

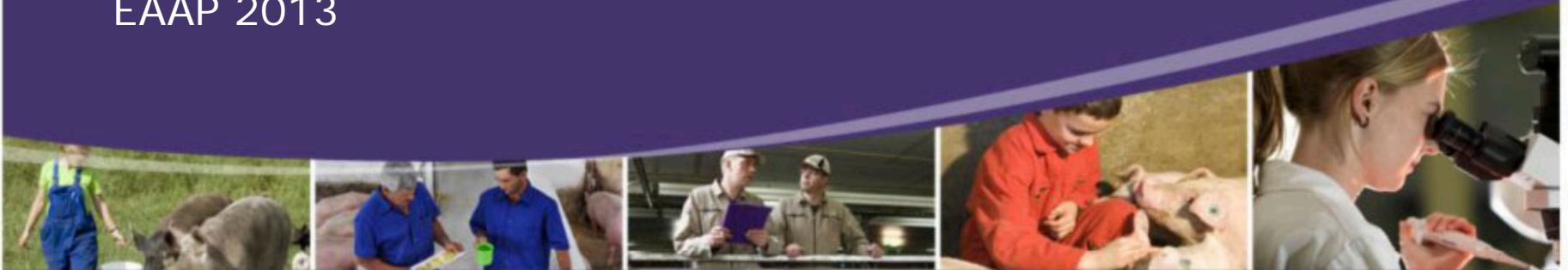
Progress in Pigs

TOPIGS

Search for pleiotropic effects in
genome regions affecting female
fertility traits in pigs

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EAAP 2013



Motivation and goal

- Marker assisted selection (MAS)
- Single step approach
- Single step + MAS
- Handle genetic correlations at the genomic level
- Unfavorable correlation

Animals and Methods

- 1,460 animals (TOPIGS sow line)
- 43,977 SNPs
- Deregressed breeding values (*Garrick et al. 2009*)
 - Number of teats (NT)
 - Average birth weight (BW_{avg})
 - Variation BW (BW_{var})
- GWAS
 - Bayesian variable selection, BayZ (*Janss, 2011*)
 - 500,000 MCMC chains
 - 5,000 burn in
 - $Pi0 = 0.999$

