QTL MAS

Analysis of submitted breeding values and applied methods

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Common task

- Predict breeding values for young individuals without phenotypes

- **11** teams provided results for qunatitative (**QT**) and 6 for binary trait (**BT**)

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True Breeding Value

- QT:

  TBV = ∑[30 additive QTLs] +

  + haplotype effects (QTLs pairs 31-32 and 33-34) +

  + the effects of imprinted QTLs (for males only).

- BT:

  TBV = ∑ 22 additive QTLs.

Methods used by Participants

- BLUP:
  - PBLUP(pedigree; univariate and bivariate),
  - TA-BLUP(specific relationship matrix),
  - G(enomic)BLUP (univariate and bivariate)
  - RR-BLUP – ridge regression
  - Spatial
- Bayes A,B,C (univariate and bivariate)
- PLSR
- Double Hierarchical Generalized Linear Models (DHGLM)
- Machine learning: Support vector , Boosting, Genome-wide Rapid Association

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Comparison criteria

- **Accuracy** - Pearson correlation between TBV and EBV
- **Regression** - linear regression coefficient TBV on EBV
- **MSD** - mean square difference (TBV-EBV) after correcting for mean

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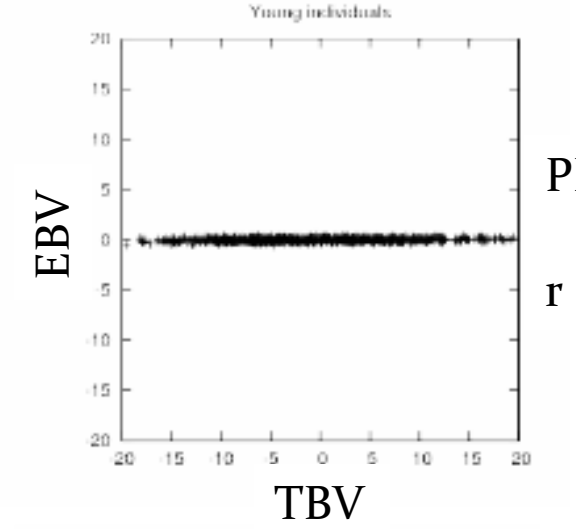
Comparison criteria cont.

- **Ranking comparison**:
  - **Shared** - percentage of IDs shared between the groups of young individuals selected on TBV and EBV
  - **Loss** - % of loss of response to selection when 10% are selected based on EBV instead of TBV

