

# **A review of the validation of national genomic evaluations**

Mohammad A. Nilforooshan

[mohammad.nilforooshan@slu.se](mailto:mohammad.nilforooshan@slu.se)

2014-05-21

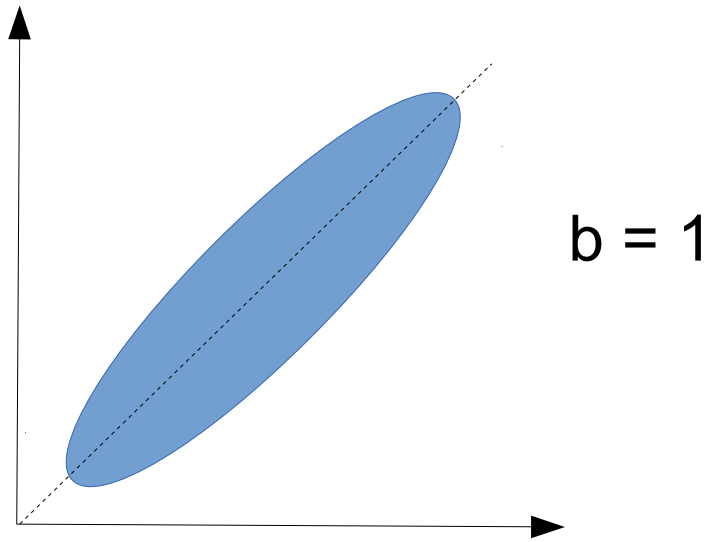
# The aim of the GEBV test

- Several countries have enrolled GMACE.
- National genomic evaluation models need to be validated to be included in GMACE.
- Mäntysaari et al. (2010) developed a model to validate national genomic evaluation models, based on predicting future genetic evaluation using daughter information from early available marker information.
- The accuracy and directional changes (bias) are the key points of this test.

# The samples

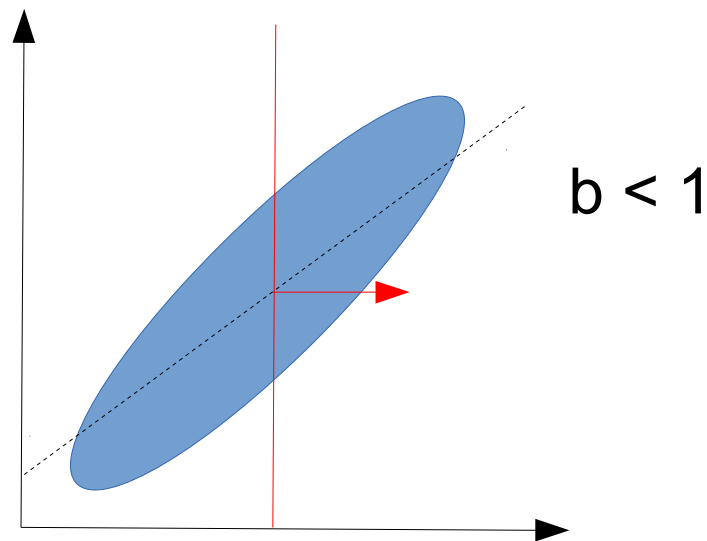
- **Candidate bulls:** young domestic bulls, had been candidate for genotyping, currently have evaluation based on 1<sup>st</sup> crop daughters.
- **Test bulls:** genotyped candidate bulls (used in a regression model)
- In the presence of non-random selection (selective genotyping):  $b_1$  &  $E(b_1) \neq 1$
- For  $E(b_1)$ , please see Interbull Bulletin 42: 56-61

# No bias, upward & downward bias

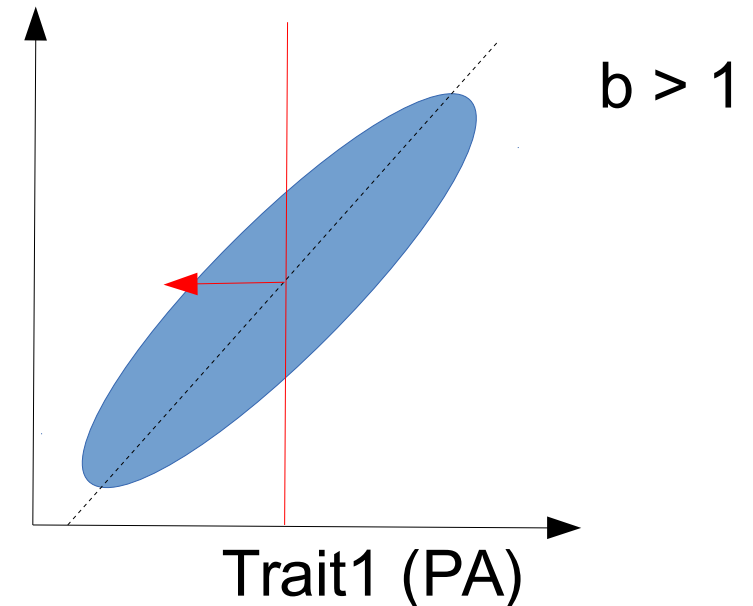


By selection, variance ratios and correlation are changed.

This change in slope can change the slope between GEBV & DYD.



Trait2  
(GEBV)



Trait1 (PA)

# The model

$$y = b_0 + b_1 \times \text{GEBVr} + e$$

$$y = b_0 + b_1 \times \text{PA} + e$$

where  $y$  is DYD or DEBV

Significant deviation of  $b_1$  from  $E(b_1)$  indicates significant bias. A two-tailed t-test is involved.

There is different accuracy for data from different bulls, therefore a weighted least squares regression model is used.

EDC weight for DEBV, and  $\text{EDC}/\text{EDC} + \lambda$  weight for DYD

# The data

- GEBV-test results since January 2013
- 357 tests (country-breed-trait), 51 repeated tests for HOL
- 38 (all) traits

- | BSW | HOL | JER | NOR | RDC | SIM |
|-----|-----|-----|-----|-----|-----|
| 18  | 259 | 399 | 1   | 36  | 4   |

AUS	BEL	CAN	CH	DE	DFS	ESP	FRA	GBR	ITA	NLD	POL	USA
8	56	123	17	7	15	44	12	23	11	2	9	30

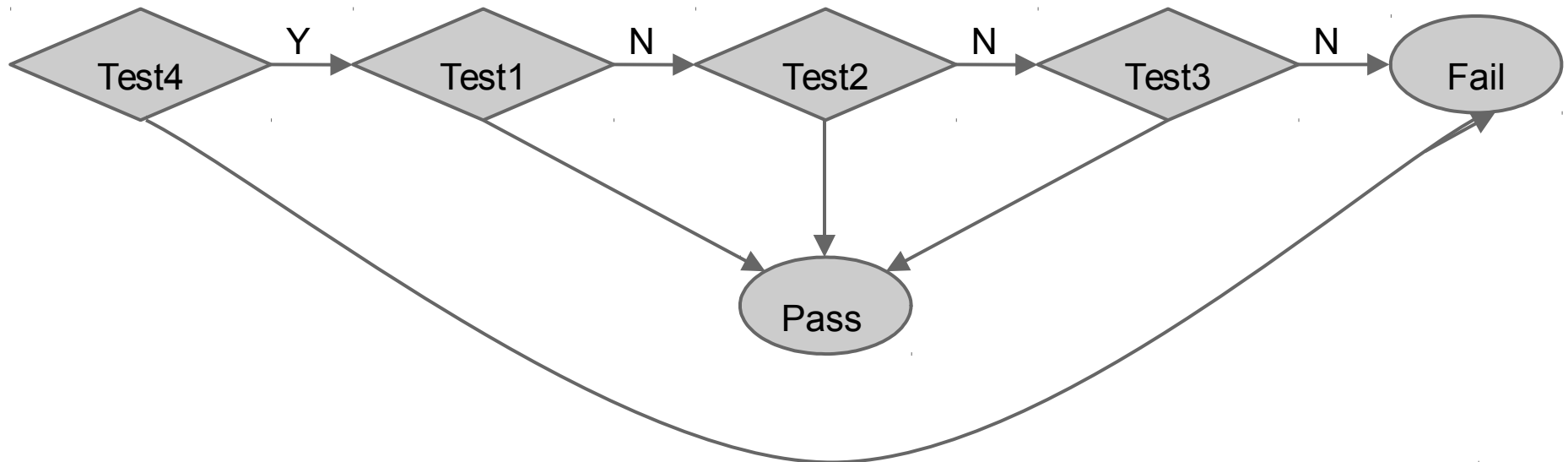
# 4 tests, Final PASS/FAIL

<b>PASS</b>	<b>Y</b>	<b>N</b>
<b>Stat test</b>	250	107
<b>Bio test</b>	136	221
<b><math>b_1 &gt; 1</math></b>	188	169
<b><math>\Delta R^2 &gt; 0</math></b>	305	52
<b>Final</b>	283	74



More strict than the Stat test,  
but helps large populations.