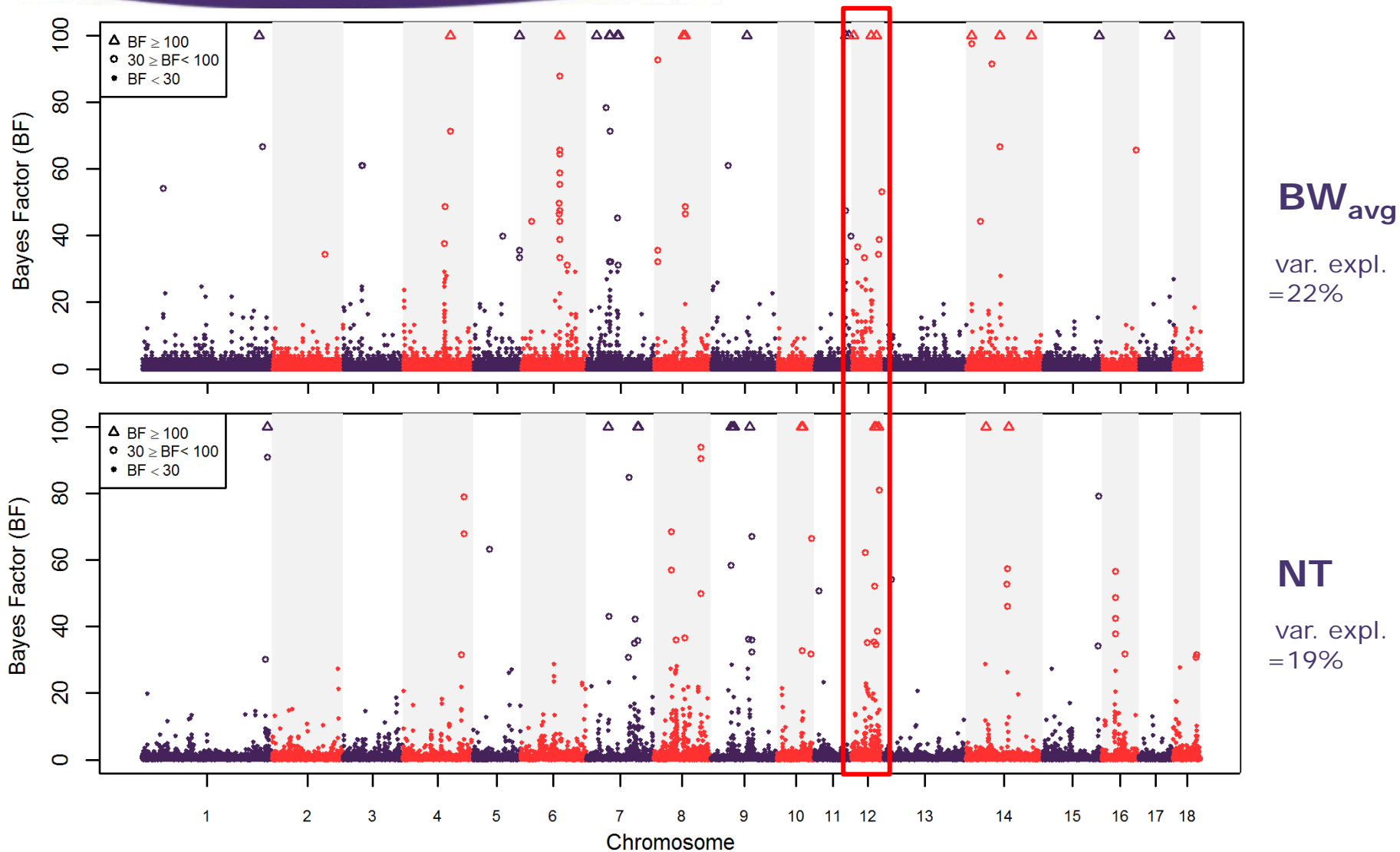
Genetic parameters

Quantitative approach