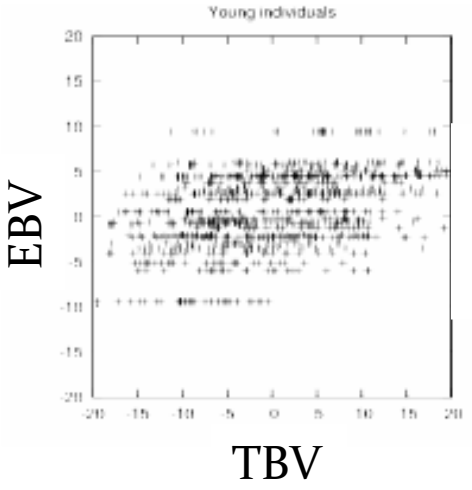
Accuracy of EBV - examples

QT



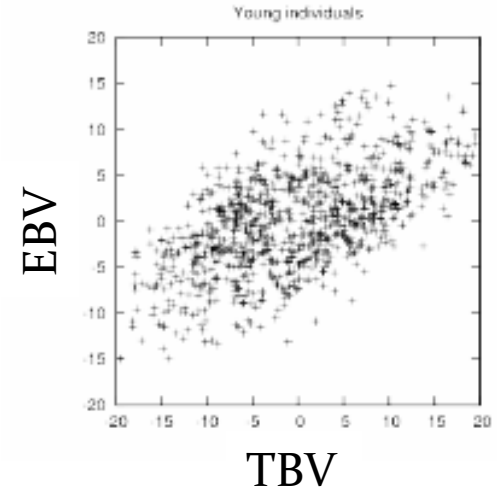
PLSR

r = 0.24



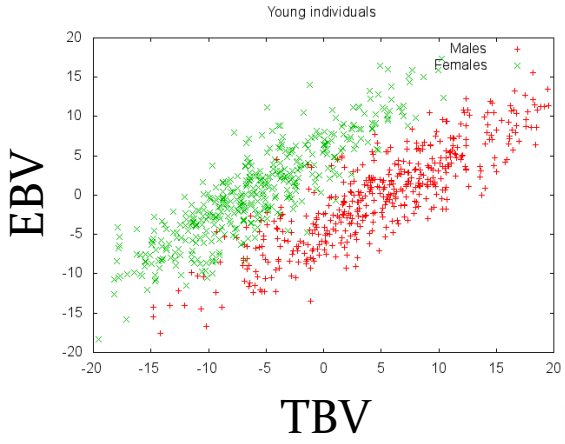
PBLUP

r = 0.39



GBLUP Bivar

