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 Laat8, 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.

References

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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 (log2 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.