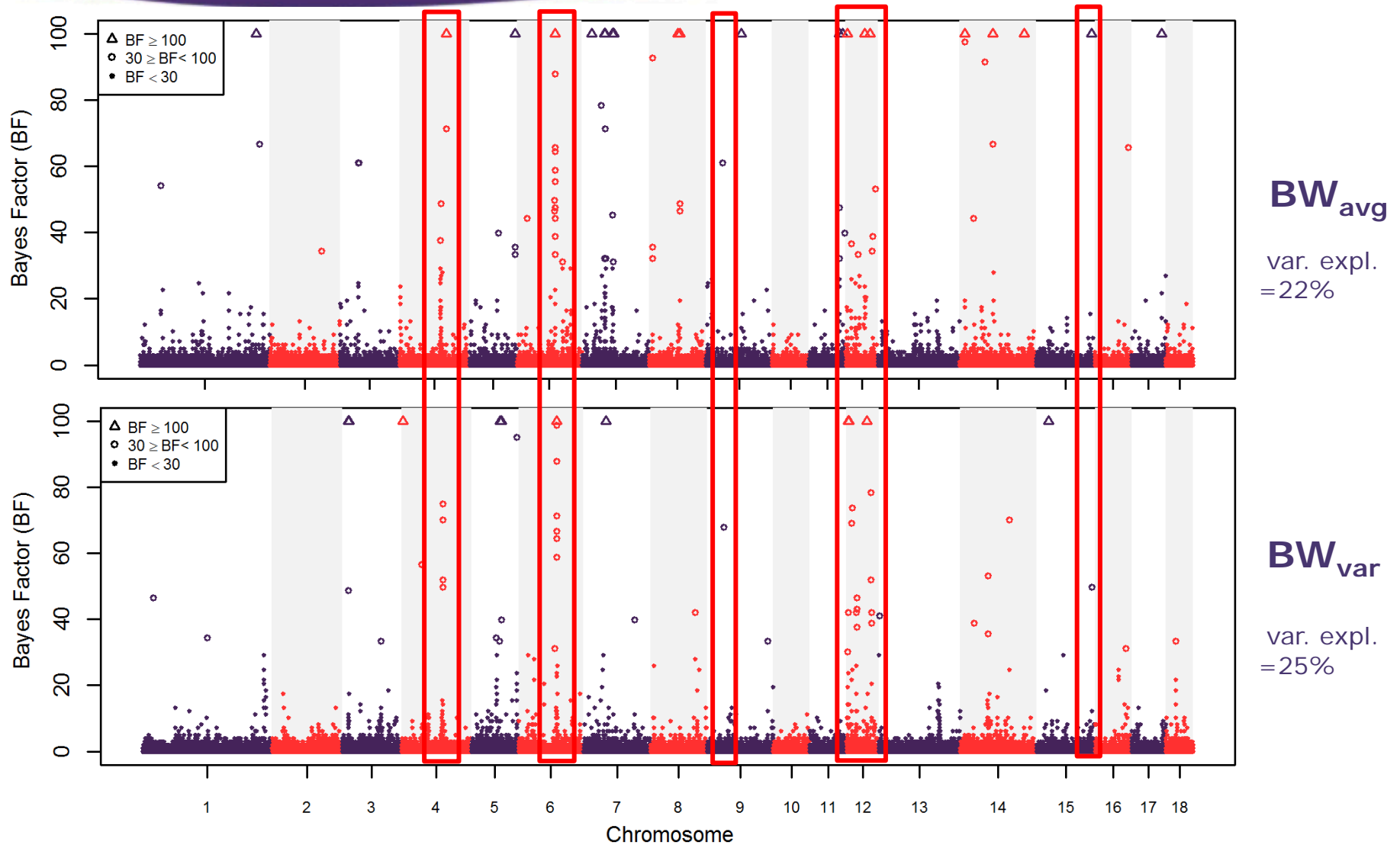
Heritabilities (diagonal) and genetic correlations (above diagonal)

