Web Figure A. The number of arrayed elements that report anomalous segregation can be estimated for each annotated class. We used an independent method to estimate the number of annotated genomic segments that segregate anomalously in our fractionation. The percentile rank of individual ratio values \(\log_2\text{(experimental signal intensity/normalized reference signal intensity)}\) within each class (ORFs, black; non-coding, red) is plotted (x-axis) against the percentile rank of that same ratio value among all spots (y-axis) for experiments #9-27. For this analysis, all spots of a designated class are analyzed, regardless of p-value.

If one supposes that each annotated class segregates stereotypically, and therefore contributes to the overall ratio rank among all spots in a consistent manner, one may model each class’s idealized contribution to the overall rank (dashed straight lines). Areas where the experimental data (solid points) departs from the model (dashed lines) represent arrayed elements reporting anomalous segregation of the corresponding genomic fragment. The grey dotted line drawn from such points of departure to the x-axis estimate that approximately 17% of SGD-annotated ORFs and 20% of annotated intergenic regions behave apart from other members of their respective classifications.
Web Figure B.

Genomic Regions Upstream of Highly Transcribed Genes Segregate Most Strongly (Single promoters only)

Web Figure B. Same as Figure 3B, except data is only from intergenic regions upstream of 1 gene, to show that the effect is not an artifact created by including double promoters, which as a class are more heavily enriched than single promoters (Figure 4), or by plotting against only the most highly transcribed of the two downstream gene
Web Figure C.

(A) Methylene bridge formation between the ε-amino group of lysine and the amide group of a peptide bond

Methylene Glycol (Formaldehyde + Water)

\[
\begin{align*}
\text{HC} & \quad \text{(CH}_3\text{)}_4\text{NH}_2 + \text{HOC}_2\text{OH} + \text{HN} \\
\text{O} & \quad \text{C} \\
\text{N} & \quad \text{H} \\
\end{align*}
\]

Lysine
Adjacent Peptide Linkage

Methylene Bridge

\[
\begin{align*}
\text{HC} & \quad \text{(CH}_3\text{)}_4\text{N}\text{CH}_2\text{N} \\
\text{O} & \quad \text{C} \\
\text{N} & \quad \text{H} \\
\end{align*}
\] + \text{H}_2\text{O}

(B) T:A

\[
\begin{align*}
\text{T} & \quad \text{A} \\
\text{C} & \quad \text{G} \\
\end{align*}
\]

\[
\begin{align*}
\text{H} & \quad \text{R} \quad \text{N} \quad \text{H} + \text{CH}_2\text{O} \quad \text{K}_1 \\
\text{R} & \quad \text{N} \quad \text{CH}_2\text{O} + \text{CH}_2\text{O} \quad \text{K}_2 \quad \text{R} \quad \text{N} \quad \text{CH}_2\text{OH}
\end{align*}
\]
Web Figure C. The reaction of formaldehyde with proteins and DNA. Adapted from an article published in *Microscopy Today* 00-1 pp. 8-12 (2000), by John A. Kiernan, http://publish.uwo.ca/~jkiernan/formglut.htm, reference (1).

(A) An example of methylene bridge formation between the ε-amino group of lysine and the amide group of the peptide bond. The initial reaction of formaldehyde with the amino group of lysine residues on proteins (red "N") is very fast and results in a methylol derivative. The derivative subsequently forms a methylene bridge through a slow condensation reaction. Such bridges most likely form between amine, amide, guanidyl, phenol, imidazole or indole groups. The only other product isolated from crosslinked proteins was Lys-CH2-Tyr. (B) Double-stranded DNA must be denatured to react with formaldehyde, in order to expose exocyclic amino groups (red arrows). Since reaction of formaldehyde with a nucleoside amino group results predominantly in a hydroxymethyl or methylol derivative, rather than a Shiff base, there is a possibility of forming a diadduct at high formaldehyde concentration (2, 3).
Web Figure D. The fractionation properties of chromatin change as a function of distance proximal to chromosome ends. This effect is illustrated by the trend lines in the above graph, and in the graphs of the 32 individual chromosome ends (see the file “Individual_Telomere_Graphs.xls” on the web page). The slope of the trend lines is up and away from the chromosome end for both classes, with the trend line of the ORFs beneath that of the intergenics in all cases.

To further illustrate this telomere position effect, the median percentile rank for all members of each class (not just the ones closest to the chromosome ends) is indicated by the dotted lines in the graph above. If there were no telomeric position effect, one would expect half of the black dots to be above the black dotted line, and half to be below. This is not the case, but the expected distribution begins to emerge as the distance from the chromosome ends increases. The same is true to a lesser extent for the ORFs (the slope of the solid red trend line is more shallow; red dots data points, blue dotted line median ORF rank).
Literature cited