

Supplemental Figure Legends

Figure S1. Reproducibility of biological replicates. Genome browser views of EE and L3 biological replicates of the repressive mark H3K9me3 and the active marks H3K4me3 and H3K79me3 in ~60kb of Chr X. The correlation coefficients between biological replicates for each ChIP factor are shown in **Table S1**.

Figure S2. Profiles of all factors on X-linked and autosomal genes in the top and bottom expression bins. Average signal profiles in the 2kb around transcript start sites (TSS) and transcript termination sites (TTS) are shown for all factors on four groups of genes: autosomal genes in the top 10% and bottom 10% of expression and X-linked genes in the top 10% and bottom 10% of expression. Groups as determined in **Figure 1** are indicated.

Figure S3. Histone marks and chromatin proteins show distinct patterns on different chromosomes and on the arms versus central region of each chromosome. Panels A-F show enlarged views of each chromosome shown in **Figure 2**. The signal intensity of all analyzed factors is shown across each chromosome. Colored cells show median signals in 1kb windows, red indicating high signal, blue low signal. Each row corresponds to a factor. The order of factors is as shown in **Figure 1** and in the key to the right. The color labels to the right of each track indicate stage, as in **Figure 1**. Marey plots of recombination distances are shown as thick black lines.

Figure S4. Histone marks across an arm-center boundary. Genome browser shots of active marks H3K4me3, H3K36me3 and H3K79me3 and repressive marks H3K9me1/2/3 in a 3Mb region and a zoom-in view in a 400kb region of Chr II illustrate the transition from arm (left) to central region (right). The transition region is highlighted in gray.

Figure S5. Profiles of factors on genes located in the centers and arms of chromosomes and in the top and bottom expression bins. Profiles of selected factors

are shown for genes in the central regions (blue) and arms (red) of chromosomes and in the top 10% (dark color) and bottom 10% (light color) of expression.

Figure S6. Distribution of genes with different expression levels and ubiquitously expressed genes by chromosome. (A) Expression of genes genome-wide in early embryos was divided into 5 equal bins. The distribution of the genes on each chromosome in those bins is shown. (B,C) Distribution of ubiquitously expressed genes, as defined in Methods, by chromosome.

Table S1. ChIP-chip profiling performed in this study, correlation coefficients of biological replicates for each ChIP factor, and GEO accession numbers.

