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

Hendrik Marks1*, Hindrik H. D. Kerstens1, Tahsin Stefan Barakat3, Erik Splinter4, René A. M. Dirks1, Guido van Mierlo1, Onkar Joshi1, Shuang-Yin Wang1, Tomas Babak5, Cornelis A. Albers2, Tüzer Kalkan6, Austin Smith6, Alice Jouneau7, Wouter de Laat6, Joost Gribnau3 and Hendrik G. Stunnenberg1*

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

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

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Fig. 5 Allele-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.