# How does a trait pass the test?



- **Test1:**  $b_1 - 2SE(b_1) < E(b_1) < b_1 + 2SE(b_1)$
- **Test2:**  $b_1 - 0.1 < E(b_1) < b_1 + 0.1$
- **Test3:**  $b_1 > 1$
- **Test4:**  $R^2M_1 > R^2M_2$



## **NOTE!!!**

In the next graphs “Pass & Fail” refers only to the statistical test!

# PASS/FAIL since January 2013

<b>Test4</b>	<b><math>\Delta R^2 &gt; 0</math></b>	<b><math>\Delta R^2 &lt; 0</math></b>
	305	52



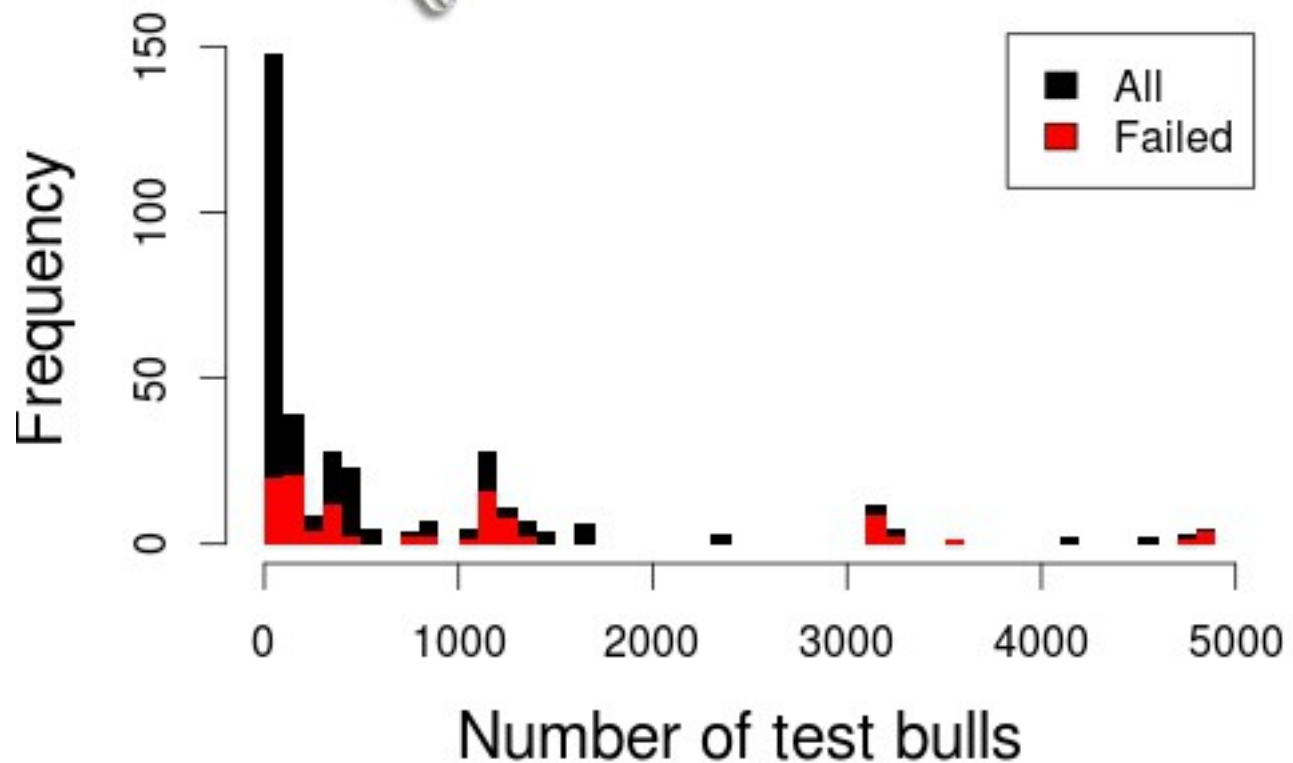
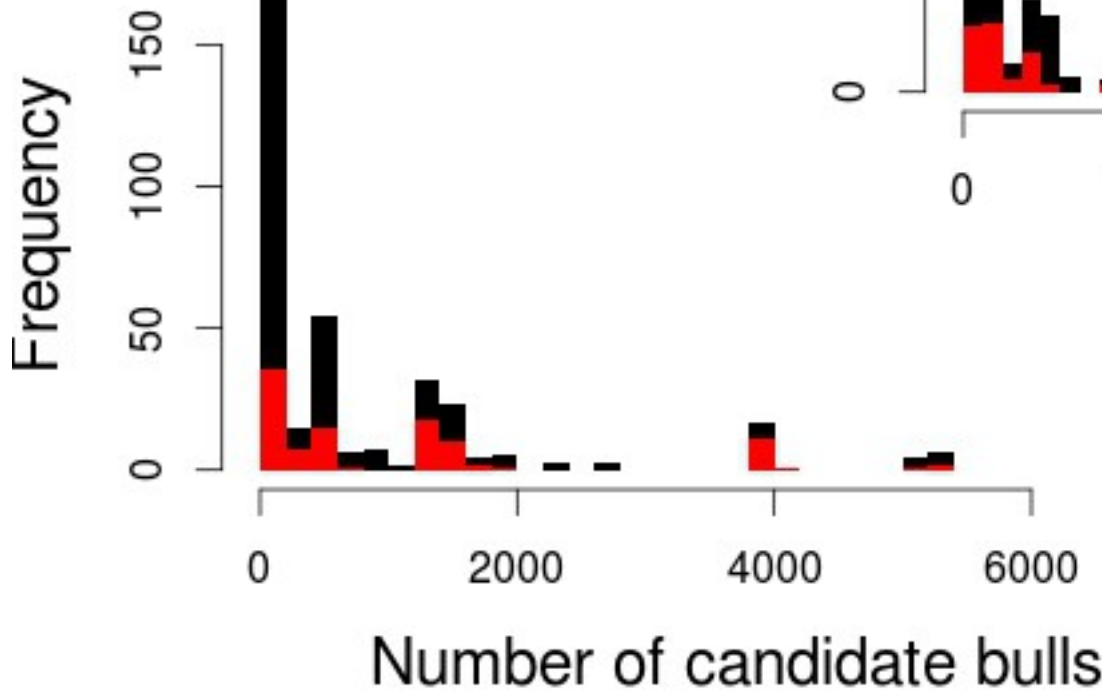
Stat test

