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

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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.

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

References
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 \(-3.5\). 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.

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.