

Figure S1

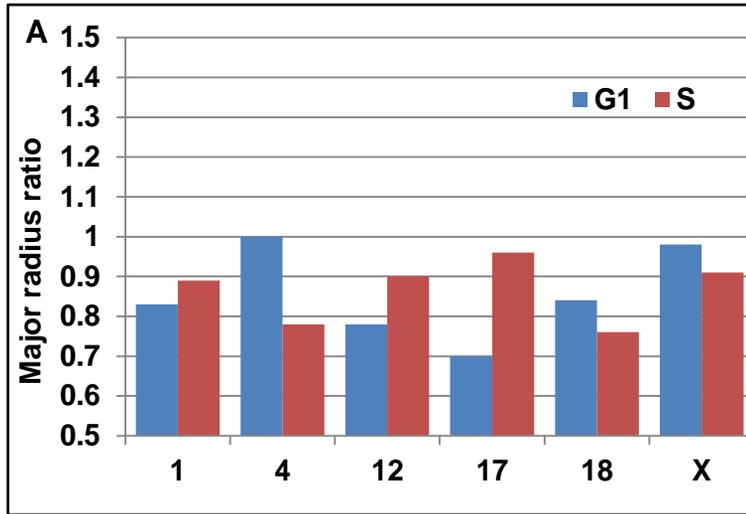


Figure S1. Positioning within CT in random constrained simulations. Random simulations constrained within CT demonstrate the most probable positions relative to the CT centers and peripheries if the points are selected randomly (MRR, see Fig 3A, C).

