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Corrigendum

Long non-coding RNA exchange during the oocyte-to-embryo transition in mice

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There should be three authors to whom correspondence should be addressed: Fugaku Aoki, Kristian Vlahovicek, and Petr Svoboda. Their details are as above:
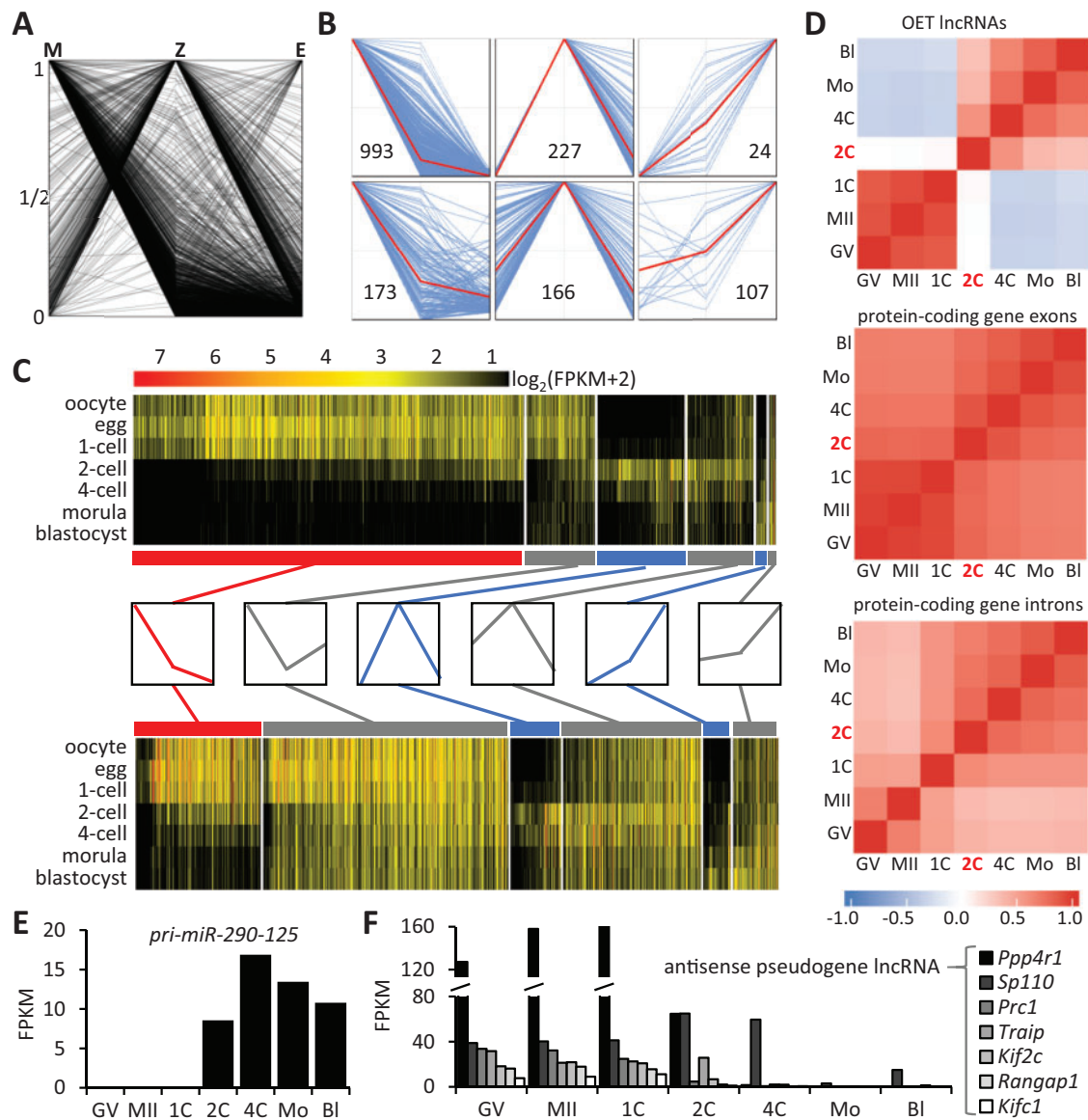The image for Figure 5 was incorrect. The correct image and caption are given below.

Figure 5. OET lncRNA population dynamics during early development. **(A)** Overview of expression patterns of OET lncRNAs. To simplify expression pattern classification, we used average FPKM values: M, maternal (GV and MII oocytes); Z, zygotic (two- and four-cell stages); and E, late preimplantation embryo (morula and blastocyst). The plot shows dynamics of all clusters where the maximum average FPKM value of each cluster in M, Z, E was set to 1. **(B)** Main expression patterns of OET lncRNAs. The six panels display six basic patterns separating maternal (top left panel), zygotic (top middle and top right panels), and maternal-zygotic lncRNA (bottom panels) expression. The red lines represent the average values per each panel. **(C)** Expression patterns of 1,600 OET lncRNAs and 19741 mRNAs. The heatmap for lncRNAs and mRNAs was assembled from the six basic patterns (shown in (B) and schematically depicted between the heatmaps with maternal in red, zygotic in blue and maternal-zygotic in grey). Clusters with M, Z, E maxima were ordered from the left to the right and ranked based on the Z value for M and E patterns and M value for Z patterns. **(D)** Expression correlations estimated from reads matching different types of sequences—exons of 1,600 lncRNA and exons and introns of protein-coding genes. The color scale on the left indicates the correlation coefficient for the analysed features. Note the negative correlation for lncRNA expression between maternal and zygotic/embryonic stages reflects the apparently mutually exclusive expression patterns observed in the upper heatmap in (C). Temporal expression patterns of miR-290-295 primary precursor **(E)** and lncRNAs carrying antisense sequences of processed pseudogenes **(F)**. Graphs depict expression values (FPKMs) for indicated lncRNAs. In (F), lncRNAs are labeled by gene names from which the pseudogene sequences in lncRNAs originated.

These corrections have been made to the full paper.