

ERRATUM Open Access

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

Janez Jenko¹, Gregor Gorjanc¹, Matthew A. Cleveland², Rajeev K. Varshney³, C. Bruce A. Whitelaw¹, John A. Woolliams¹ and John M. Hickey^{1*}

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.

Author details

¹The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Easter Bush, Midlothian, Scotland, UK. ²Genus plc., 100 Bluegrass Commons Blvd., Suite 2200, Hendersonville, TN 37075, USA. ³International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India.

Received: 23 July 2015 Accepted: 23 July 2015 Published online: 11 September 2015

Reference

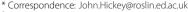
 Jenko J, Gorjanc G, Cleveland MA, Varshney RK, Whitelaw CBA, Woolliams JA, et al. Potential of promotion alleles by genome editing to improve quantitative traits in livestock breeding programs. Genet Sel Evol. 2015;47:55.

Submit your next manuscript to BioMed Central and take full advantage of:

- Convenient online submission
- Thorough peer review
- No space constraints or color figure charges
- Immediate publication on acceptance
- Inclusion in PubMed, CAS, Scopus and Google Scholar
- Research which is freely available for redistribution

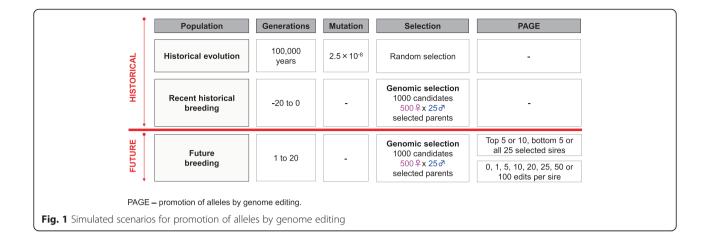
Submit your manuscript at www.biomedcentral.com/submit

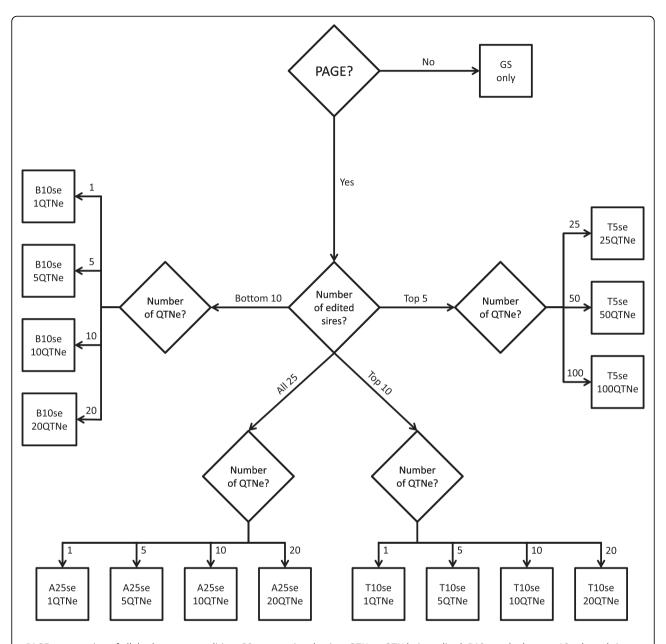




¹The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Easter Bush, Midlothian, Scotland, UK







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