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

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ERRATUM

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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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1. 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.

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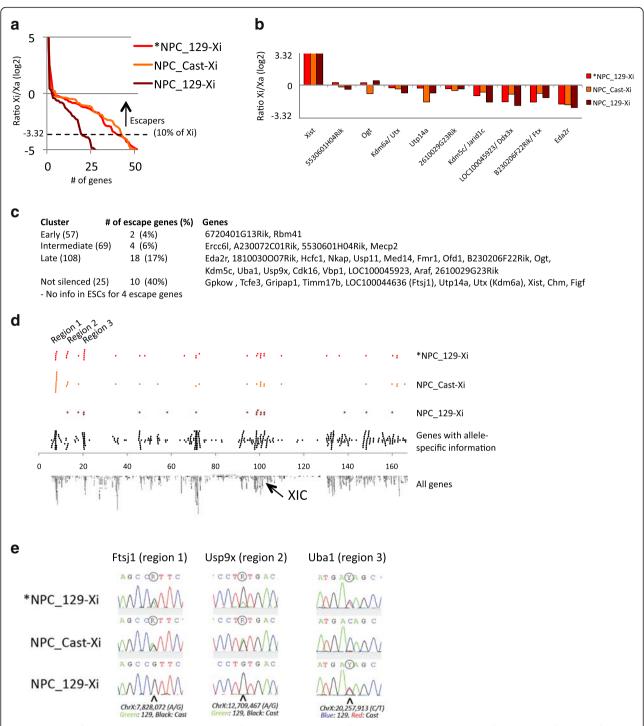Marks *et al. Genome Biology* (2016) 17:22

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Fig. 5 llele-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