Figure S2

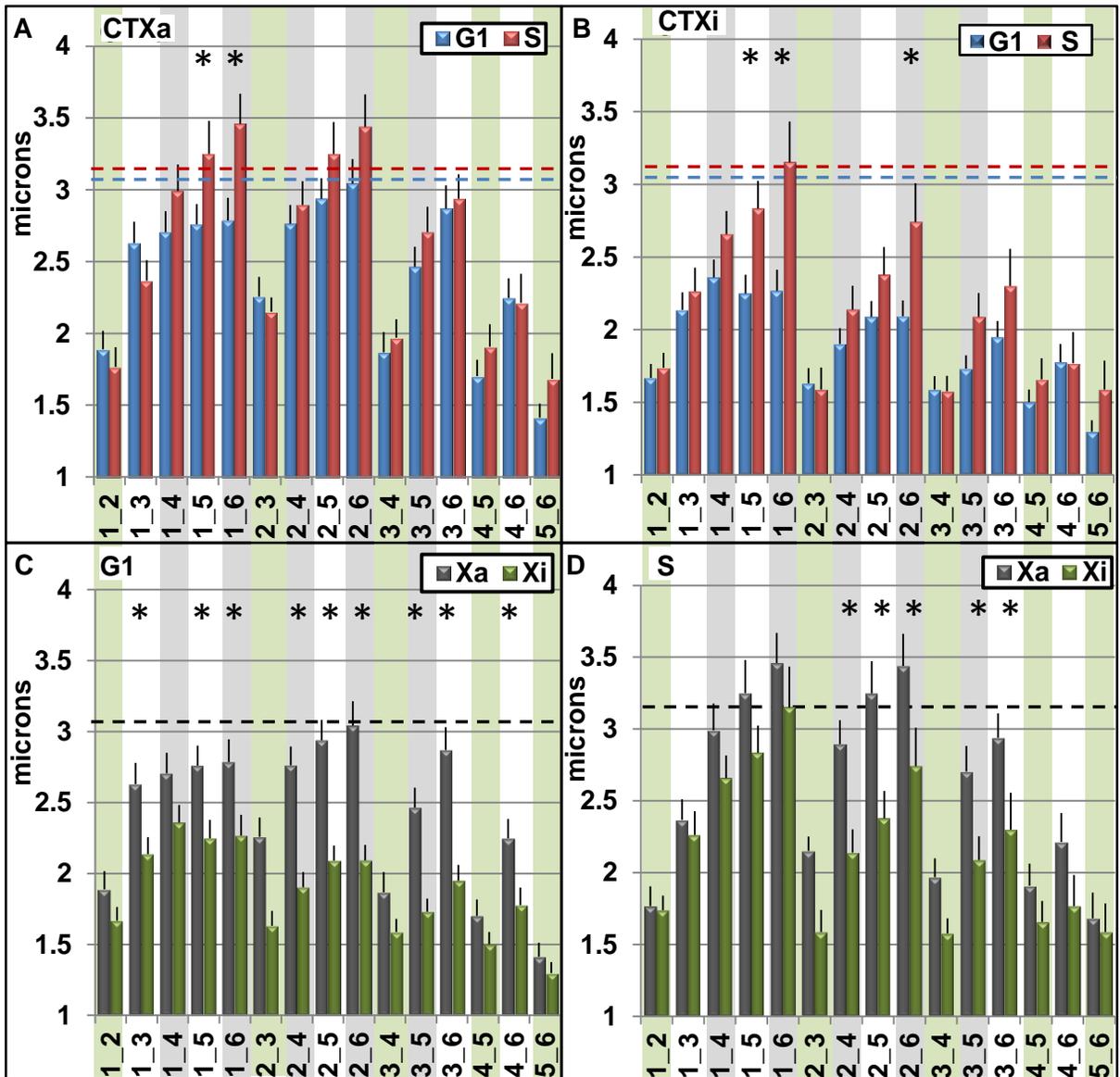


Figure S2. Pairwise probe distances between intrachromosomal regions in CTX. 15 pairwise distances between the 6 different regions are determined for CTXa (A) and CTXi (B) in G1 (blue) and S (red). Comparisons between Xa (grey) and Xi (green) are presented in G1 (C) and in S (D). The average values for simulations of randomly generated points constrained within the CT are shown as dashed lines. *indicates significant differences between G1 and S (t test, $p < 0.05$).

Figure S3

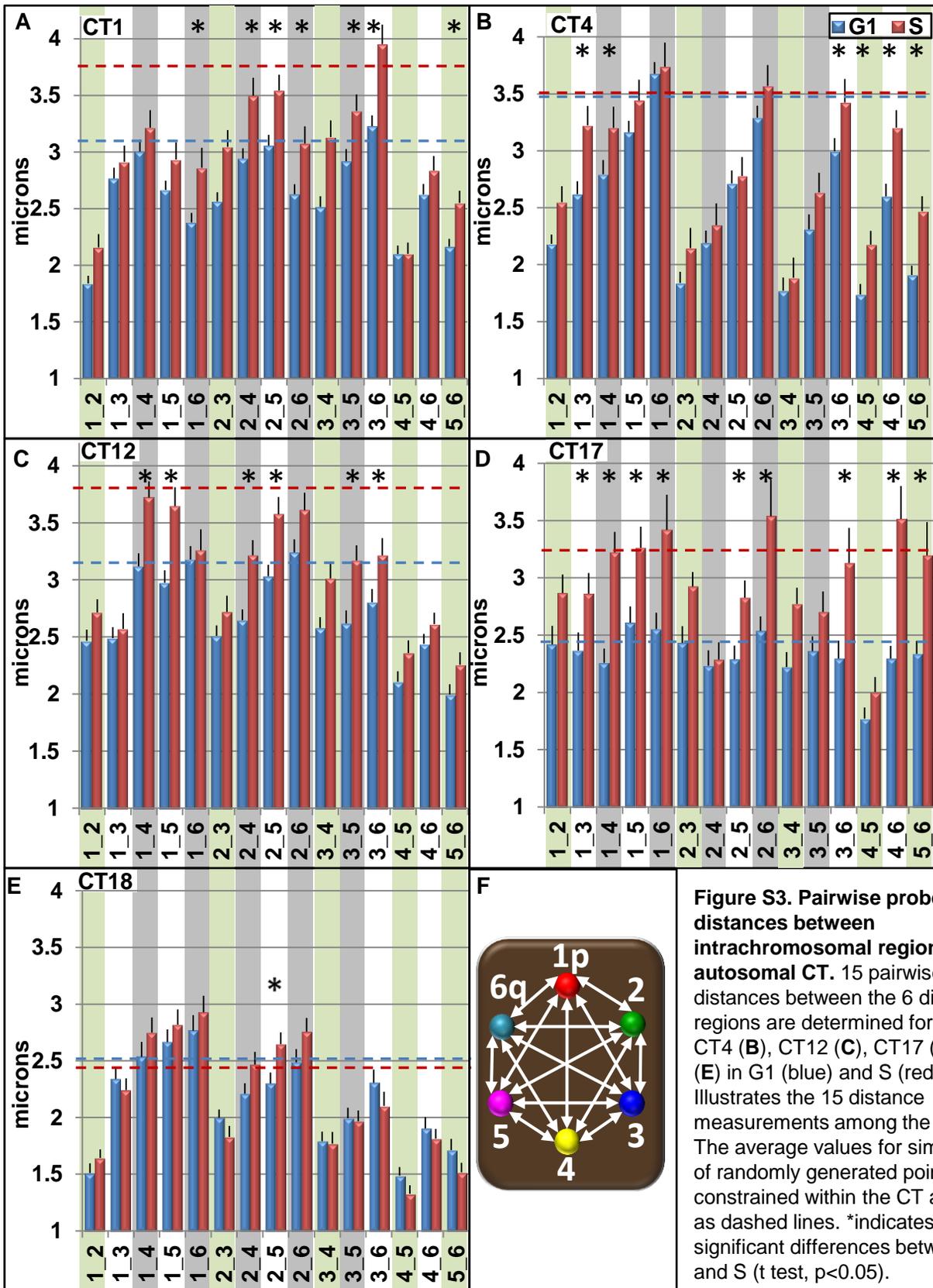


Figure S3. Pairwise probe distances between intrachromosomal regions in autosomal CT. 15 pairwise distances between the 6 different regions are determined for CT1 (A), CT4 (B), CT12 (C), CT17 (D), CT18 (E) in G1 (blue) and S (red). (F) Illustrates the 15 distance measurements among the 6 probes. The average values for simulations of randomly generated points constrained within the CT are shown as dashed lines. *indicates significant differences between G1 and S (t test, $p < 0.05$).