	NT	BW _{avg}	BW _{var}
NT	0.46	0.00	0.00
BW _{avg}		0.41	0.51
BW _{var}			0.14

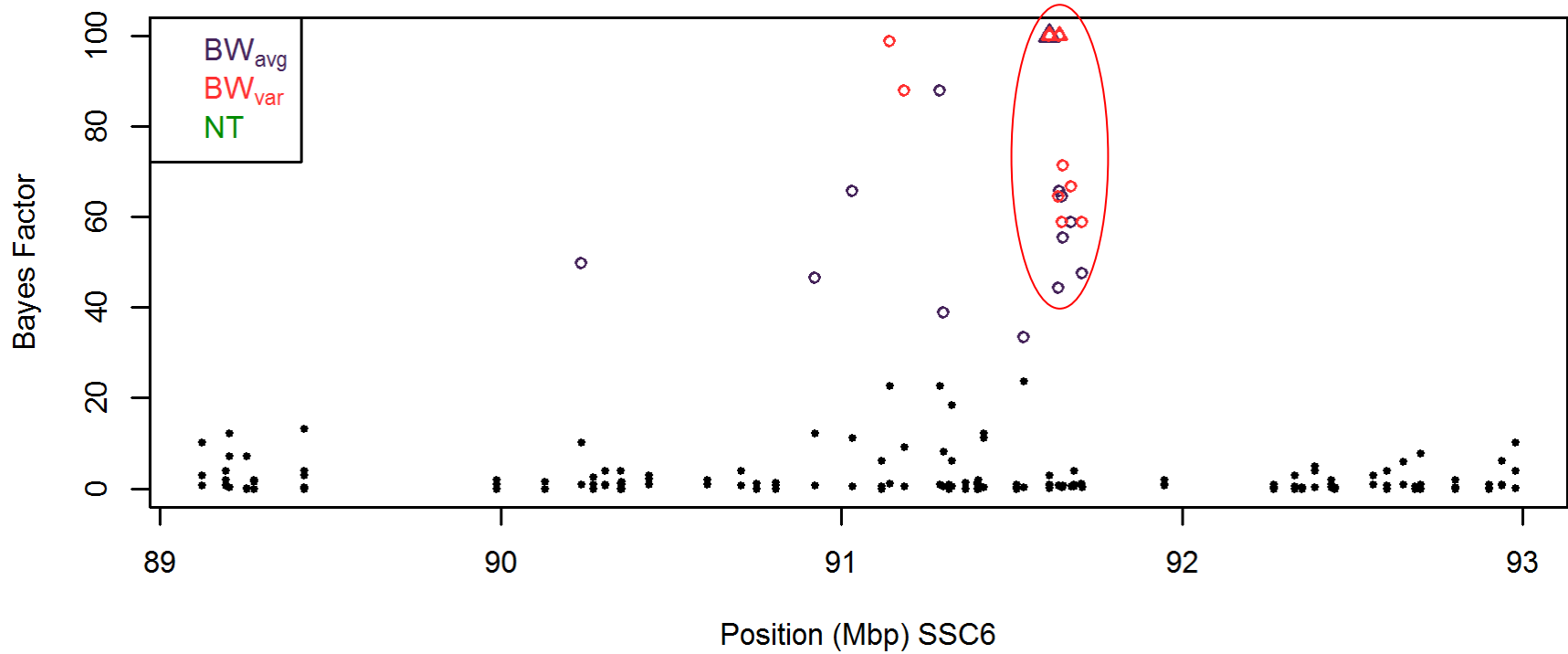
GWAS: BW_{avg} and NT



