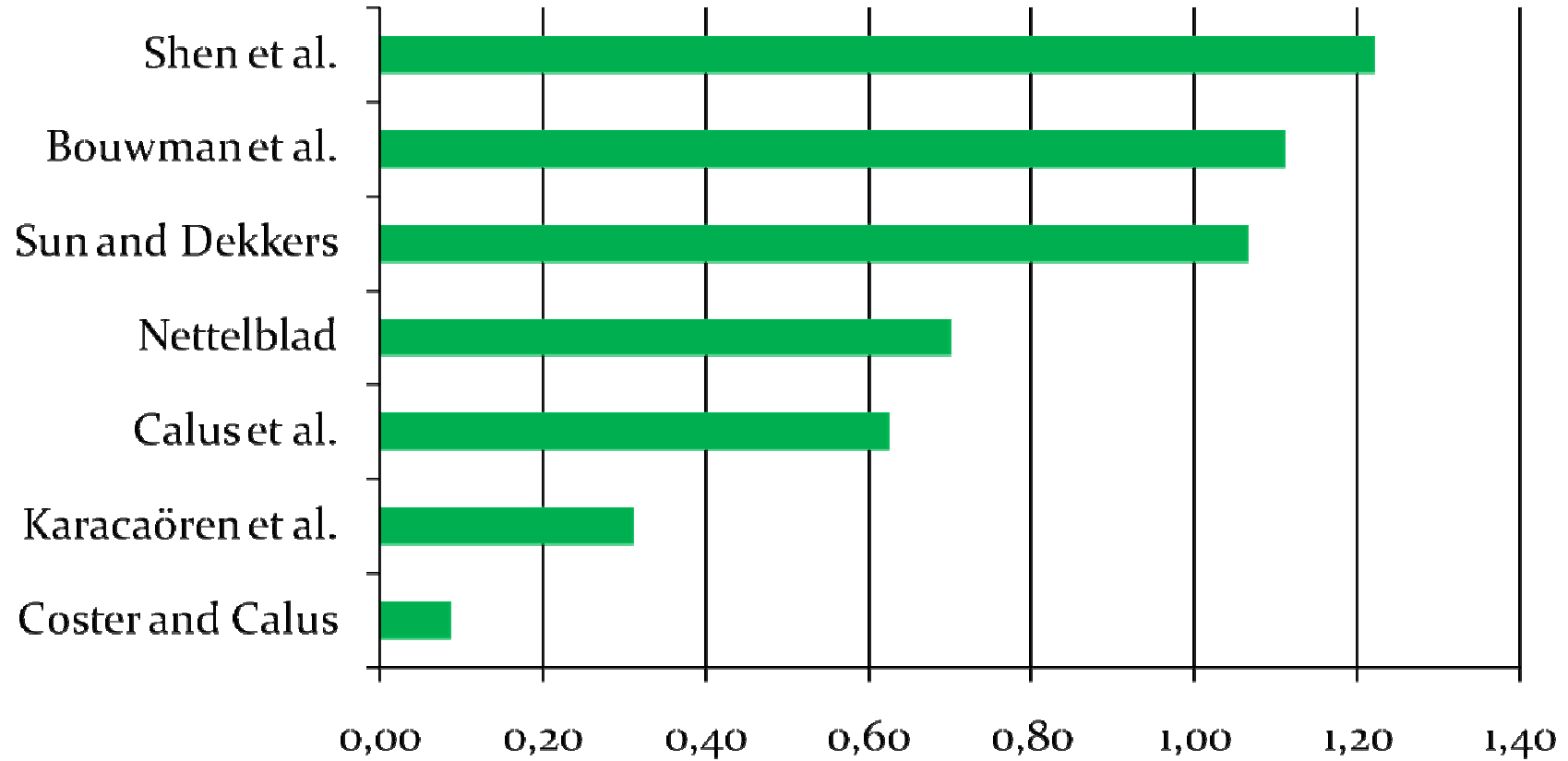
MAS

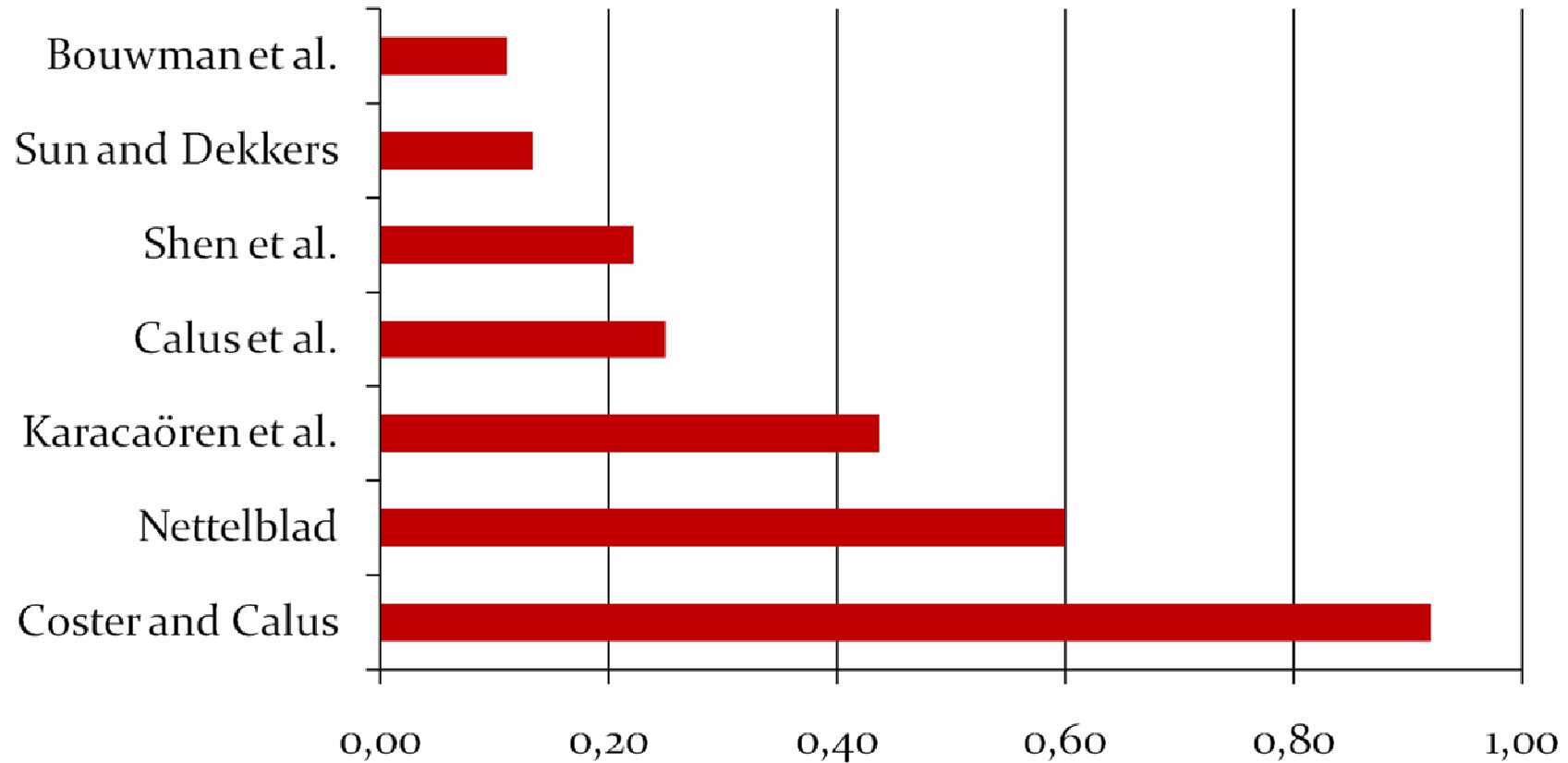
# Success rate

QT



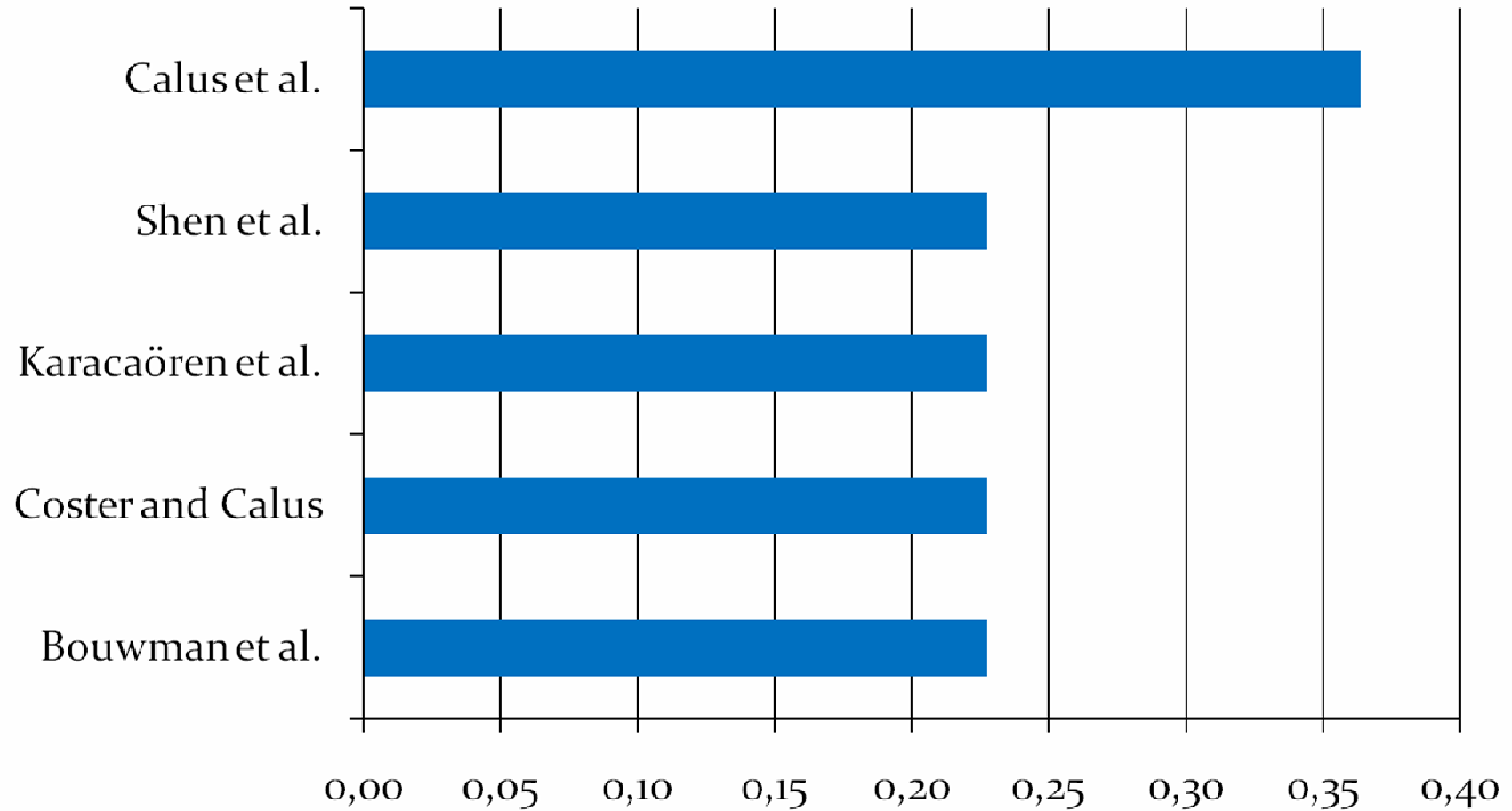
# Mapped / reported QT





<b>Authors</b>	<b>Method</b>	<b>Reported positions</b>	<b>Mapped QTLs</b>	<b>Mean dist.</b>	<b>FALSE</b>
1. Bouwman et al.	Bayesian	5	5	0.30 Mb	0
2. Calus et al.	BayesC	24	8	0.33 Mb	14
3. Coster and Calus	PLSR	22	5	0.77 Mb	17
4. Karacaören et al.	GRAMMAR	50	5	0.33 Mb	41
5. Shen et al.	DHGLM	6	5	0.45 Mb	2