rr = 0.62



BayesC Bivar

r= 0.67

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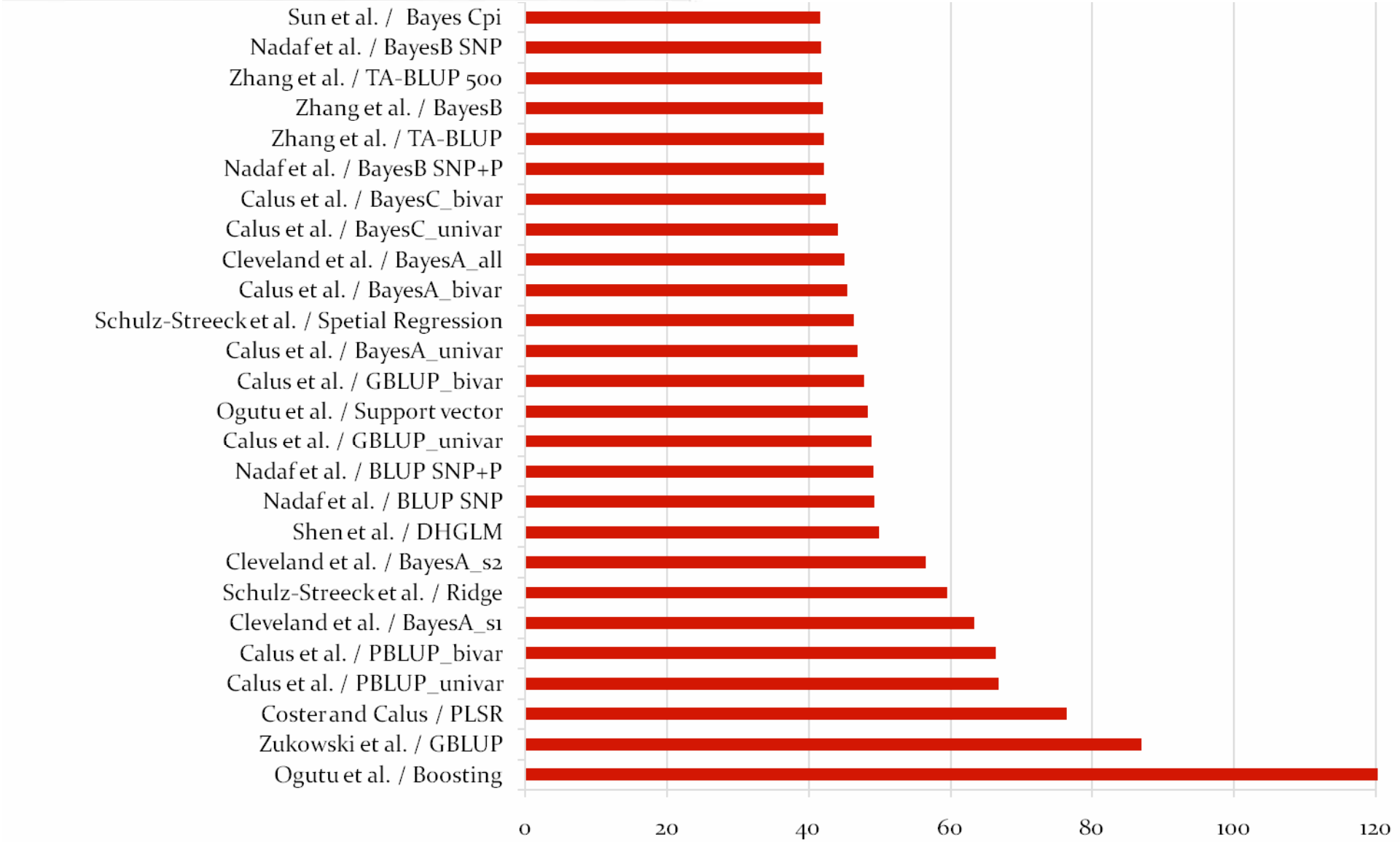
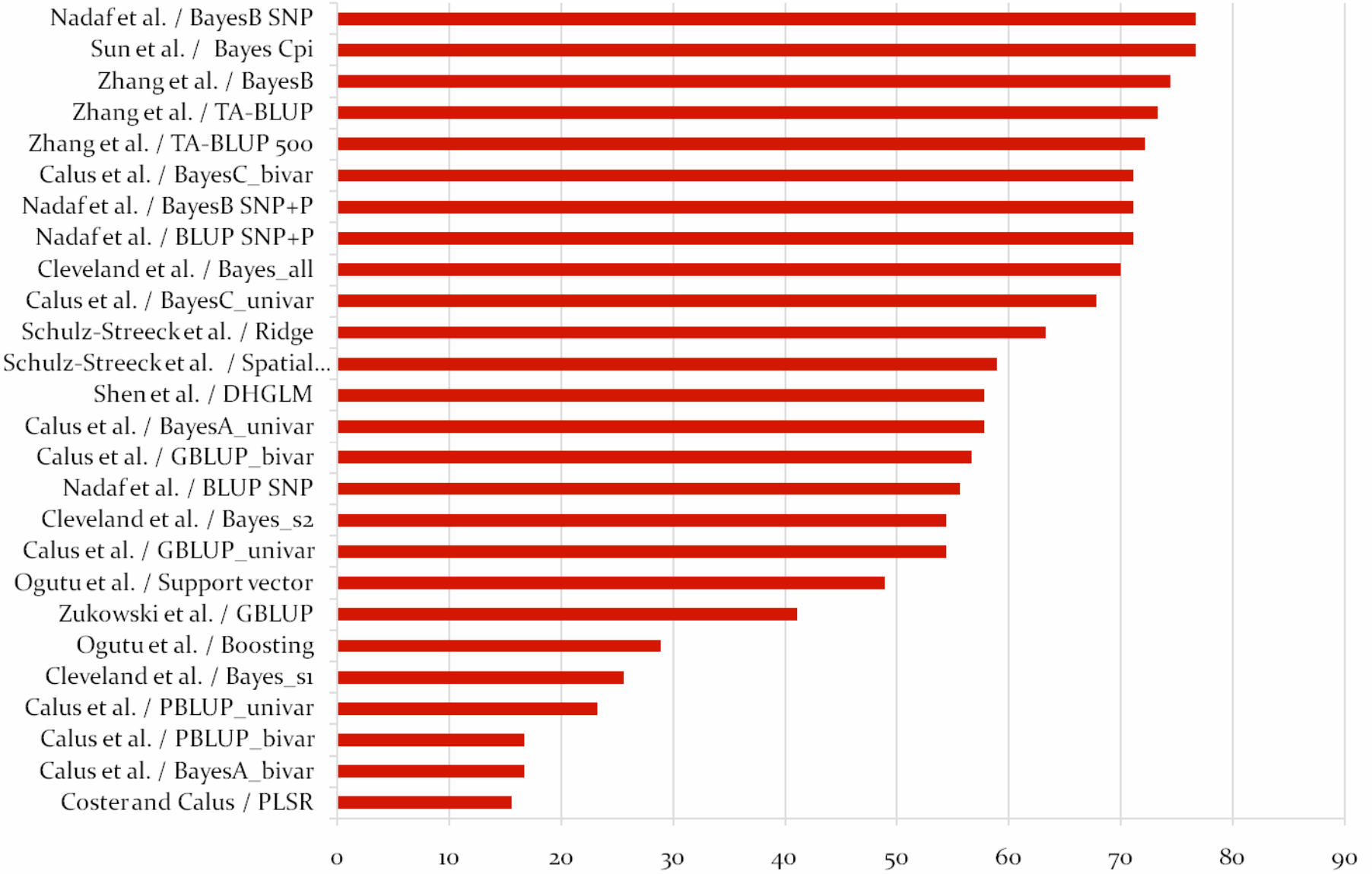
Accuracy and regression QT