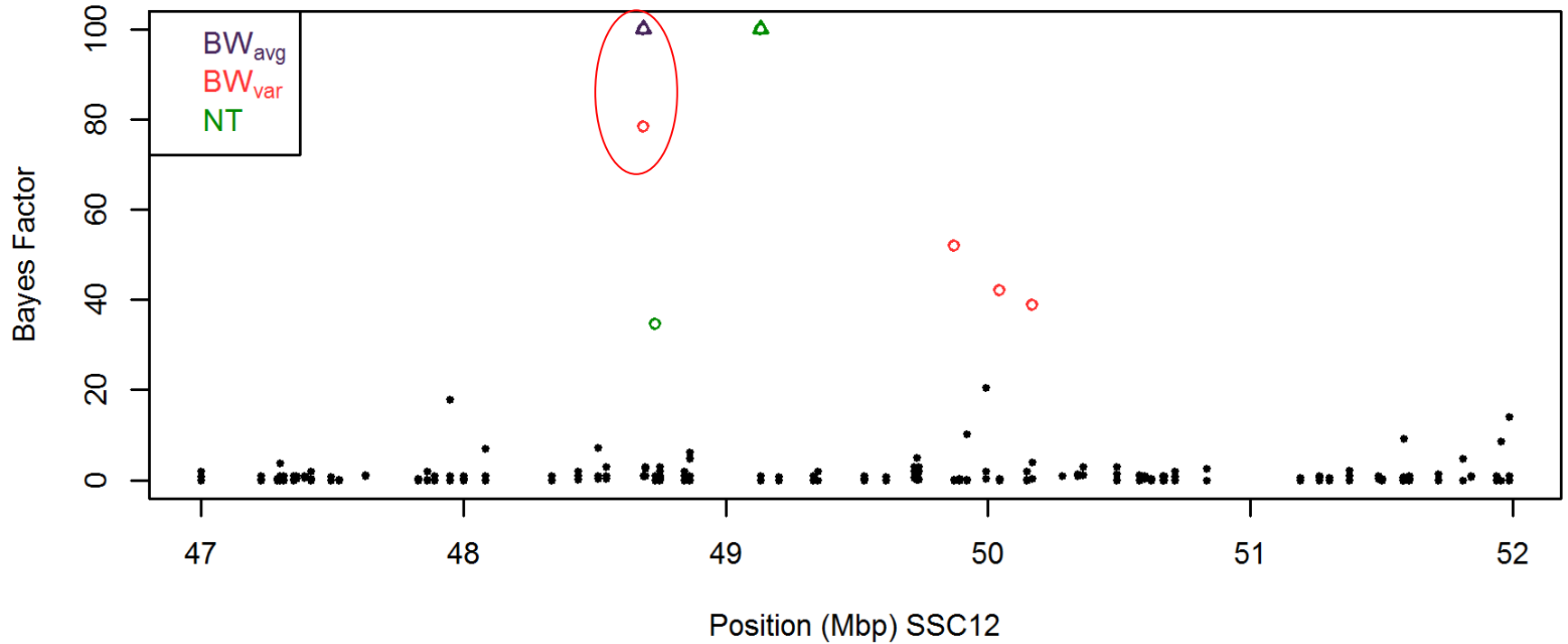
GWAS: BW_{avg} and BW_{var}



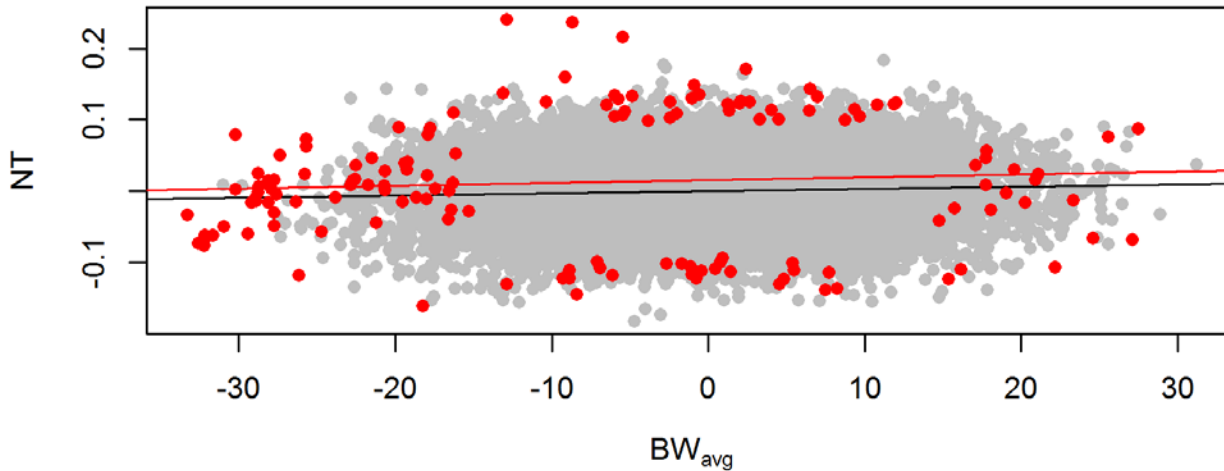
Zoom SSC6



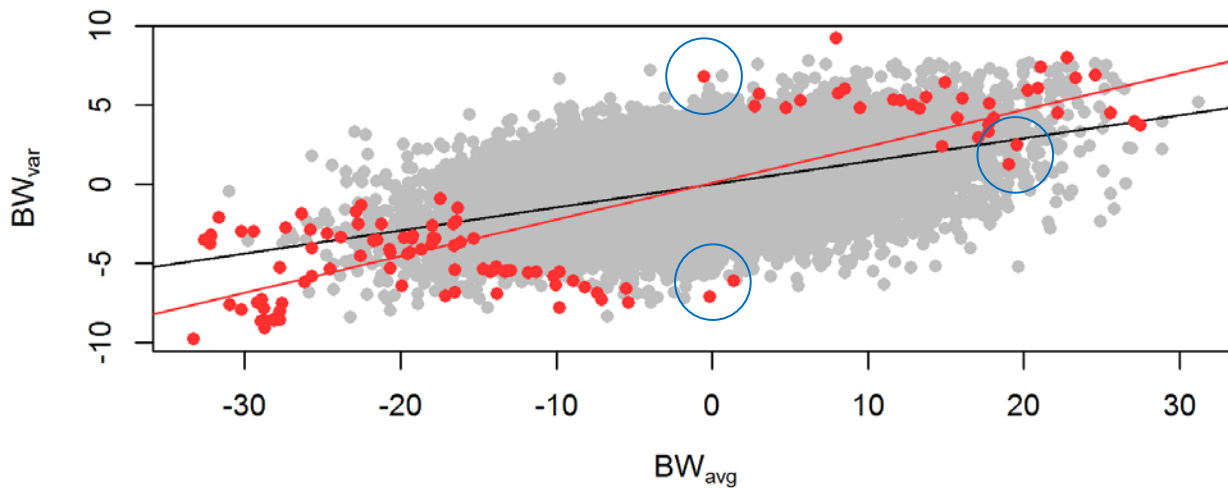