Figure S4

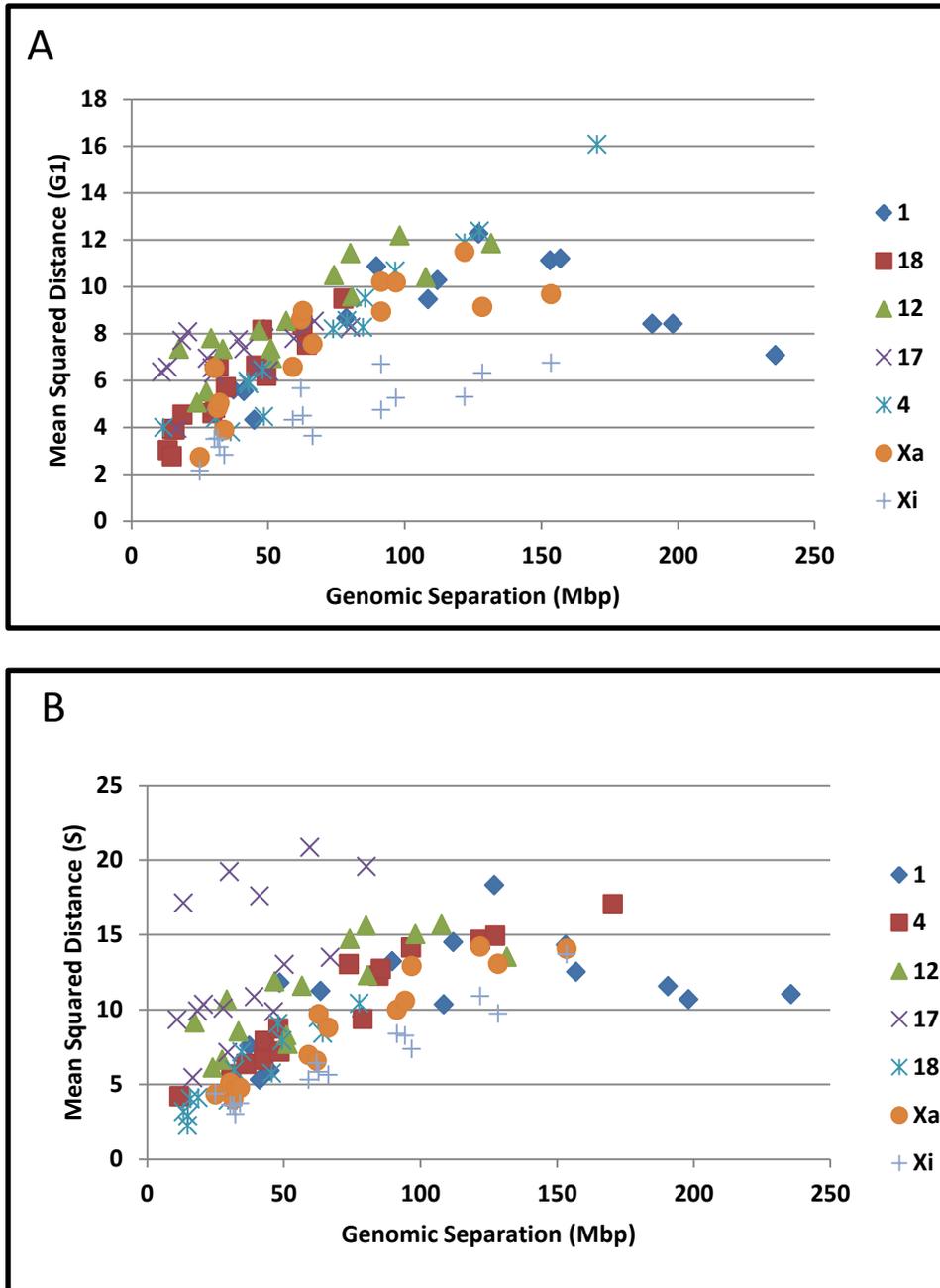


Figure S4. Relation between mean squared distances and genomic separation. The mean squared distances were plotted against their genomic separation (Mbp) for all the CT in G1 (A) and S (B) phase.