MSD QT


Sun et al. / Bayes Cpi
Nadaf et al. / BayesB SNP
Zhang et al. / TA-BLUP 500
Zhang et al. / BayesB
Zhang et al. / TA-BLUP
Nadaf et al. / BayesB SNP+P
Calus et al. / BayesC_bivar
Calus et al. / BayesC_univar
Cleveland et al. / BayesA_all
Calus et al. / BayesA_bivar
Schulz-Streeck et al. / Spetial Regression
Calus et al. / BayesA_univar
Calus et al. / GBLUP_bivar
Ogutu et al. / Support vector
Calus et al. / GBLUP_univar
Nadaf et al. / BLUP SNP+P
Nadaf et al. / BLUP SNP
Shen et al. / DHGLM
Cleveland et al. / BayesA_s2
Schulz-Streeck et al. / Ridge
Cleveland et al. / BayesA_s1
Calus et al. / PBLUP_bivar
Calus et al. / PBLUP_univar
Coster and Calus / PLSR
Zukowski et al. / GBLUP
Ogutu et al. / Boosting
0
20
40
60
80
100
120

Shared QT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Nadaf et al. / BLUP SNP+P
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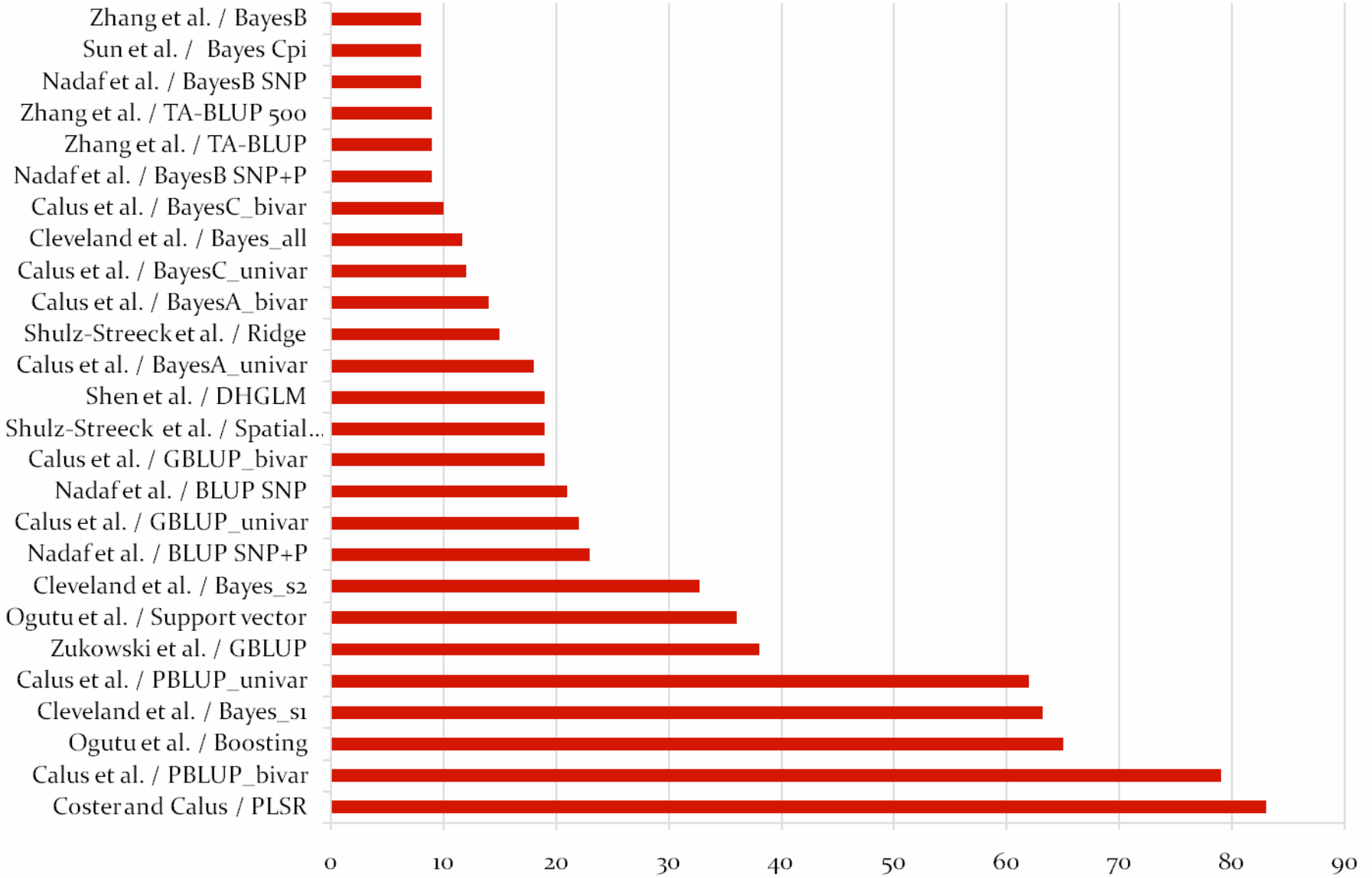
Loss (%) QT



