Human postmeiotic sex chromatin and its impact on sex chromosome evolution

Supplemental Material

Figure S1. Immunostaining and combined DNA FISH using paraffin sections of human testis. (**A**) H3K9me3 and X-paint. (**B**) CBX1 and X paint. (**C**) CBX3 and Y paint. (**D**) Double immunostaining using anti-centromere antibody and anti-CBX3 antibody. Representative pictures of primary spermatocytes (boxed region) are magnified in the bottom panels denoted with ('). All images are wide-field images. Bar: 20μm

Figure S2. Maintenance of silencing from MSCI to postmeiotic silencing. (**A)** Distribution of recovery rate of the genes repressed at PS (see text). Recovery rate is calculated according to this equation: Recovery rate = $(E_{RS}-E_{PS}) / (E_{SG}-E_{PS})$. (B) Expression average of genes repressed at PS. Spermatogonia (GS), pachytene spermatocytes (PS), and round spermatids (RS). ** $p < 10^{-4}$. Tukey's Multiple Comparison Test.

Table S1. List of each group of human X-linked genes based on the expression profiles.

Table S2. Expression profiles of human Y-linked genes.

Table S3. Expression profiles of human X-linked genes which have homologues on the Y chromosome.

Table S4. List of human X-linked multicopy genes and their expression profiles. Definition of groups is described in this study.

Table S5. List of multicopy genes on the mouse X chromosome and their expression profiles. Definition of groups is described in our previous study (Namekawa et al. 2006).

Table S6. Expression profiles of human X-retrotransposed genes and their X-linked homologues.

Table S7. Expression profiles of mouse X-retrotransposed genes and their X-linked homologues.

Table S8. Comparison of Group C genes between mice and humans. Genes which show consistent expression patterns between humans and mice are listed in the upper panels. Genes which show inconsistent expression patterns between humans and mice are listed in the lower panels. We identified 66 human Group C genes comprising 6 multicopy genes and 60 single-copy genes (Table S1). However, 5 genes among 60 single-copy genes are intergenic transcriptions and do not have formal nomenclature. Therefore, in this Table S8 we do not include these intergenic transcriptions. In our previous study, we identified 51 mouse Group C genes (Namekawa et al. 2006), but we have reexamined the microarray data and identified 4 additional genes in the mouse Group C (total 55 genes). Therefore, we listed 55 genes as mouse Group C genes in this table.

Table S9. List of K_a/K_s values of escape genes and non-escape genes. Escape genes include genes that escape postmeiotic silencing in humans. Non-escape genes include genes consistently repressed by postmeiotic silencing both in humans and in mice.