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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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. 

<table>
<thead>
<tr>
<th>Cluster</th>
<th># of escape genes (%)</th>
<th>Genes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Early (57)</td>
<td>2 (4%)</td>
<td>Ercc6l, A230072C01Rik, S530601H04Rik, Meccp2</td>
</tr>
<tr>
<td>Intermediate (69)</td>
<td>4 (6%)</td>
<td>Eads2r, 1810030007Rik, Hcfc1, Nkap, Usp11, Med14, Fmr1, Odf1, B230206F22Rik, Ogt, Kdm5c, Uba1, Usp9x, Cdk16, Vbp1, LOC100045923, Araf, 2610029623Rik</td>
</tr>
<tr>
<td>Late (108)</td>
<td>18 (17%)</td>
<td>Gpkow, Tcfe3, Grippap1, Tmm17b, LOC100044636 (Ftsj1), Utp14a, Utx (Kdm6a), Xist, Chm, Figf</td>
</tr>
<tr>
<td>Not silenced (25)</td>
<td>10 (40%)</td>
<td></td>
</tr>
</tbody>
</table>

- No info in ESCs for 4 escape genes

**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.