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Ranking of the best group*methods based on all measurements

QT

1. Nadaf et al. - BayesB SNP
2. Sun et al. - Bayes Cpi
3. Nadaf et al. - BayesB SNP+P
4. Zhang et al. - BayesB
5. Zhang et al. - TA-BLUP 500
6. Zhang et al. - TA-BLUP
7. Calus et al. - BayesC_bivar
8. Calus et al. - BayesC_univar
9. Calus et al. - BayesA_bivar
10. Schulz-Streeck et al. - RR
11. Calus et al. - GBLUP_bivar
12. Schulz-Streeck et al. - Spatial
13. Calus et al. - BayeaA_univar
14. Calus et al. - GBLUP_univar
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18. Ogutu et al. - Boosting
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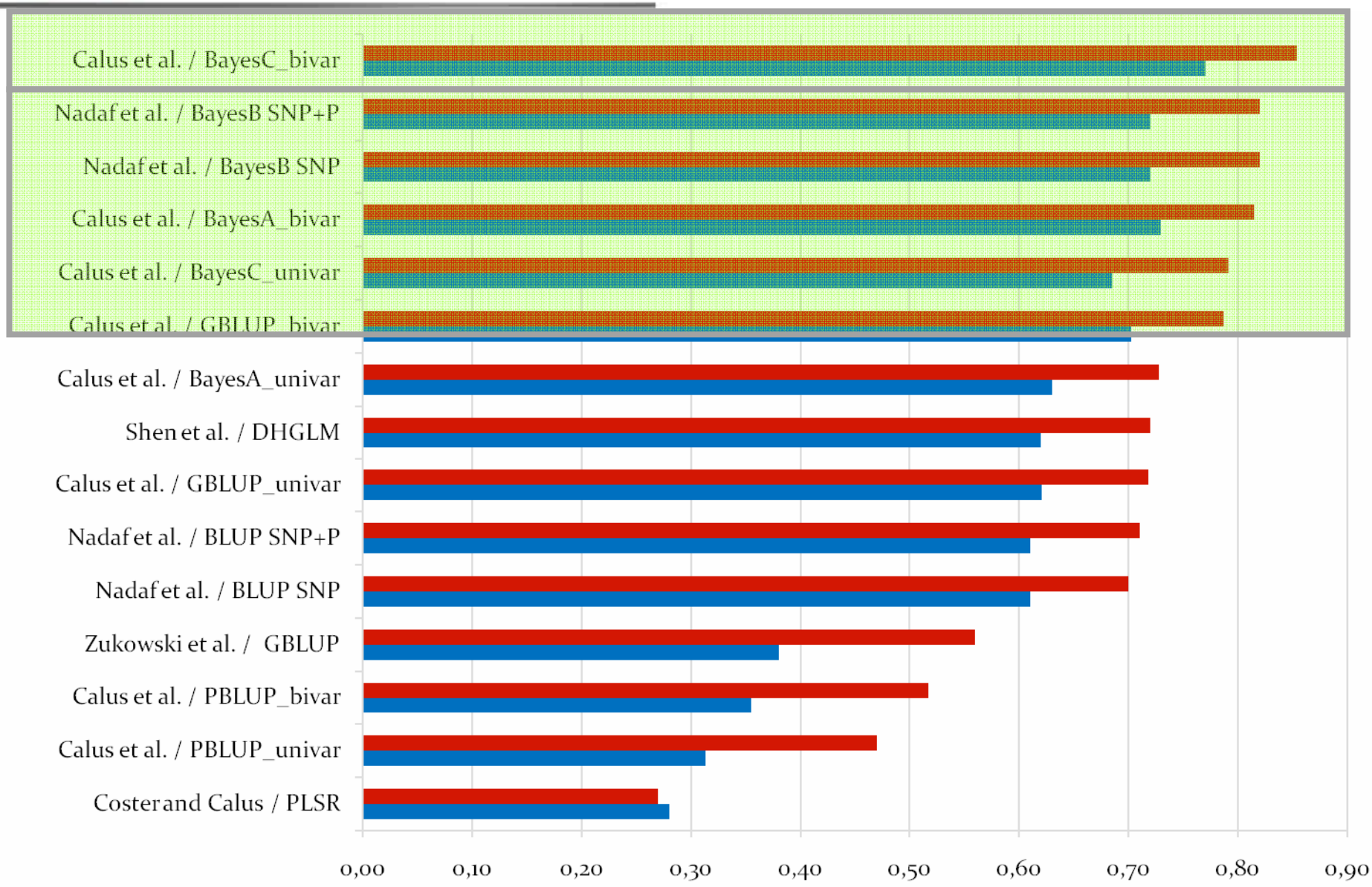
Accuracy and regression BT