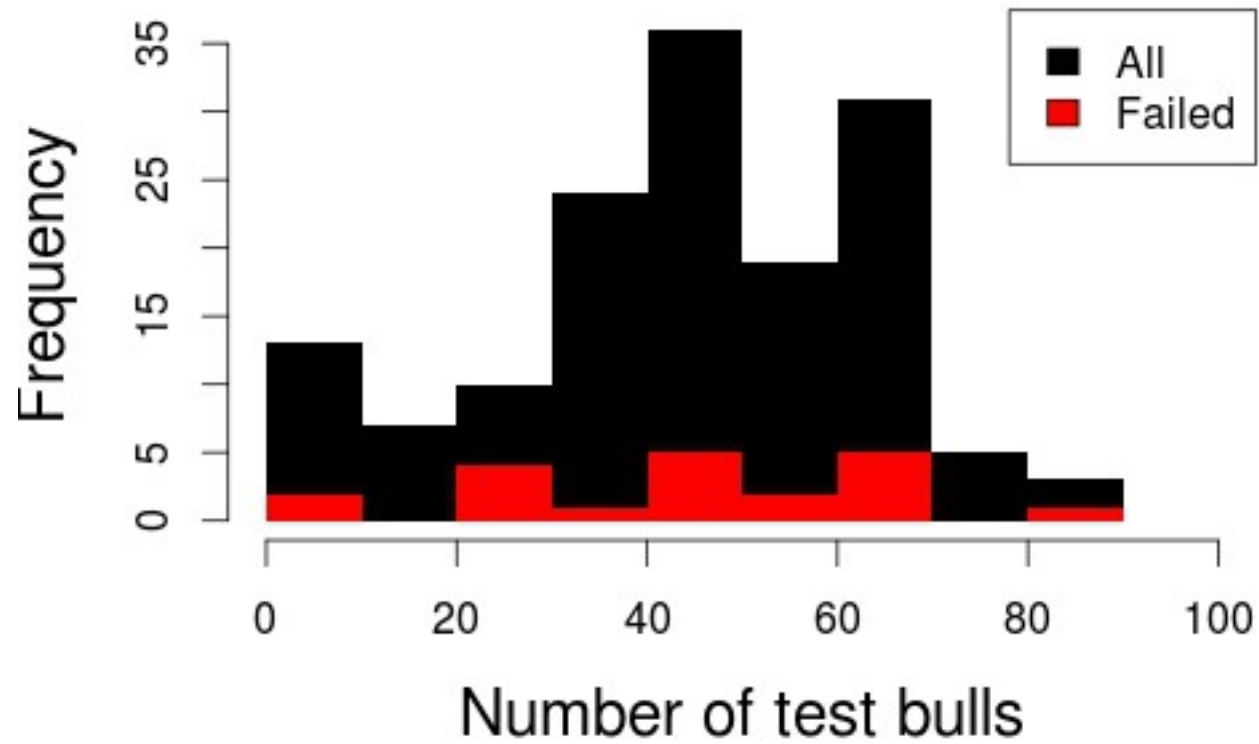
<b>Tests 1&amp;2</b>	<b>Y</b>	<b>N</b>
<b>Y</b>	110	17
<b>N</b>	96	82

Bio test

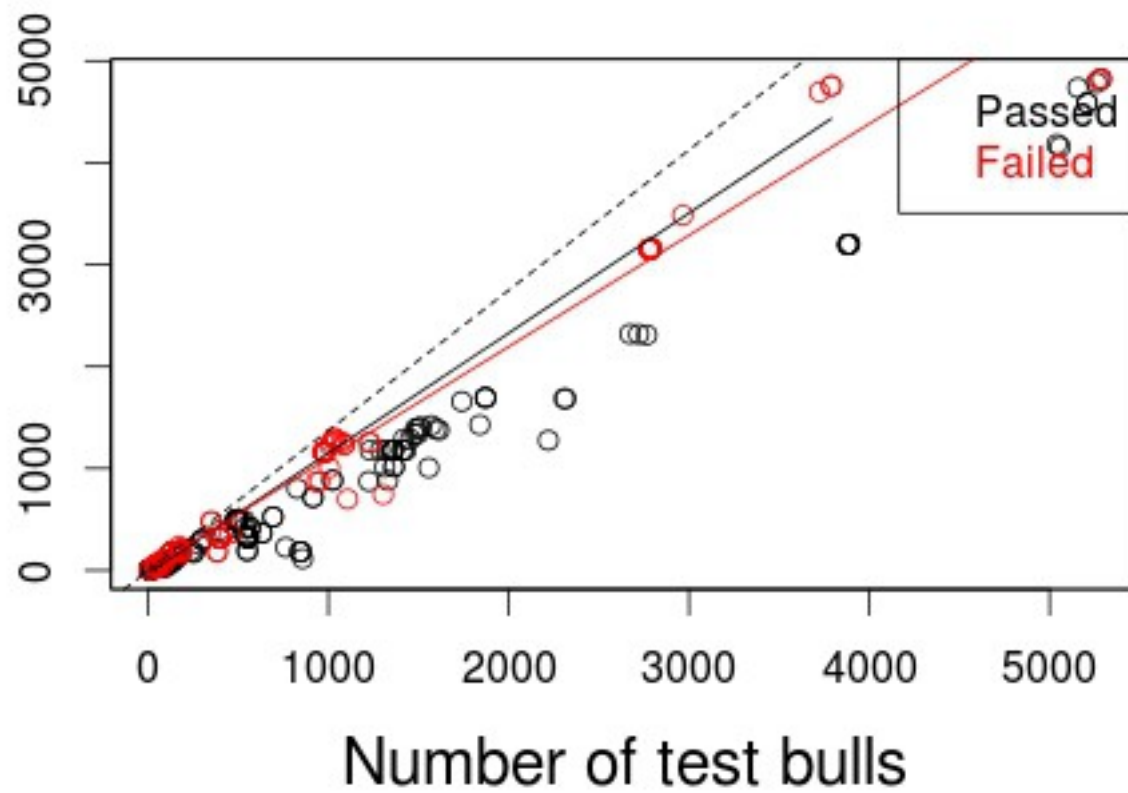
<b>Test3</b>	<b><math>b_1 &gt; 1</math></b>	<b><math>b_1 &lt; 1</math></b>
	60	22

