Erratum to: Potential of promotion of alleles by genome editing to improve quantitative traits in livestock breeding programs

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After the publication of this work [1], we noticed that Figs. 1 and 2 were accidentally interchanged. The correct version order of Figs. 1 and 2 are provided here. The original article was corrected.

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Reference
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**Simulated scenarios for promotion of alleles by genome editing**

| Population           | Generations | Mutation | Selection                              | PAGE                                      |
|----------------------|-------------|----------|----------------------------------------|-------------------------------------------|
| Historical evolution | 100,000 years | $2.5 \times 10^{-5}$ | Random selection                        | -                                         |
| Recent historical breeding | -20 to 0 | -        | Genomic selection 1000 candidates $500 \times 25 \sigma^2$ selected parents | -                                         |
| Future breeding      | 1 to 20     | -        | Genomic selection 1000 candidates $500 \times 25 \sigma^2$ selected parents | Top 6 or 10, bottom 5 or all 25 selected sires 0, 1, 5, 10, 20, 25, 50 or 100 edits per sire |

**PAGE** – promotion of alleles by genome editing.

**Fig. 1** Simulated scenarios for promotion of alleles by genome editing
PAGE? 

Yes 

No 

GS only 

Number of edited sires? 

Bottom 10 

Top 5 

Number of QTNe? 

B10se 1QTNe 

B10se 5QTNe 

B10se 10QTNe 

B10se 20QTNe 

1 

5 

10 

20 

A25se 1QTNe 

A25se 5QTNe 

A25se 10QTNe 

A25se 20QTNe 

T10se 1QTNe 

T10se 5QTNe 

T10se 10QTNe 

T10se 20QTNe 

25 

50 

100 

T5se 25QTNe 

T5se 50QTNe 

T5se 100QTNe 

PAGE – promotion of alleles by genome editing; GS – genomic selection; QTNe – QTN being edited; B10se – the bottom 10 selected sires edited; A25se – all of the 25 selected sires edited; T10se – the top 10 selected sires edited; T5se – the top 5 selected sires edited

Fig. 2 Overall design of the simulation