Figure S5

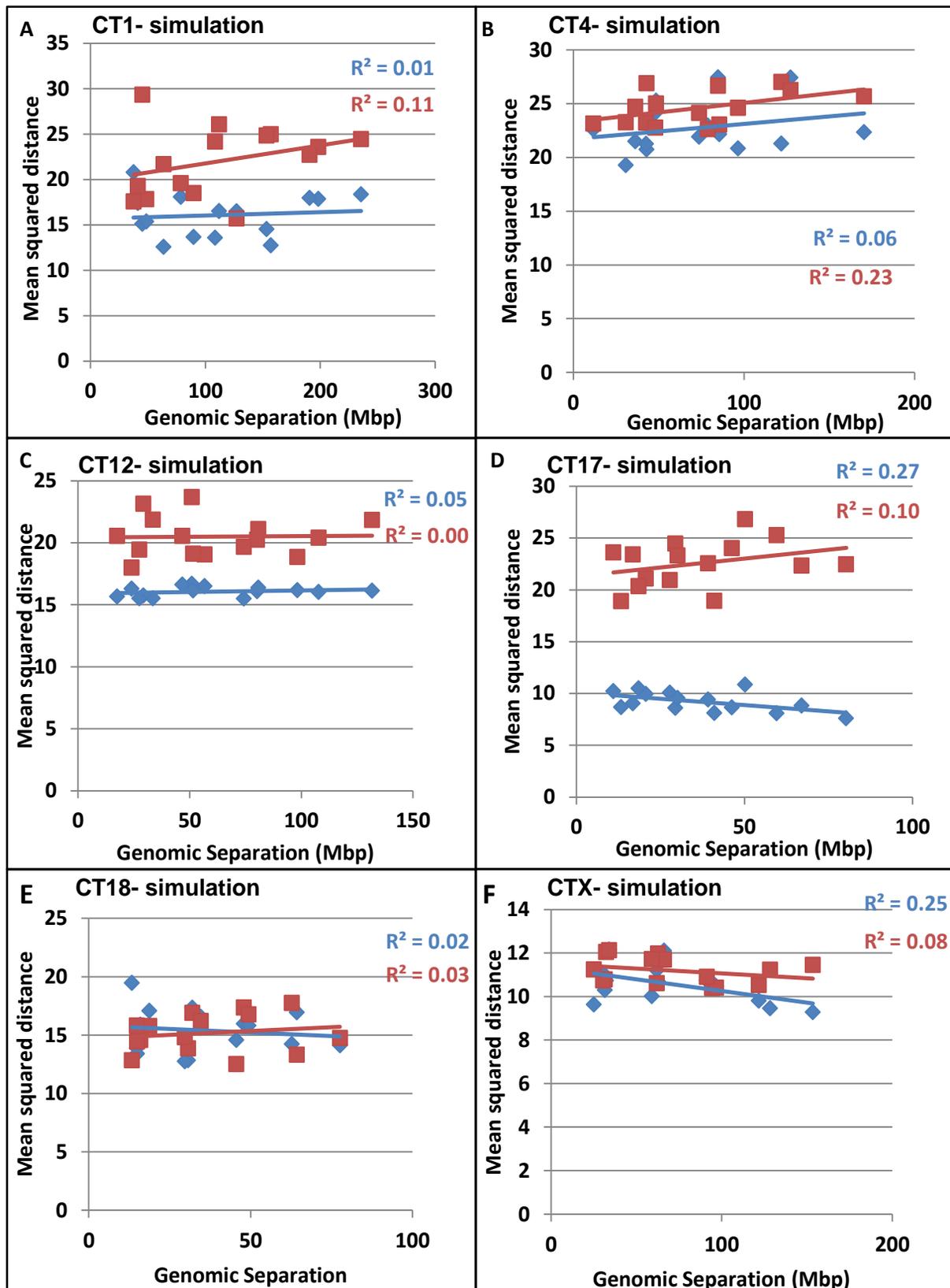


Figure S5. The relationship between mean squared distances and the genomic separation for random simulations. The mean squared interphase distances between the randomly generated six probes (a total of 15 distances) were plotted against their genomic separation for CT1 (A), 4 (B), 12 (C), 17 (D), 18 (E), X (F). Linear trendlines are shown for G1 (blue) and S (red). r^2 values for the linear trendlines are displayed on the graphs.

Figure S6.