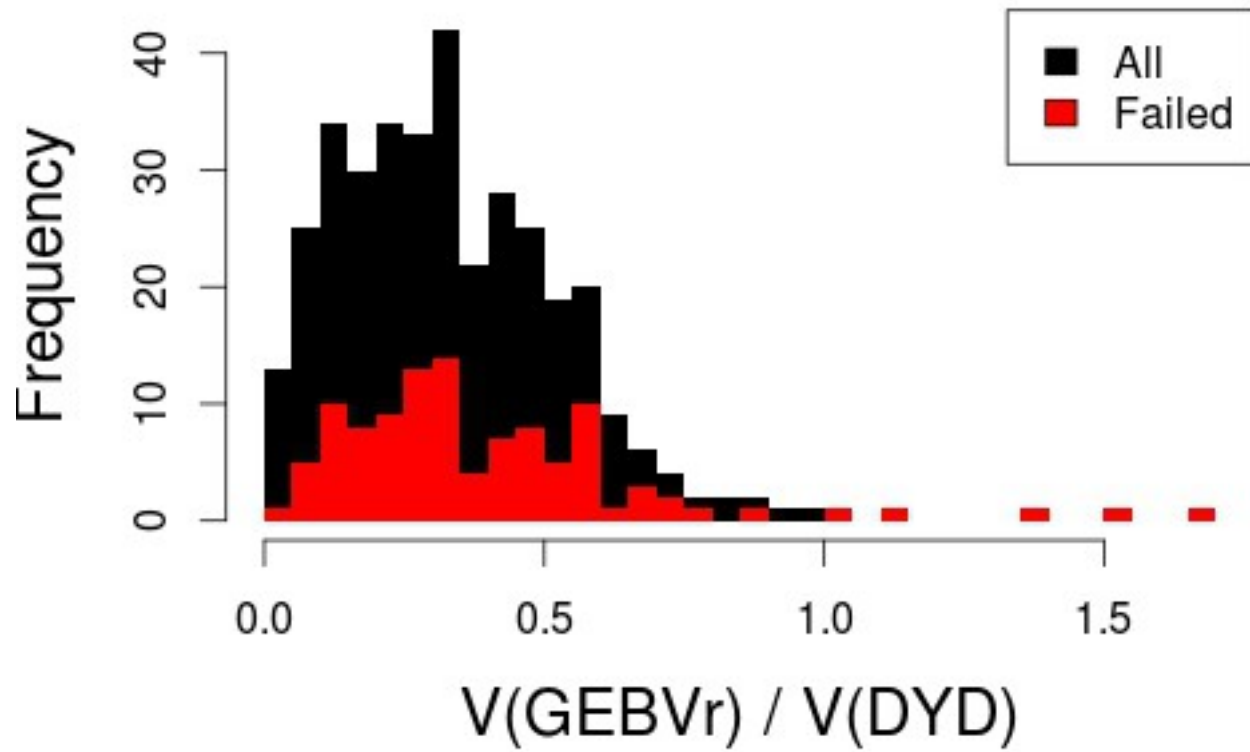


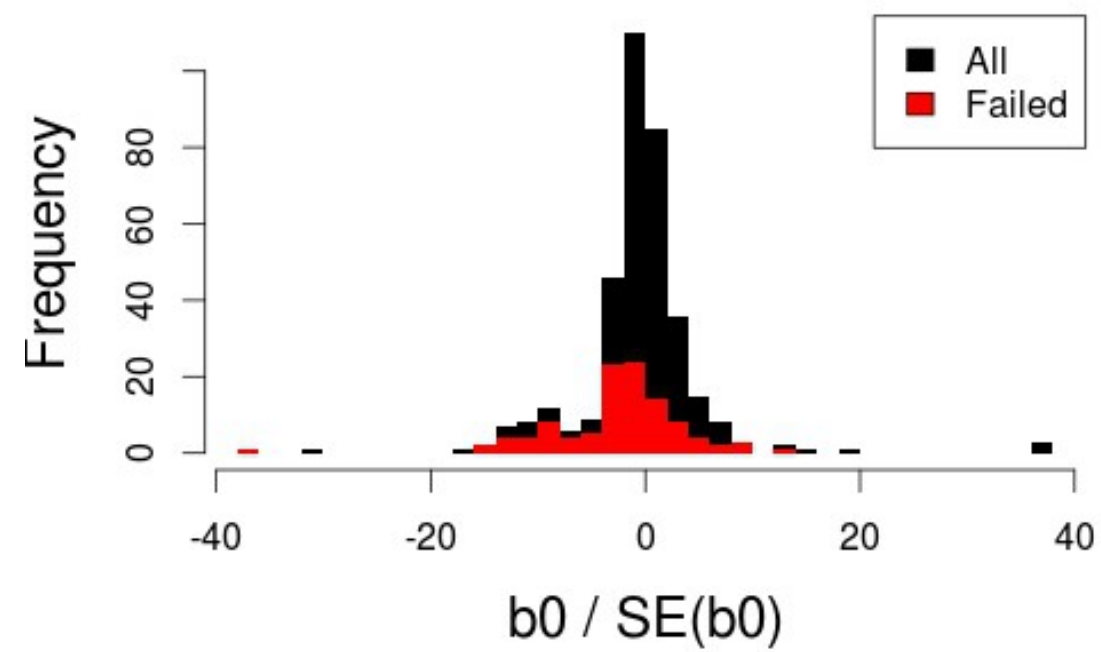
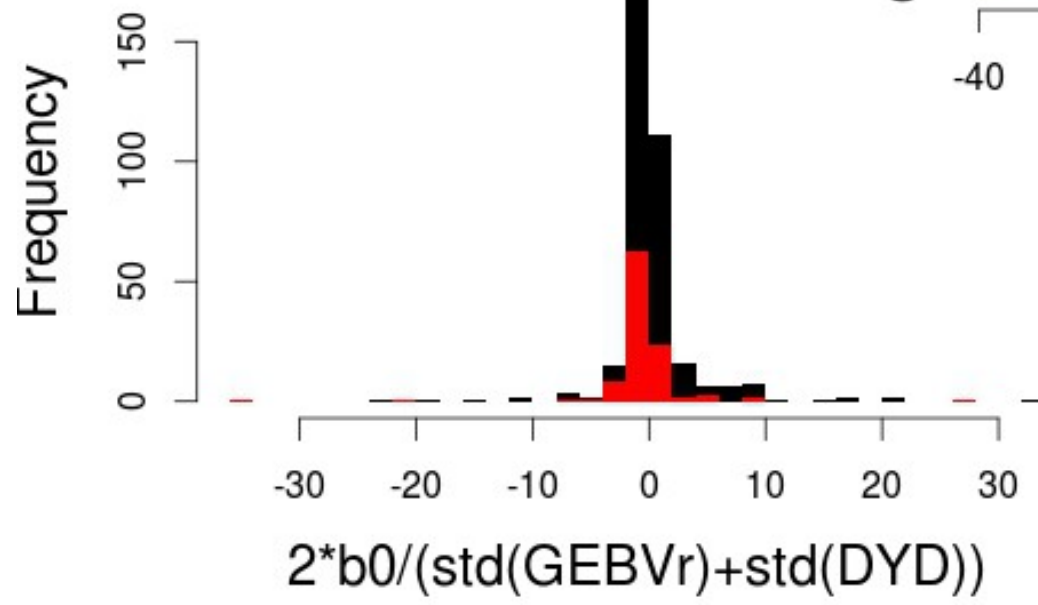


