

Supplementary Note 1: Additional information for Supplementary Figure 12

The analyses of Supplementary Figure 12 are based on the human and chicken sex-averaged recombination rates as reported in Kong et al. 2002 *Nature Genetics* 31:241-247 and Elferink et al. 2010 *BMC Genetics* 2010 11:11, with recombination rates for the Z and X corrected to 2/3 of the reported homogametic rate.

Recombination data for the human genome is available from the UCSC genome browser as an average over one megabase intervals on the 2006 assembly of the human genome, which includes the finished sequence of the human X chromosome. Recombination data for the chicken genome is available in approximately half-megabase intervals. For the Z chromosome, we mapped the locations of markers from Elferink et al. onto our assembly using BLAT.

For each interval, we tabulated the corresponding G+C content and LINE density. We then segmented the data by recombination rate, using 1 cM/Mb bins. For both G+C content and LINE density, we performed a Mann-Whitney U test on each bin, comparing the location of data for the Z chromosome to the chicken autosomes. We repeated this analysis with the data from humans, comparing the location of data from the X chromosome with the human autosomes.

Consistent with the predictions of a model of biased gene conversion towards GC, we observed no statistically significant difference in G+C content between intervals on the Z and X chromosomes and intervals on autosomes with similar rates of crossing over.

Models of transposable element distribution based on ectopic exchange or NAHR-mediated deletion predict that LINEs will be more abundant in regions where crossing over is rare. We observe this trend in both the chicken and human genomes. However, the LINE density of Z and X chromosomes is significantly different from autosomal regions with similar rates of crossing over. Additional mechanisms of LINE element accumulation are necessary to account for the enrichment we observe.

On the Z chromosome, we observed statistically significant ($P < 0.05$) differences in LINE density between intervals on the Z chromosome and intervals on chicken autosomes with a similar rates of crossing over, in bins up to 7 cM/Mb, beyond which significance tests are impossible due to the low number of Z intervals.

On the X chromosome, we observed statistically significant ($P < 0.05$) differences in LINE density between intervals on the X chromosome and intervals on human autosomes with a similar rates of crossing over, in bins up to 3 cM/Mb, beyond which significance tests are impossible due to the low number of X intervals.