

**Figure S1**

Bar chart showing the average log2 expression ratio in X*E*O*Sry* versus X*E,Z2*O*Sry* for all genes, spermatogonia-specific genes and pachytene-specific genes. For this analysis, ‘spermatogonia-specific’ and ‘pachytene-specific’ were defined as those showing at least a tenfold decrease in transcript abundance between B spermatogonia and pachytene spermatocytes in Namekawa et al (2006). This was to ensure that autosomal genes chosen as a comparator set are an appropriate match for the X chromosome genes, which are transcribed in B spermatogonia but silenced by MSCI during pachynema.

\* The X chromosome is globally upregulated in X*E*O*Sry* (p = 4.5 x 10-39)

\*\* Autosomal and X spermatogonia-specific genes are upregulated and autosomal pachytene-specific genes are downregulated in X*E*O*Sry* (p < 1 x 10-7for each subset).

\*\*\* X spermatogonia-specific genes are more strongly upregulated than autosomal spermatogonia-specific genes in X*E*O*Sry* (p = 4.80 x 10-8).