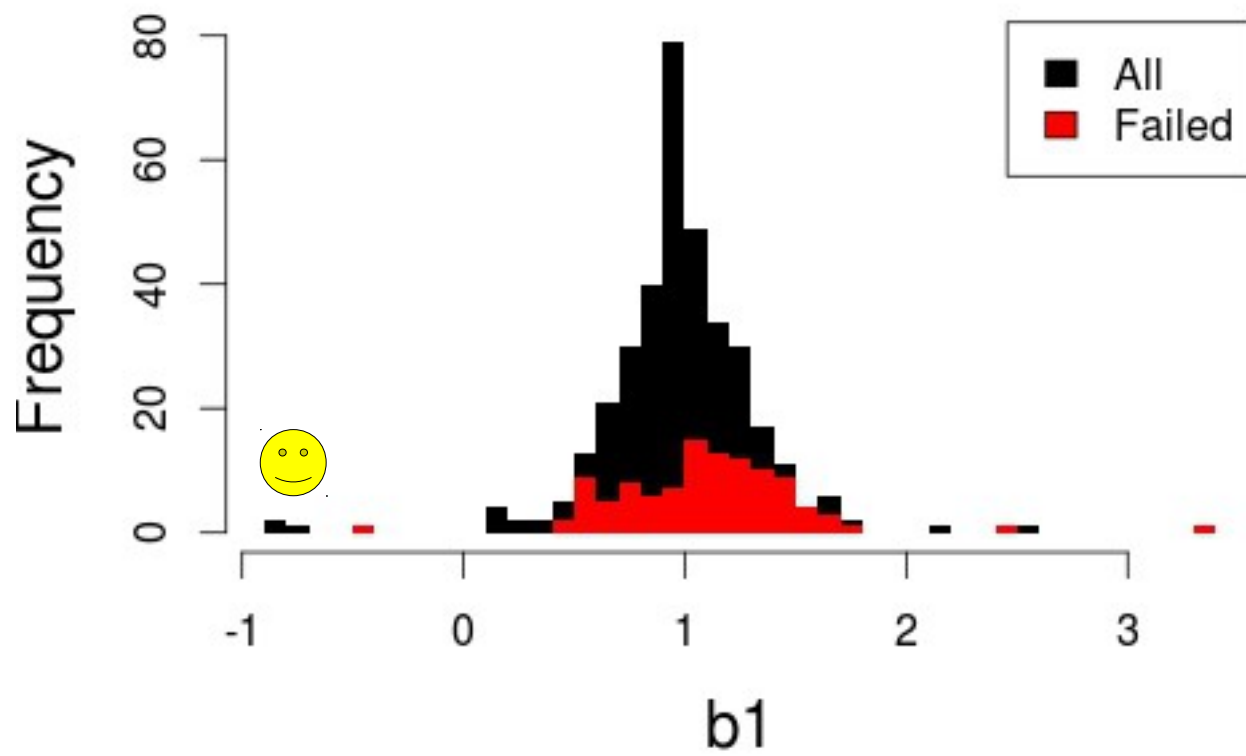


Number of candidate bulls

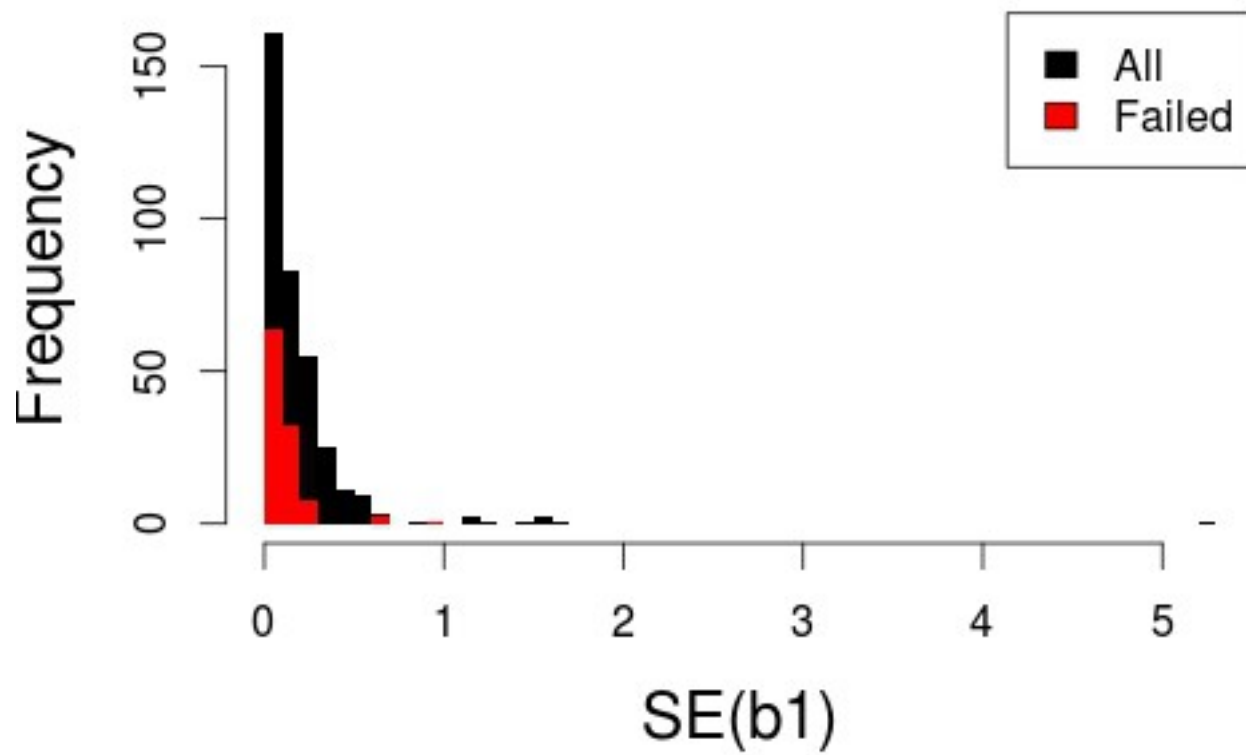


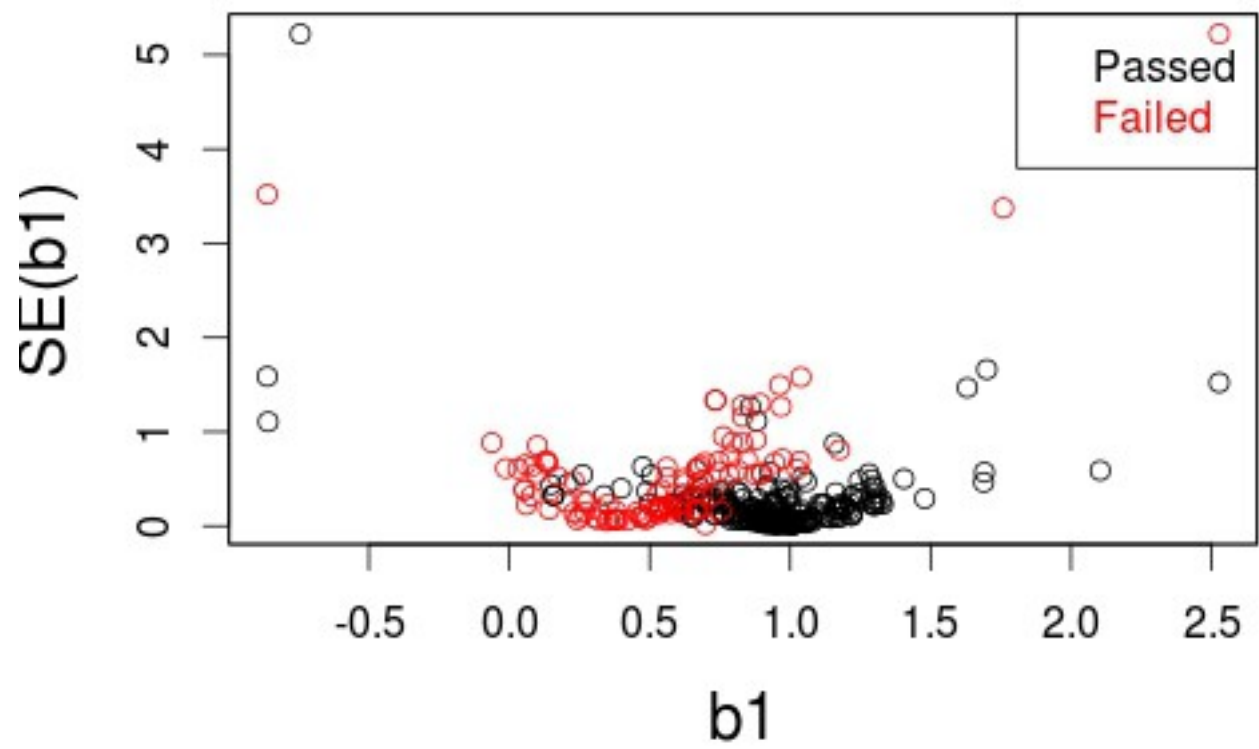