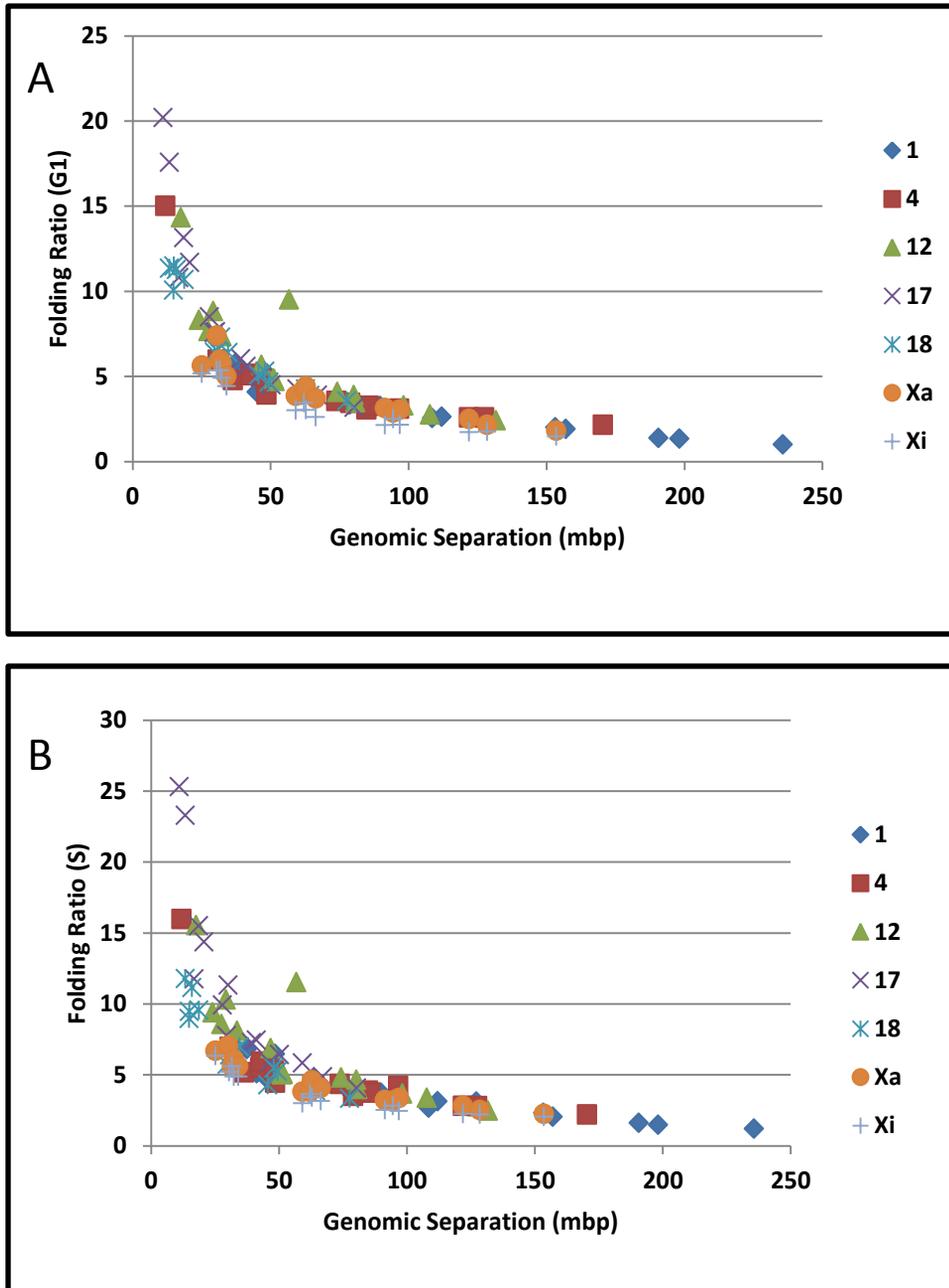


Figure S6. Folding Ratios. The folding ratios (FRs) for the 15 distances in each CT were plotted against their genomic separation (Mbp) for all the CT in G1 (A) and S phase (B).

Figure S7

	coefficient	exponent
4 G1	39.6	0.05
4 S	49	0.07
17 G1	24	0.12
17 S	8.6	0.04
18 G1	48.4	0.1
18 S	143.7	0.15
Xa G1	10.4	0.03
Xa S	86.9	0.08
Xi G1	9.5	0.02
Xi S	14.03	0.03

Figure S7. Coefficients and exponents of the folding ratio trendlines. The values for the coefficients and exponents of the trendlines obtained from the plot of the difference between random and experimental folding ratios against their genomic separation (see Fig 6 and 7) are shown for CT4, 17, 18, Xa and Xi in G1 and S phase. CT1 and 12 fit a quadratic trendline.

Figure S8.