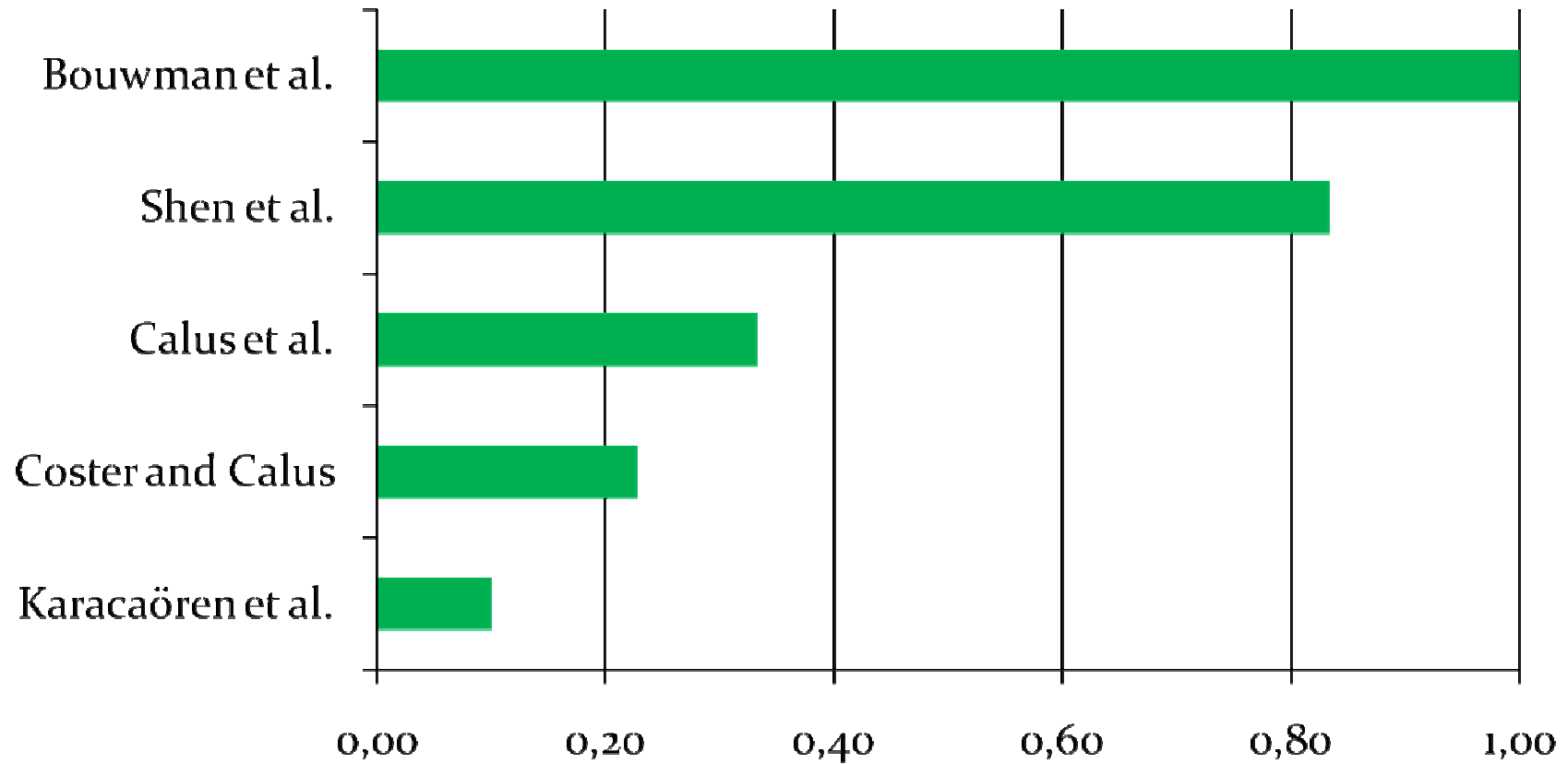


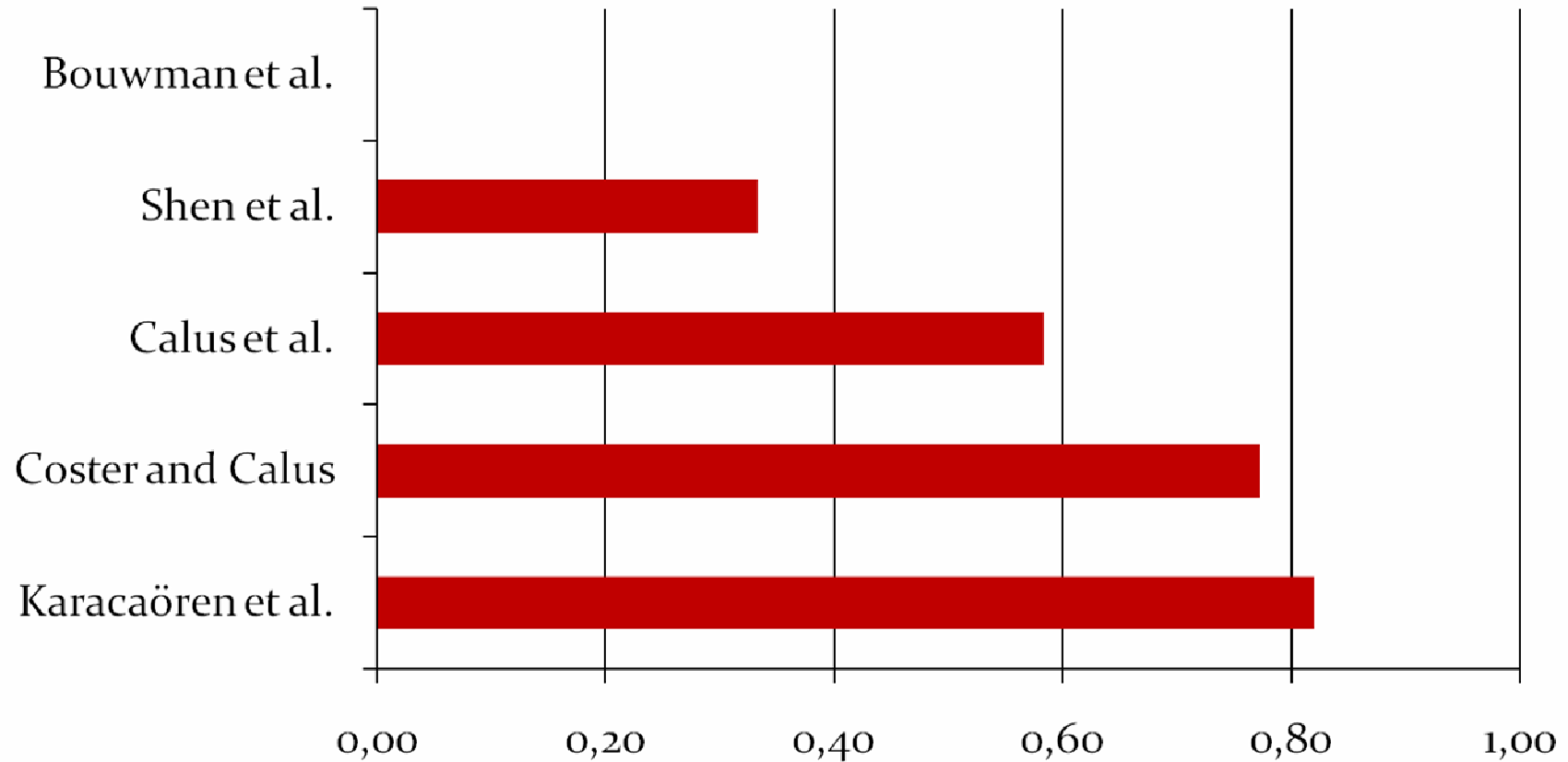


MAS

# Mapped / reported

BT





# Summary

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- Epistatic QTLs were closely linked and therefore one or both SNPs were often found as a single QTL
- Bayesian methods were more powerful for detecting QTLs
- Differences among methods increased with trait complexity
- Imprinted QTL – difficult to detect even if on chip

Congratulations to the authors !!!  
Thank you for sharing the results !!!