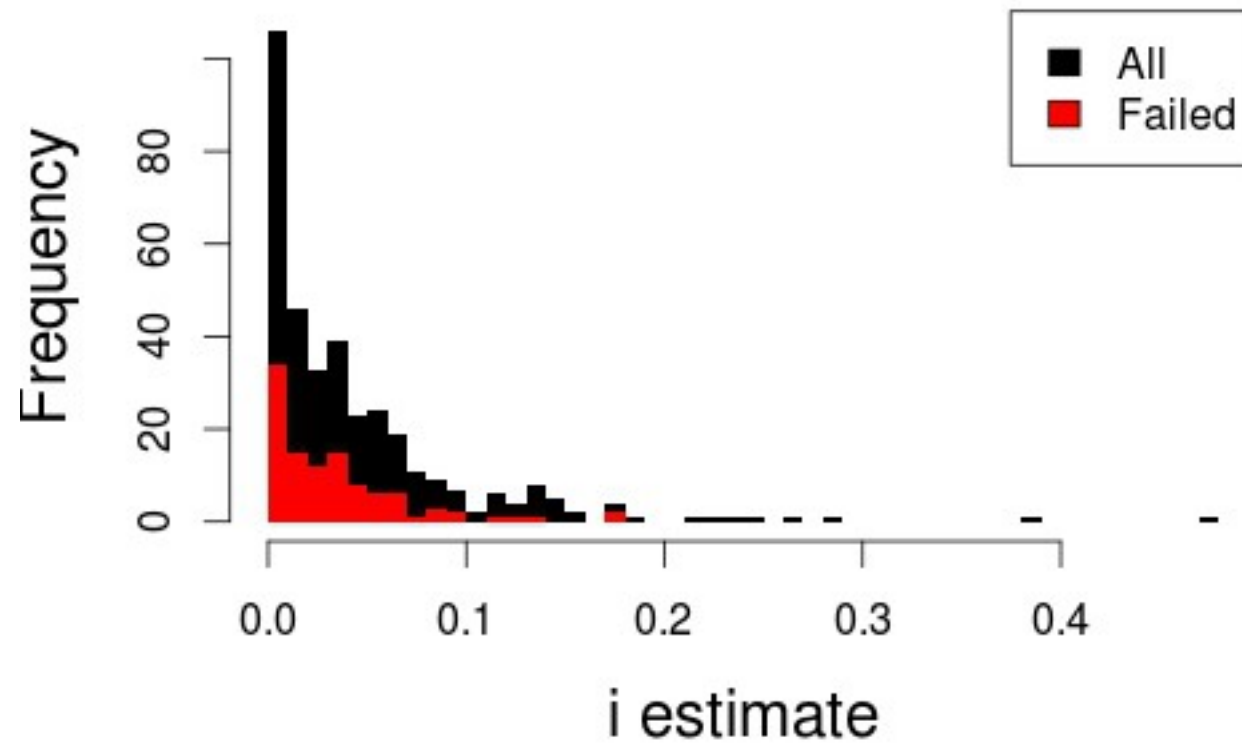






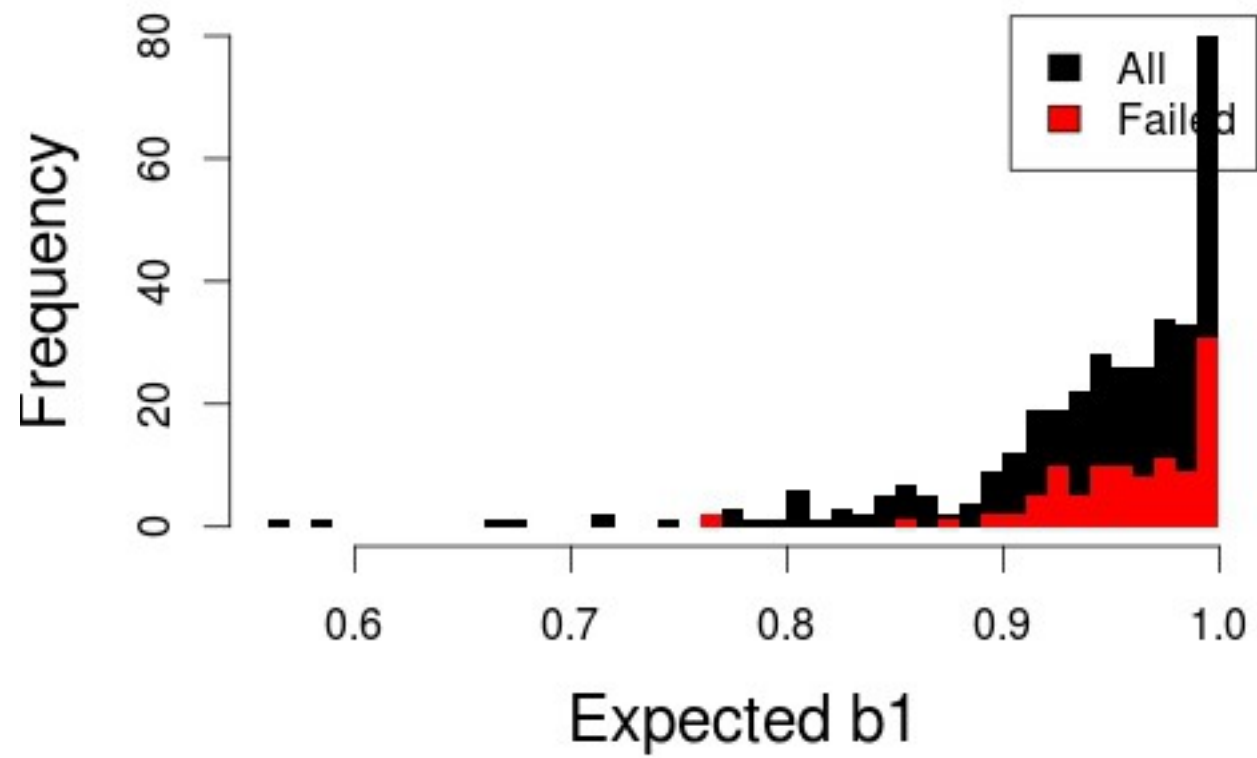


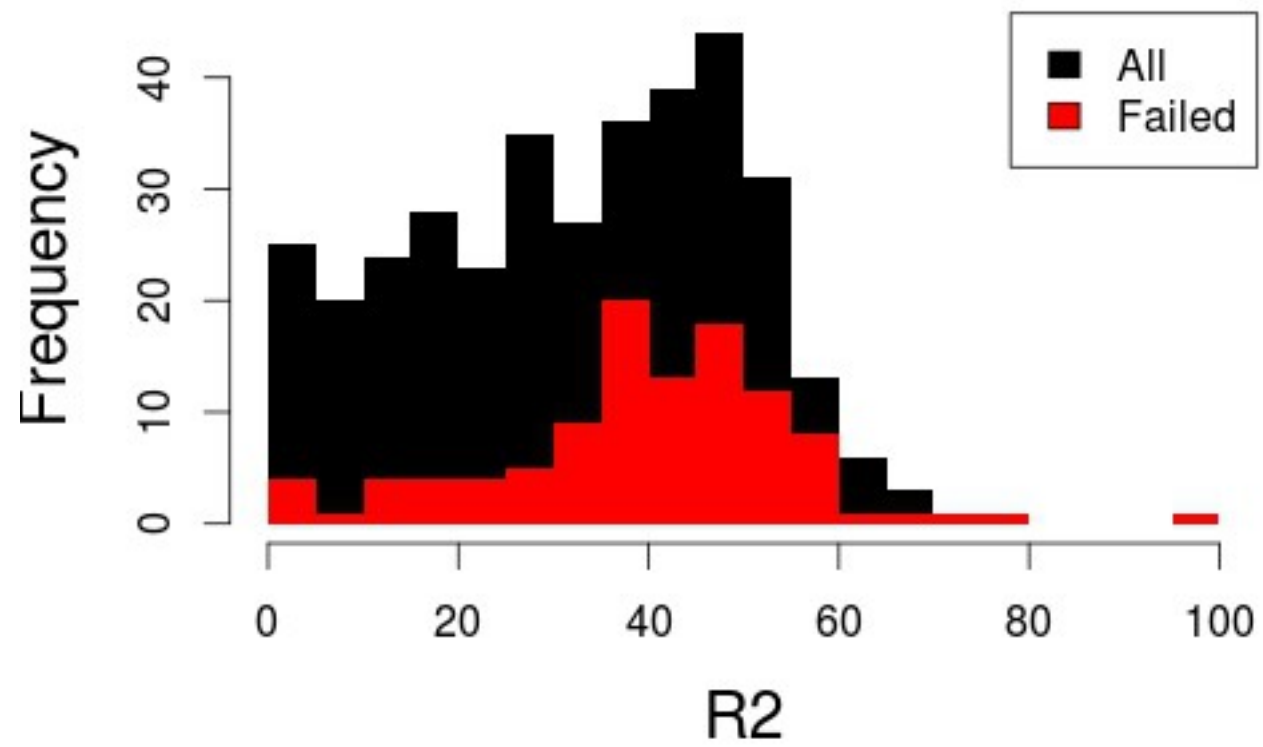