Zoom SSC12



Correlation: SNP effects



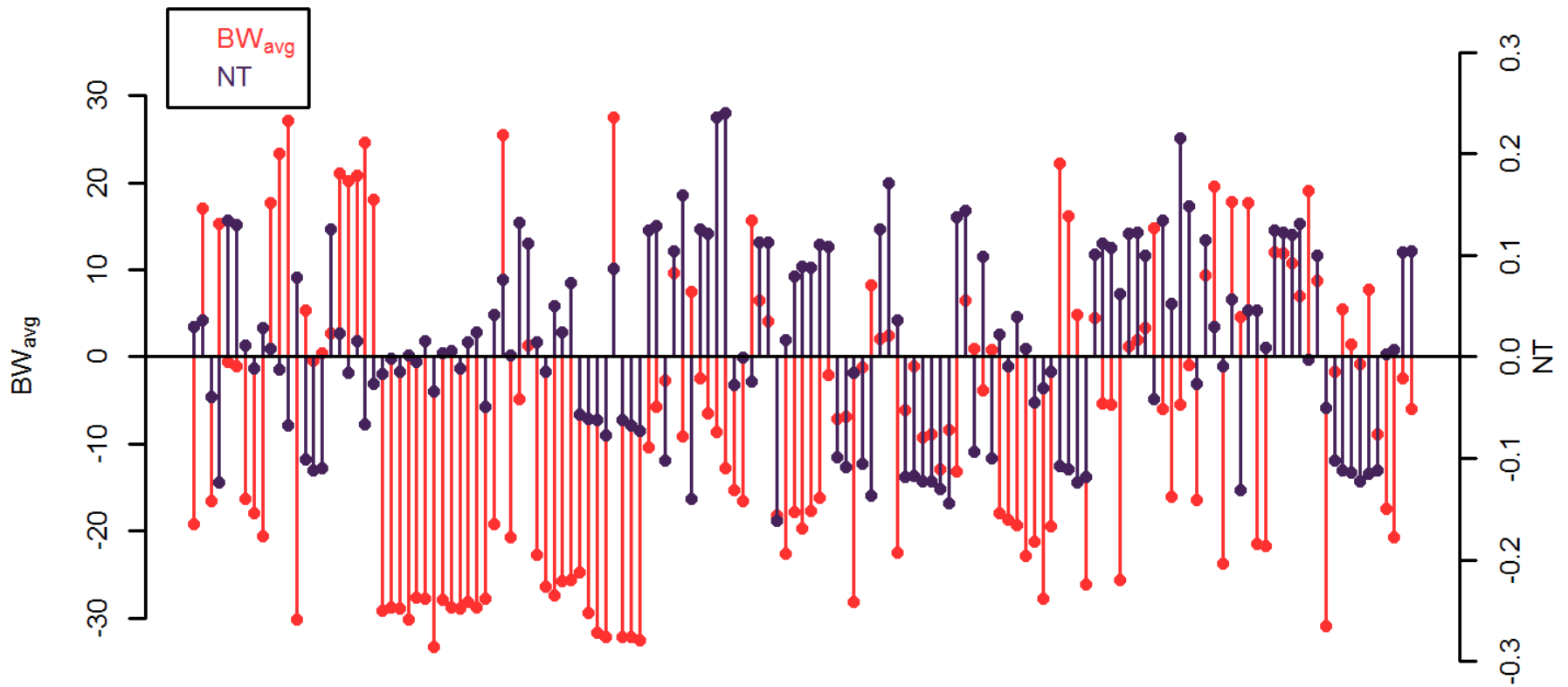
- All SNPs $r = 0.05$
- Signf. SNPs $r = 0.08$