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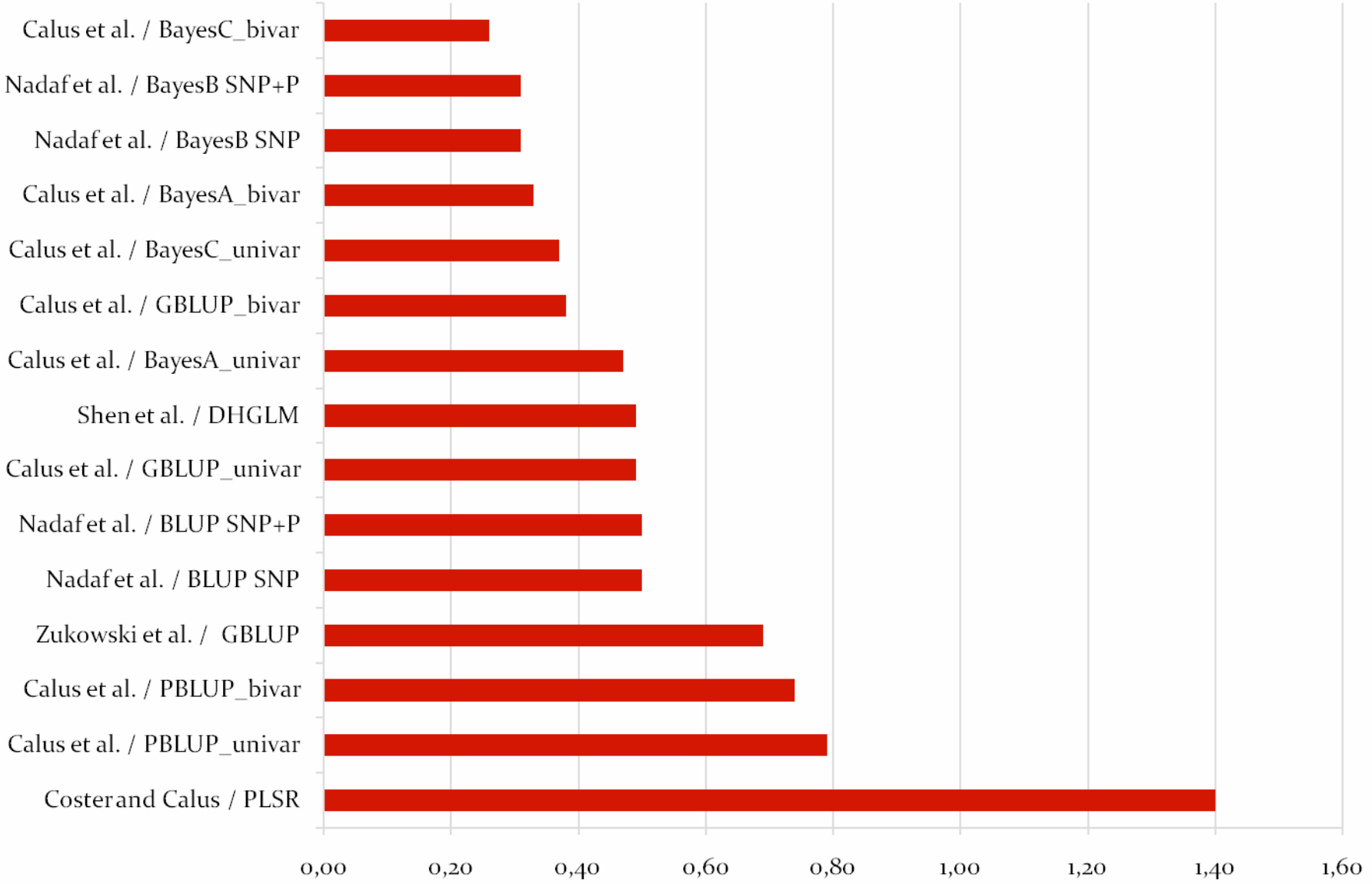
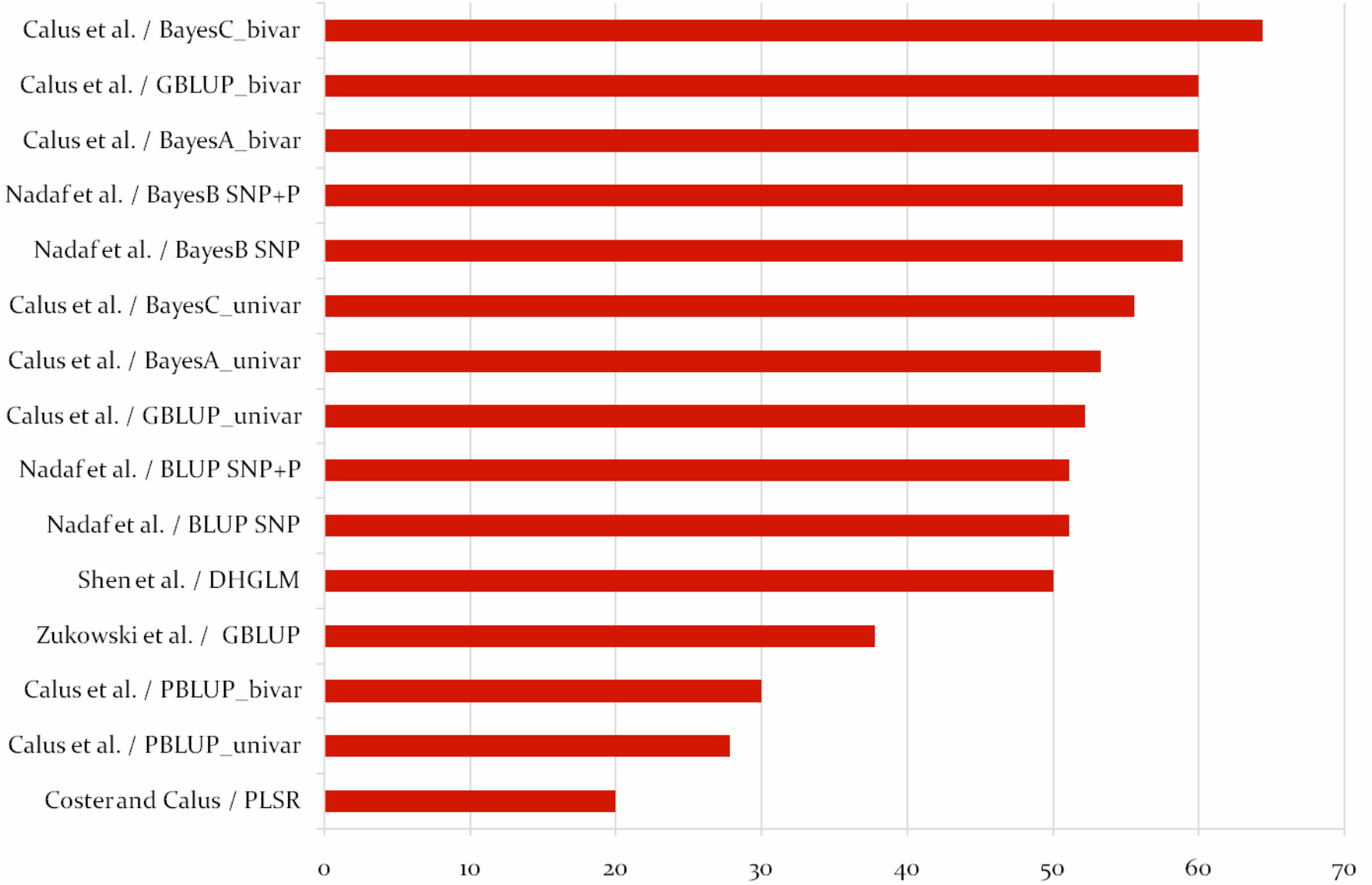
MSD BT