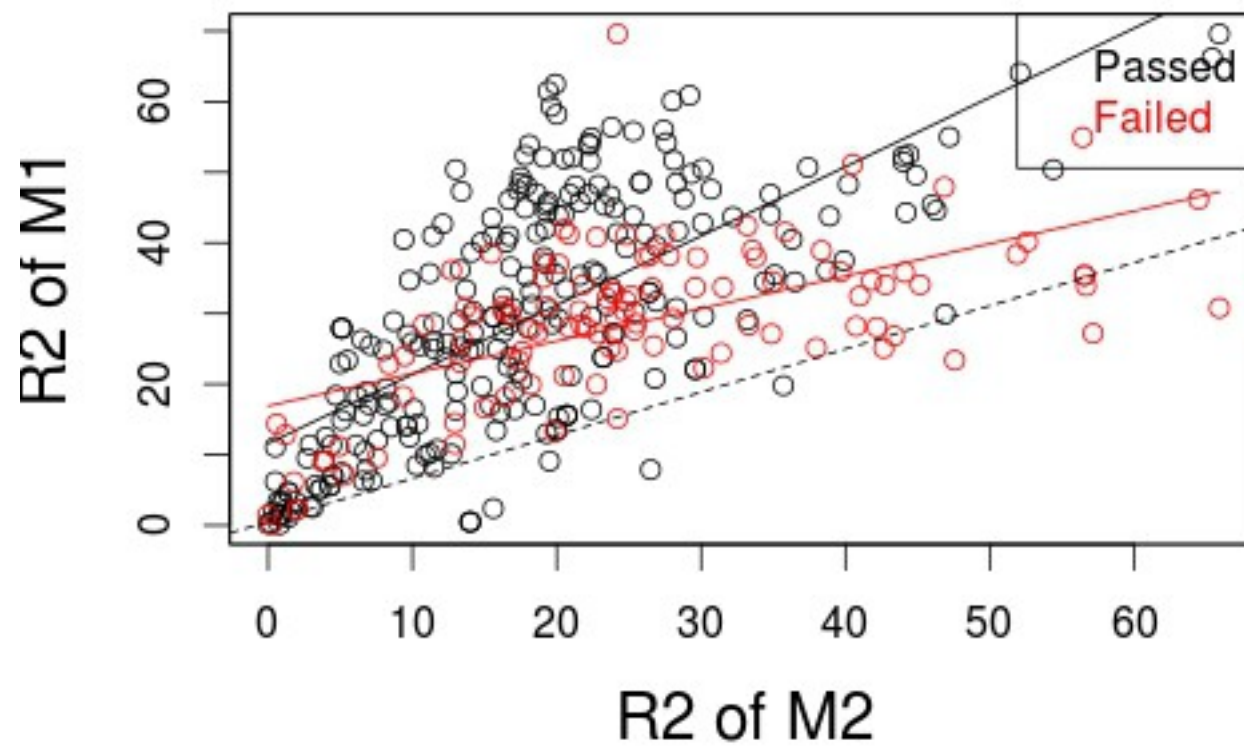


$$i = S/\sigma$$

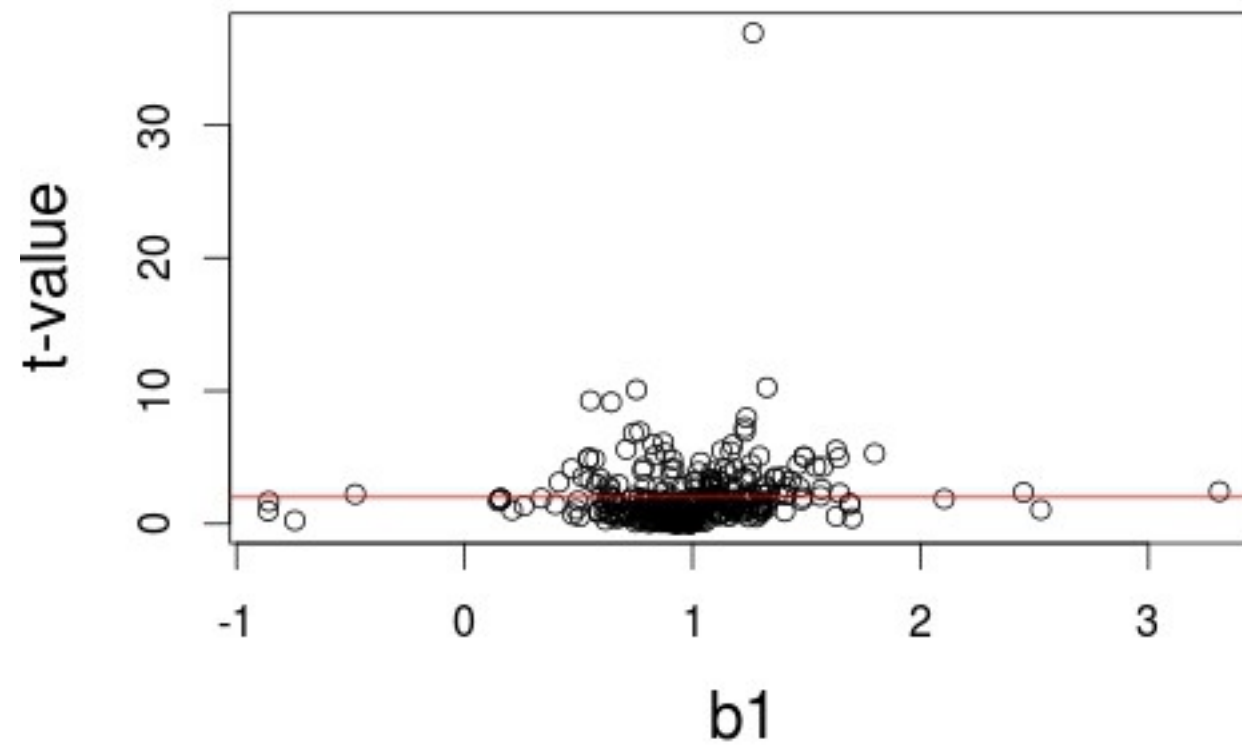
Higher  $i$ , lower  $b_1$ , lower  $E(b_1)$