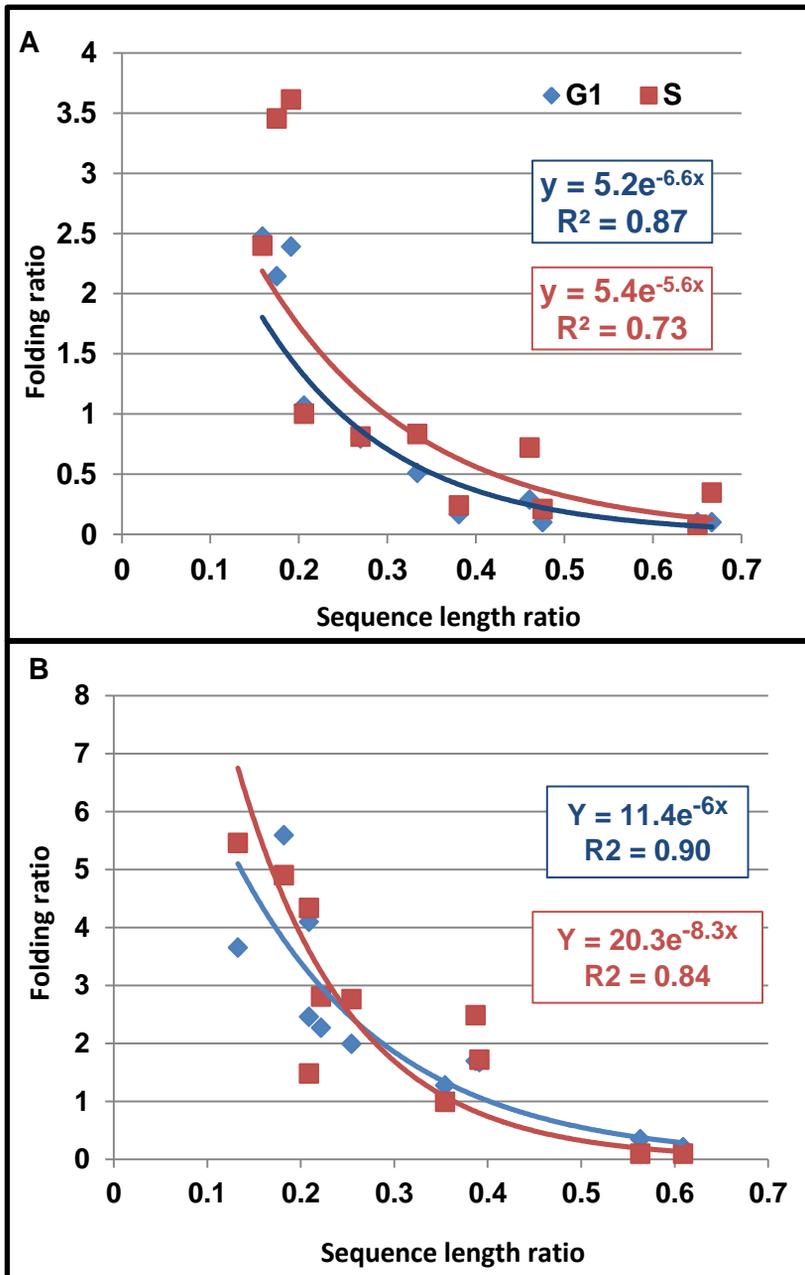


Figure S8. The first two-thirds of CT1 and CT12 fit exponential trendlines. FRr-FRe values for only the first two thirds of CT1 (A) and CT12 (B) were plotted against the sequence length expressed as a ratio to the maximum sequence length. Exponential trendlines were calculated for these partial datasets of CT1 and CT12.

