### ERRATUM

**Open Access** 



# Erratum to: Dynamics of gene silencing during X inactivation using allele-specific RNA-seq

Hendrik Marks<sup>1\*</sup>, Hindrik H. D. Kerstens<sup>1</sup>, Tahsin Stefan Barakat<sup>3</sup>, Erik Splinter<sup>4</sup>, René A. M. Dirks<sup>1</sup>, Guido van Mierlo<sup>1</sup>, Onkar Joshi<sup>1</sup>, Shuang-Yin Wang<sup>1</sup>, Tomas Babak<sup>5</sup>, Cornelis A. Albers<sup>2</sup>, Tüzer Kalkan<sup>6</sup>, Austin Smith<sup>6</sup>, Alice Jouneau<sup>7</sup>, Wouter de Laat<sup>4</sup>, Joost Gribnau<sup>3</sup> and Hendrik G. Stunnenberg<sup>1\*</sup>

After the publication of this work [1], we noticed there was an error in Fig. 5 where -1,0 and 1 are incorrectly displayed in the y-axis in panel b. Please see the corrected Fig. 5 below. We apologize for this error.

#### Author details

<sup>1</sup>Radboud University, Faculty of Science, Department of Molecular Biology, Radboud Institute for Molecular Life Sciences (RIMLS), Nijmegen 6500HB, The Netherlands. <sup>2</sup>Radboud University, Faculty of Science, Department of Molecular Developmental Biology, Radboud Institute for Molecular Life Sciences (RIMLS), Nijmegen 6500HB, The Netherlands. <sup>3</sup>Department of Reproduction and Development, Erasmus MC, University Medical Center, Rotterdam, The Netherlands. <sup>4</sup>Hubrecht Institute, University Medical Center Utrecht, Uppsalalaan 8, Utrecht 3584CT, The Netherlands. <sup>5</sup>Biology Department, Queen's University, Kingston, ON, Canada. <sup>6</sup>Wellcome Trust-Medical Research Council Stem Cell Institute, University of Cambridge, Tennis Court Road, Cambridge CB2 1QR, UK. <sup>7</sup>INRA, UMR1198 Biologie du Développement et Reproduction, Jouy-en-Josas F-78350, France.

#### Received: 25 January 2016 Accepted: 25 January 2016 Published: 5 February 2016

#### References

 Marks H, Kerstens HH, Barakat TS, Splinter E, Dirks RAM, van Mierlo G, et al. Dynamics of gene silencing during X inactivation using allele-specific RNA-seq. Genome Biol. 2015;16:149.

\* Correspondence: H.Marks@ncmls.ru.nl; H.Stunnenberg@ncmls.ru.nl <sup>1</sup>Radboud University, Faculty of Science, Department of Molecular Biology, Radboud Institute for Molecular Life Sciences (RIMLS), Nijmegen 6500HB, The Netherlands

## Submit your next manuscript to BioMed Central and we will help you at every step:

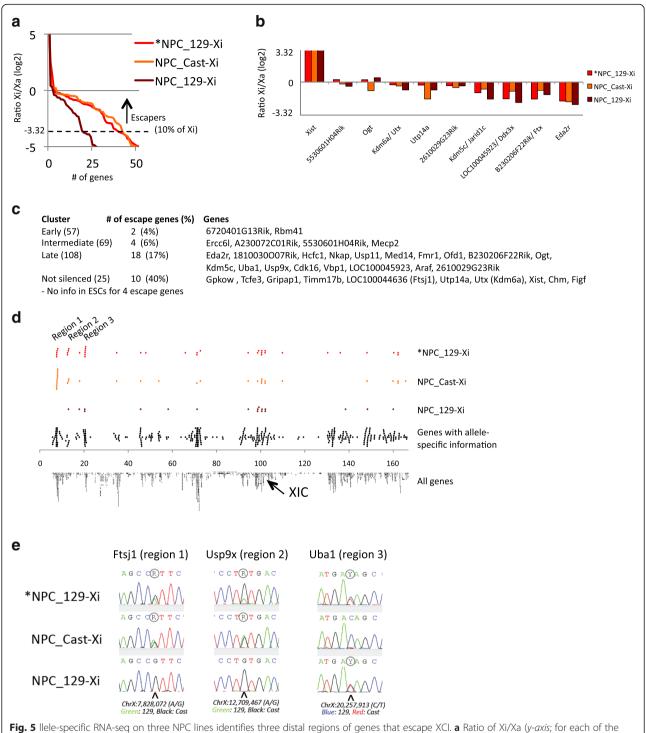
- We accept pre-submission inquiries
- Our selector tool helps you to find the most relevant journal
- We provide round the clock customer support
- Convenient online submission
- Thorough peer review
- Inclusion in PubMed and all major indexing services
- Maximum visibility for your research

Submit your manuscript at www.biomedcentral.com/submit





© 2016 Marks et al. **Open Access** This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The Creative Commons Public Domain Dedication waiver (http://creativecommons.org/publicdomain/zero/1.0/) applies to the data made available in this article, unless otherwise stated.



**Fig. 5** Ilele-specific RNA-seq on three NPC lines identifies three distal regions of genes that escape XCI. **a** Ratio of Xi/Xa (*y-axis*; for each of the three NPC lines sorted from highest to lowest) for genes showing a log2 ratio of at least –5. We set the cutoff for escape on 10 % relative expression from the Xi versus the Xa (log 2 ratio of > –3.32; similar to Yang et al. [37]). **b** Xi/Xa ratio of genes that escape XCI in all three NPC lines. **c** Distribution of the escape genes identified in \*NPC\_129-Xi over the four clusters as characterized in Fig. 4a. **d** Localization of the escape genes within each NPC line over the linear X chromosome (see also Table 1). The *black dots* on the *fourth row* represent all X-linked genes for which high-confidence allele-specific ratios were obtained in NPCs. **e** Validation of the escape genes within the three escape regions by Sanger sequencing of cDNA. See Additional file 1: Figure S13 for the full panel of 13 genes that we validated, and for further details