Shared BT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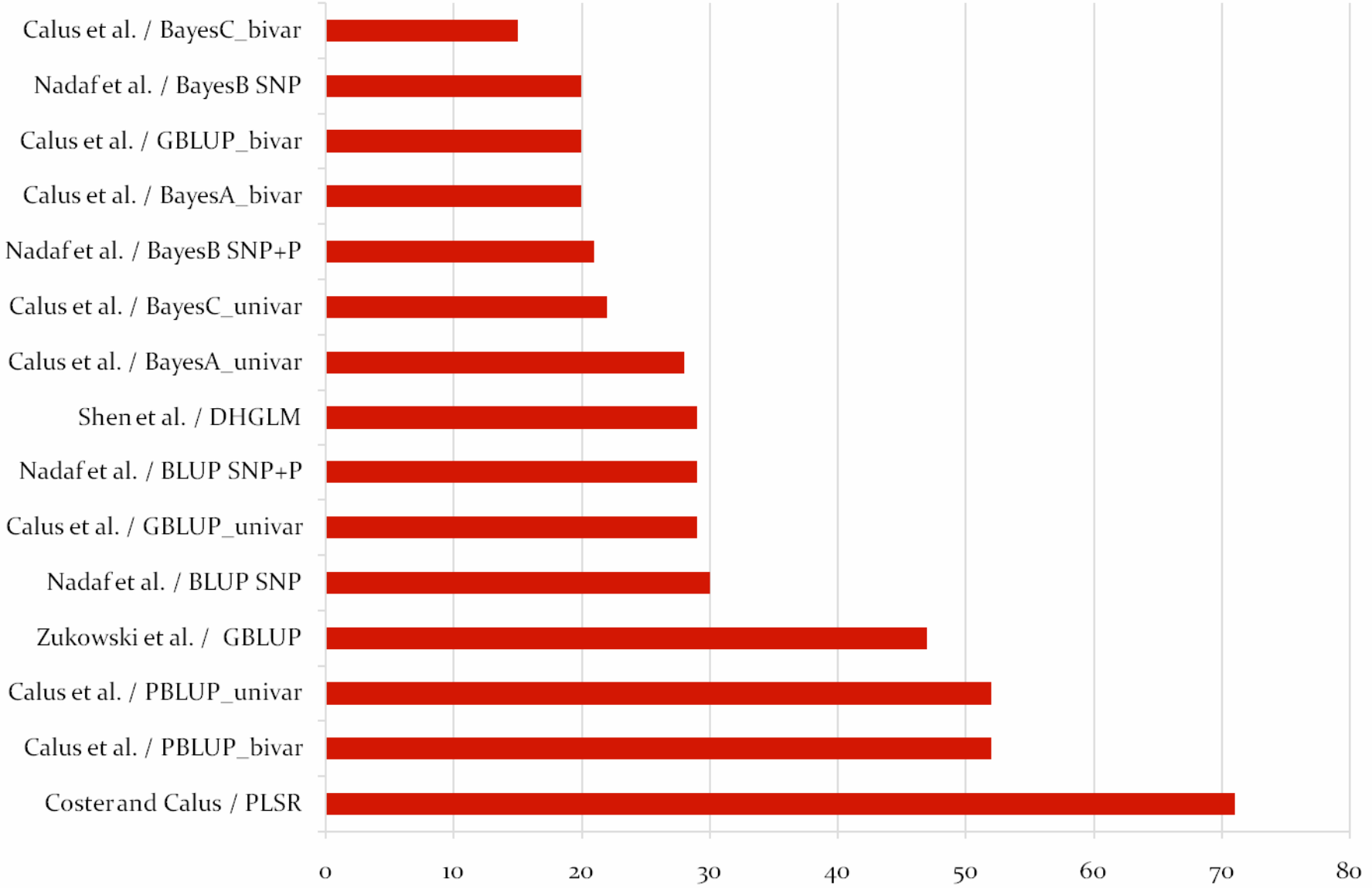
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15. Coster and Calus - PLSR

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Summary

- For QT:
  - BayesB, TA-BLUP, BayesC, RR-BLUP > GBLUP, Spatial, BayesA > PBLUP, Machine Learning
- For BT:
  - BayesC, BayesB, BayesA, GBLUP > Other methods
- Bivariate > Univariate for the same method
- Bayes and TA-BLUP methods better for complex genetic architecture

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Thank you for sharing the results !!!

Congratulations to the authors !!!

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