Figure S9. CT1

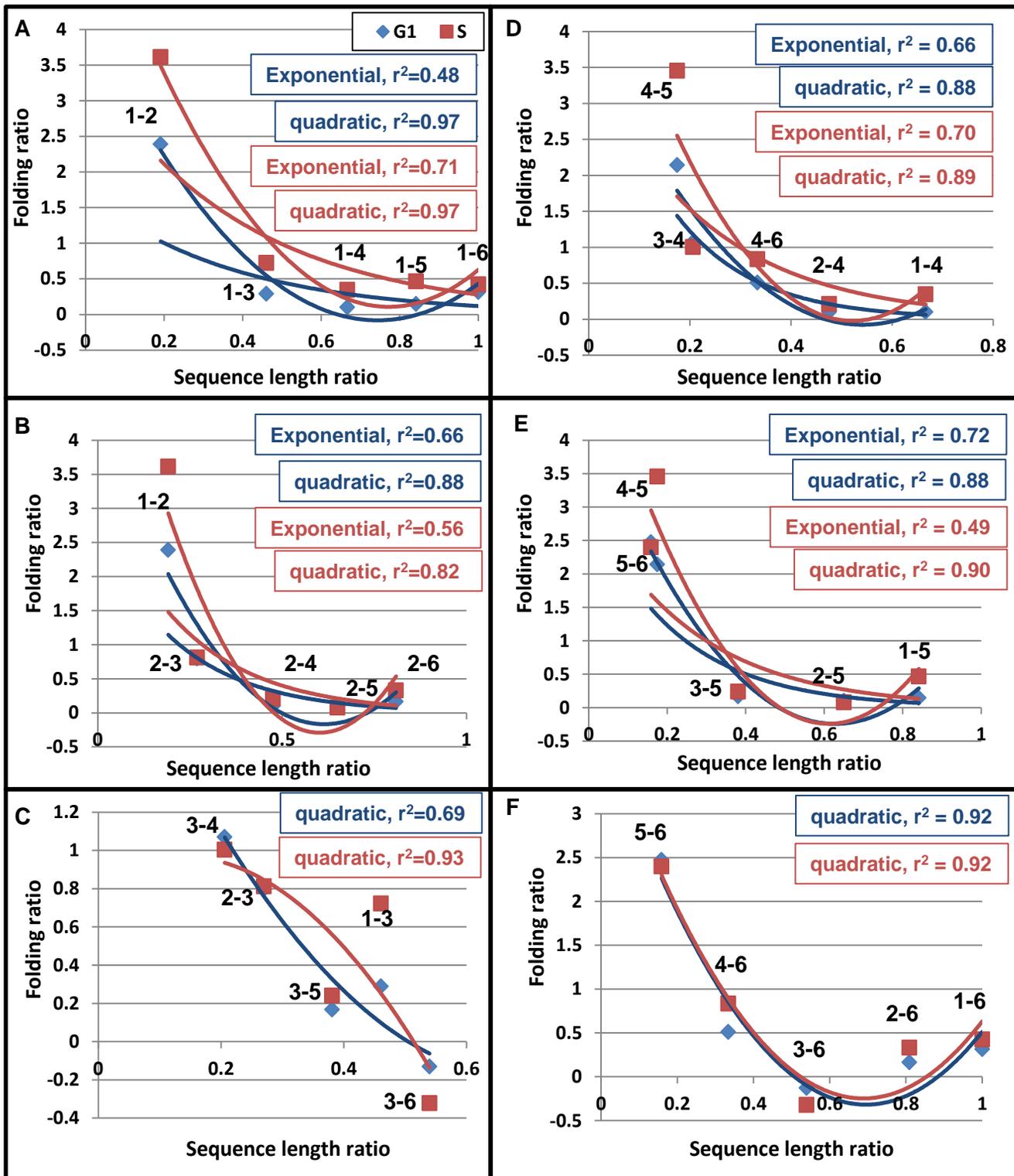


Figure S9. Variations in non-randomness across CT1. The folding ratio (FR) is defined as the spatial distance (microns) between any two given regions divided by their respective sequence length. A higher number indicates a greater distance per Mbp. Six points were randomly generated within the experimental CT space. The folding ratios for those randomly generated regions (FRr) were calculated. The experimental FRs (FRe) were then subtracted from these random FRs to determine the level of non-randomness across sequence lengths. The FRr-FRe values for all distances relative to position 1 (A), 2 (B), 3 (C), 4 (D), 5 (E), and 6 (F) are shown for CT1. Trendlines are exponential. Blue is G1 and red is S.

Figure S10. CT4

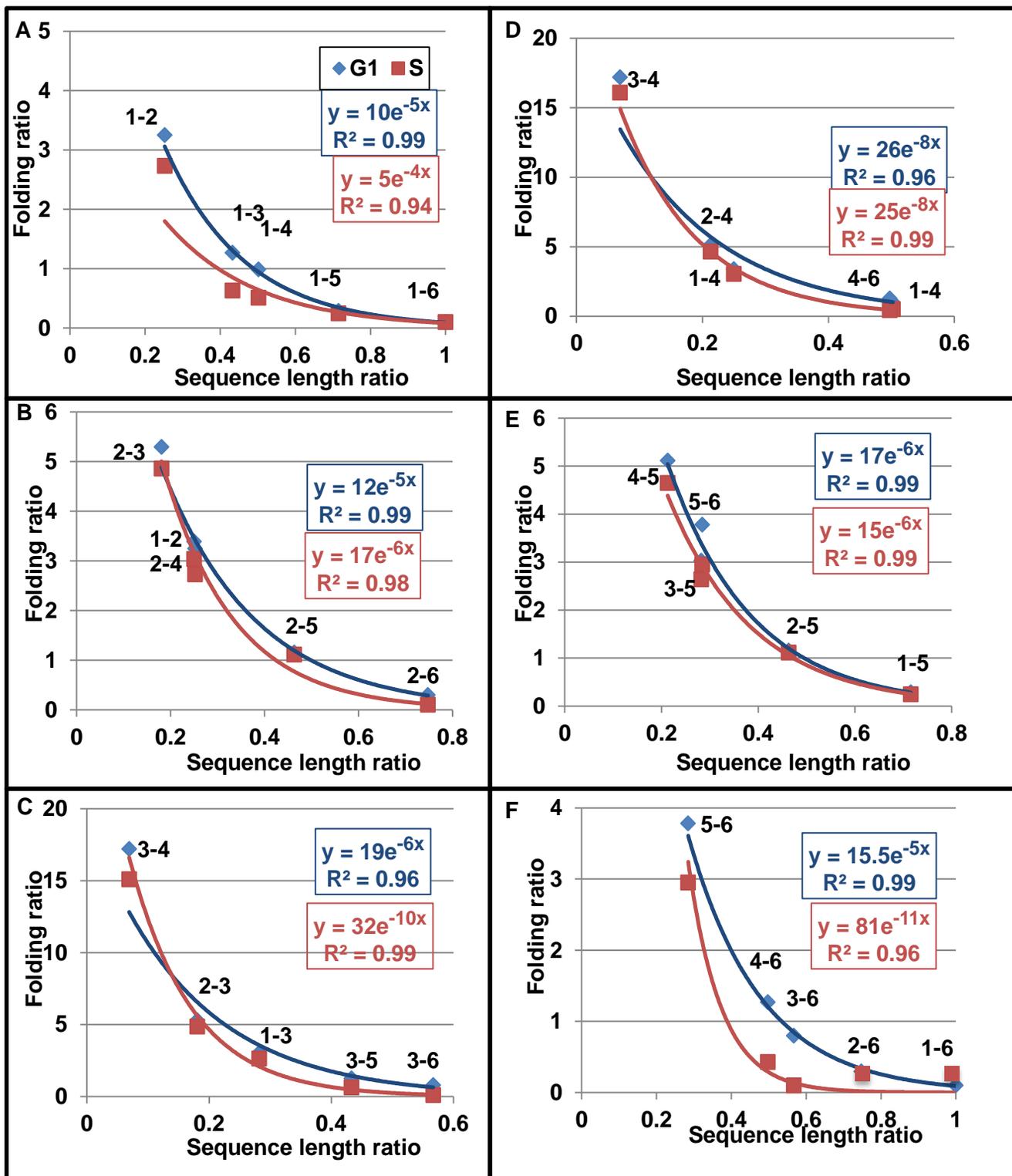


Figure S10. Variations in non-randomness across CT4. The folding ratio (FR) is defined as the spatial distance (microns) between any two given regions divided by their respective sequence length. A higher number indicates a greater distance per Mbp. Six points were randomly generated within the experimental CT space. The folding ratios for those randomly generated regions (FRr) were calculated. The experimental FRs (FRe) were then subtracted from these random FRs to determine the level of non-randomness across sequence lengths. The FRr-FRe values for all distances relative to position 1 (A), 2 (B), 3 (C), 4 (D), 5 (E), and 6 (F) are shown for CT4. Trendlines are exponential. Blue is G1 and red is S.