- All SNPs $r = 0.51$
- Signf. SNPs $r = 0.82$

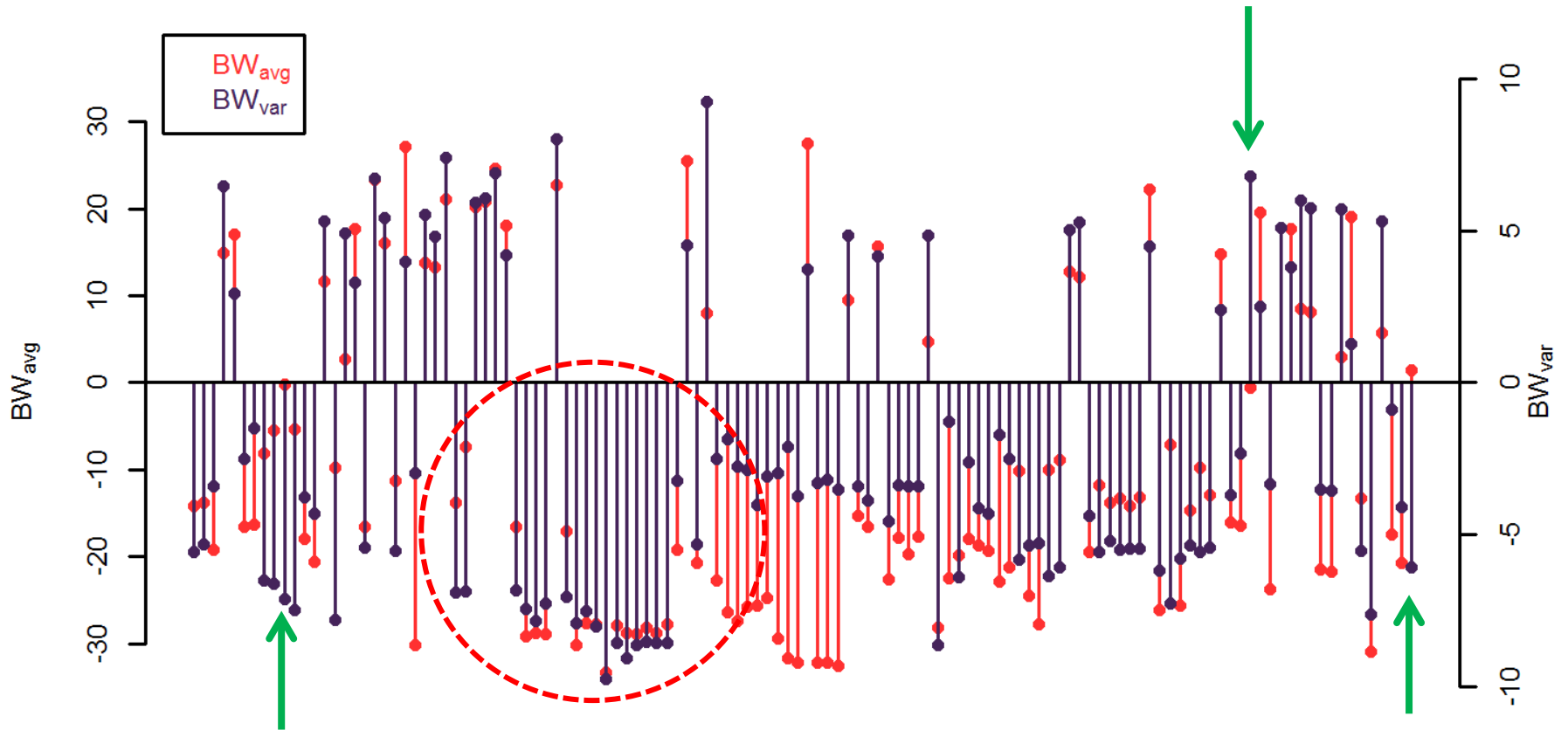
BW_{avg} and NT

Posterior mean - Signif. SNPs



BW_{avg} and BW_{var}

Posterior mean - Signif. SNPs



Final considerations

- A deeper look at this issue is required
- Correlation between SNP effects of the evaluated traits matched their genetic correlations
- Genomics may not be very useful to break down the unfavorable correlations between BW_{avg} and BW_{var}



Thank you!