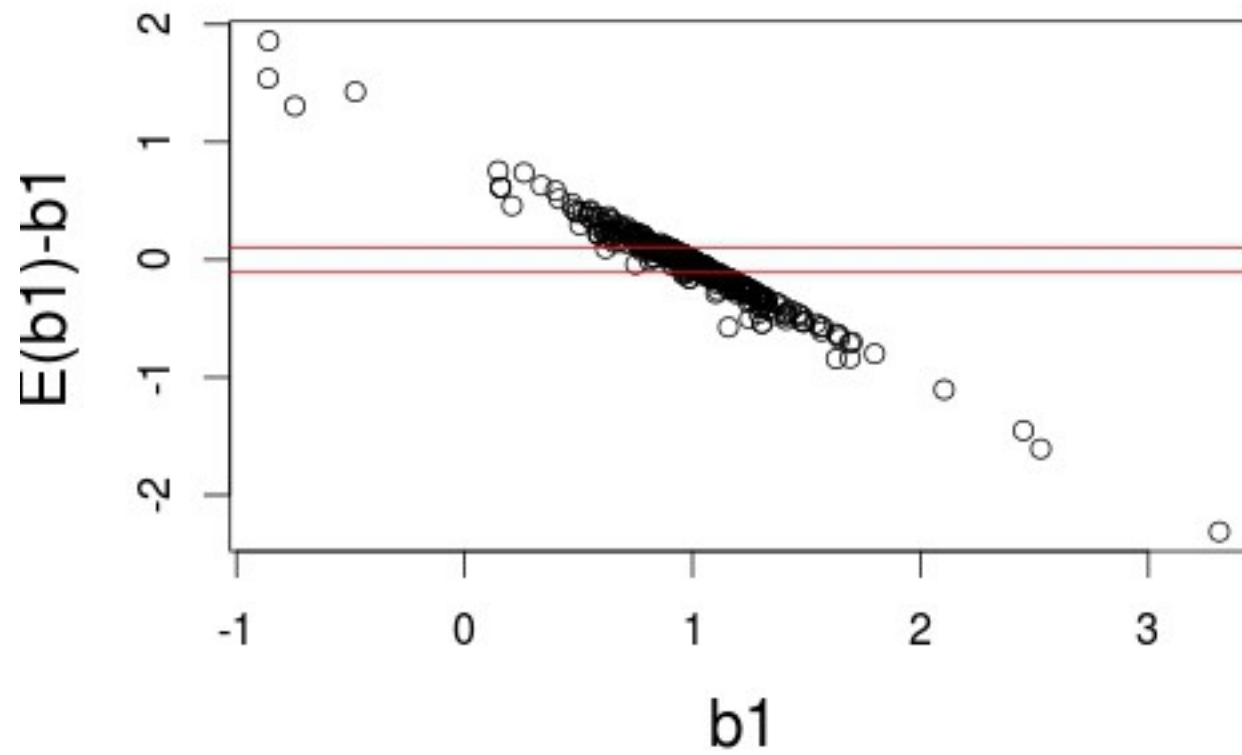




### Statistically pass/fail

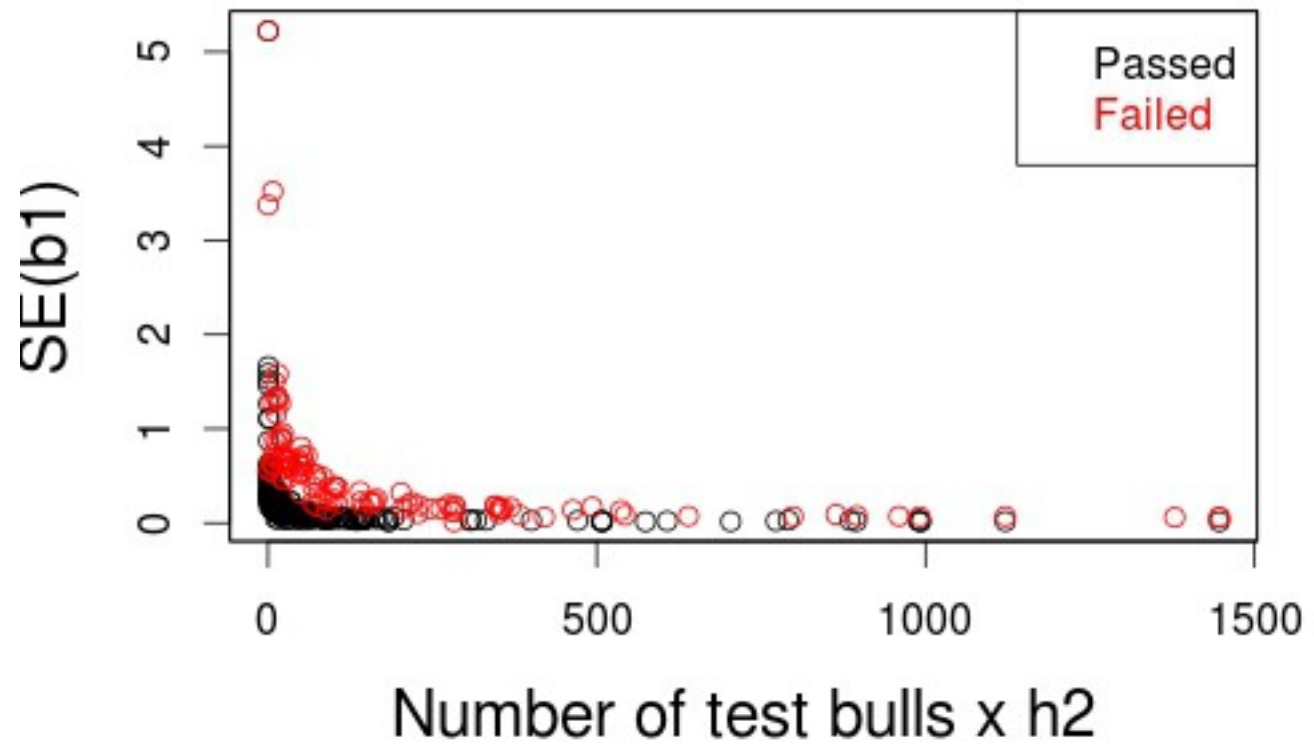


## Biologically pass/fail

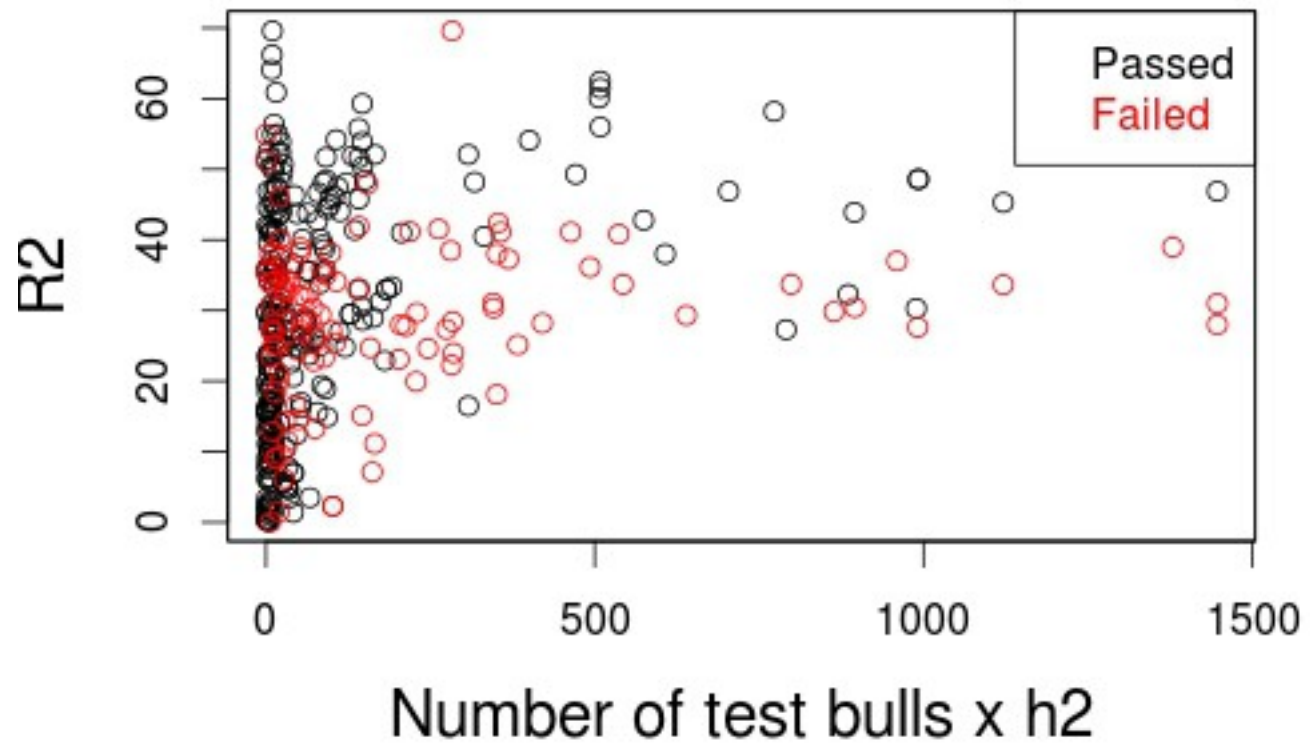


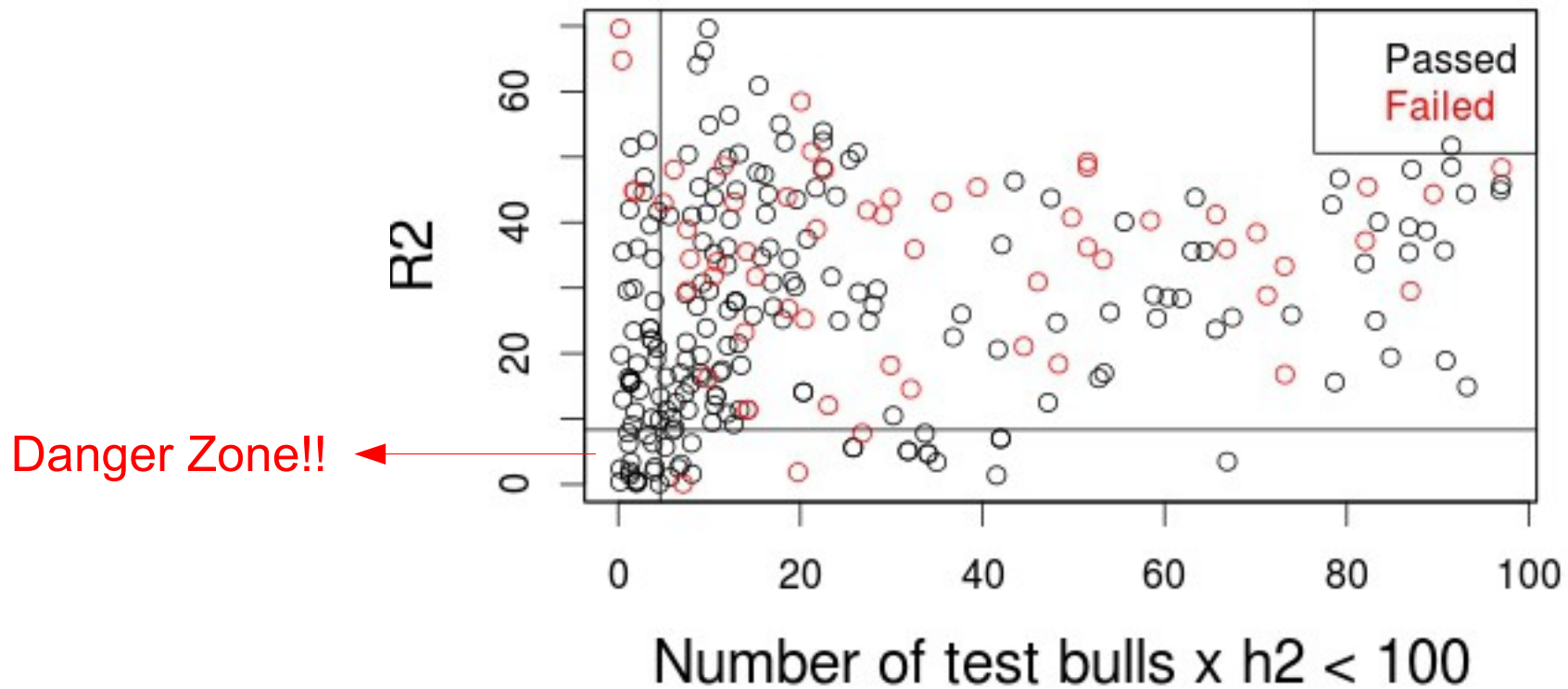
$$b_1 - 0.1 < E(b_1) < b_1 + 0.1$$
$$-0.1 < E(b_1) - b_1 < 0.1$$











Vertical line = 5

e.g.,  $h^2 = 0.25$  & #test = 20

e.g.,  $h^2 = 0.50$  & #test = 10

# Remarks and conclusion

- The current GEBV-test is a good & sound method.
- Modifications and fine tuning are required and under study.
- There has been high interest both from ITBC and the countries that traits should pass the test. Open data edits and new rules put the test under question (my personal opinion).
- In the future, with more animals being genotyped,  $b_1$  &  $E(b_1)$  may reach to 1, other validation methods may be required.
- What complicates this situation is that countries have different genotyping speed, and in need of different validation methods.

# Remarks and conclusion

- The current GEBV-test is a good & sound method.
- Modifications and fine tuning are required and under study.
- There has been high interest both from ITBC and the countries that traits should pass the test. Open data edits and new rules put the test under question (my personal opinion).
- In the future, with more animals being genotyped,  $b_1$  &  $E(b_1)$  may reach to 1, other validation methods may be required.
- What complicates this situation is that countries have different genotyping speed, and in need of different validation methods.

Thanks for your attention