Figure S11. CT12

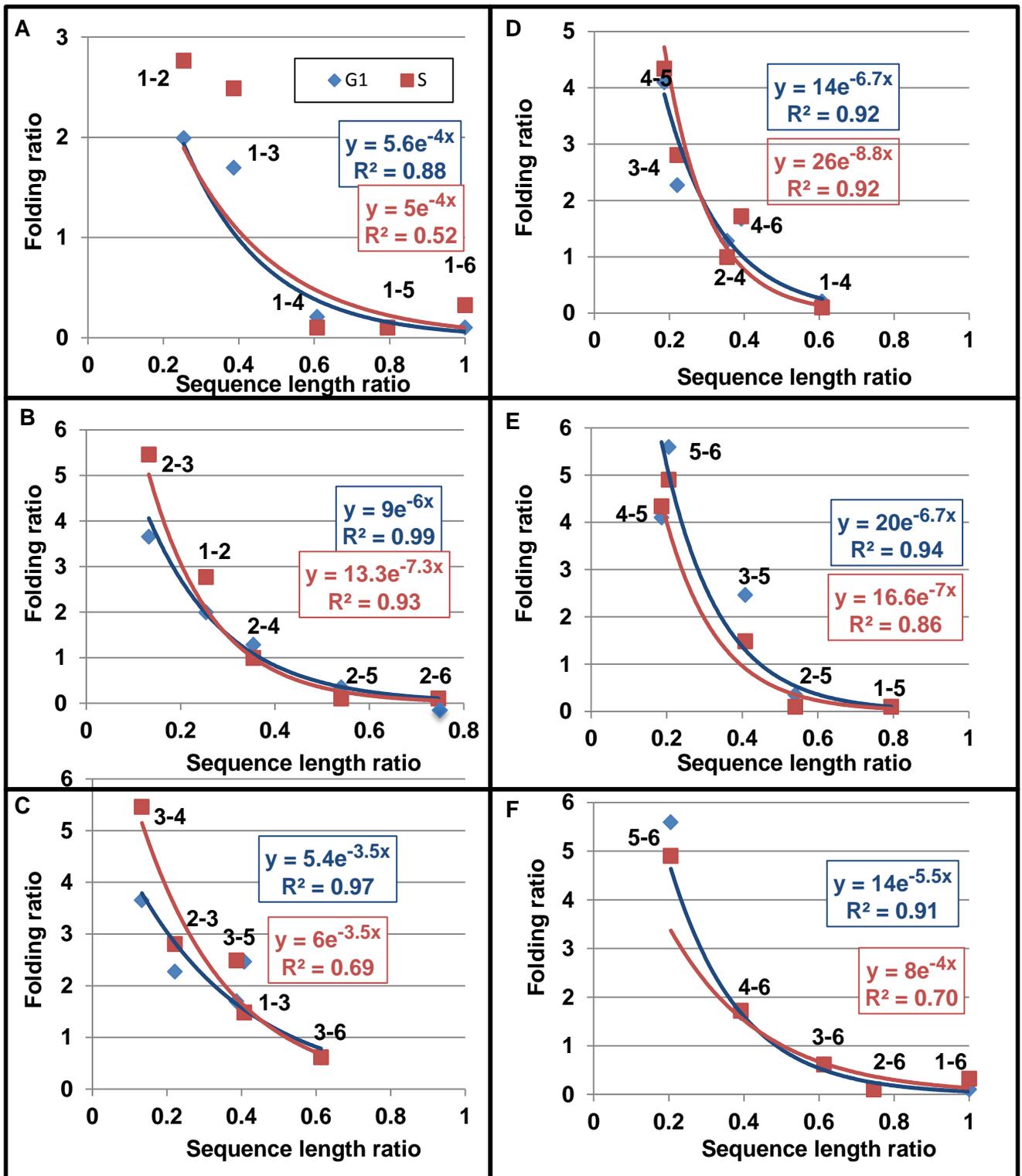


Figure S11. Variations in non-randomness across CT12. The folding ratio (FR) is defined as the spatial distance (microns) between any two given regions divided by their respective sequence length. A higher number indicates a greater distance per Mbp. Six points were randomly generated within the experimental CT space. The folding ratios for those randomly generated regions (FRr) were calculated. The experimental FRs (FRe) were then subtracted from these random FRs to determine the level of non-randomness across sequence lengths. The FRr-FRe values for all distances relative to position 1 (A), 2 (B), 3 (C), 4 (D), 5 (E), and 6 (F) are shown for CT12. Trendlines are exponential. Blue is G1 and red is S.

Figure S12. CT17

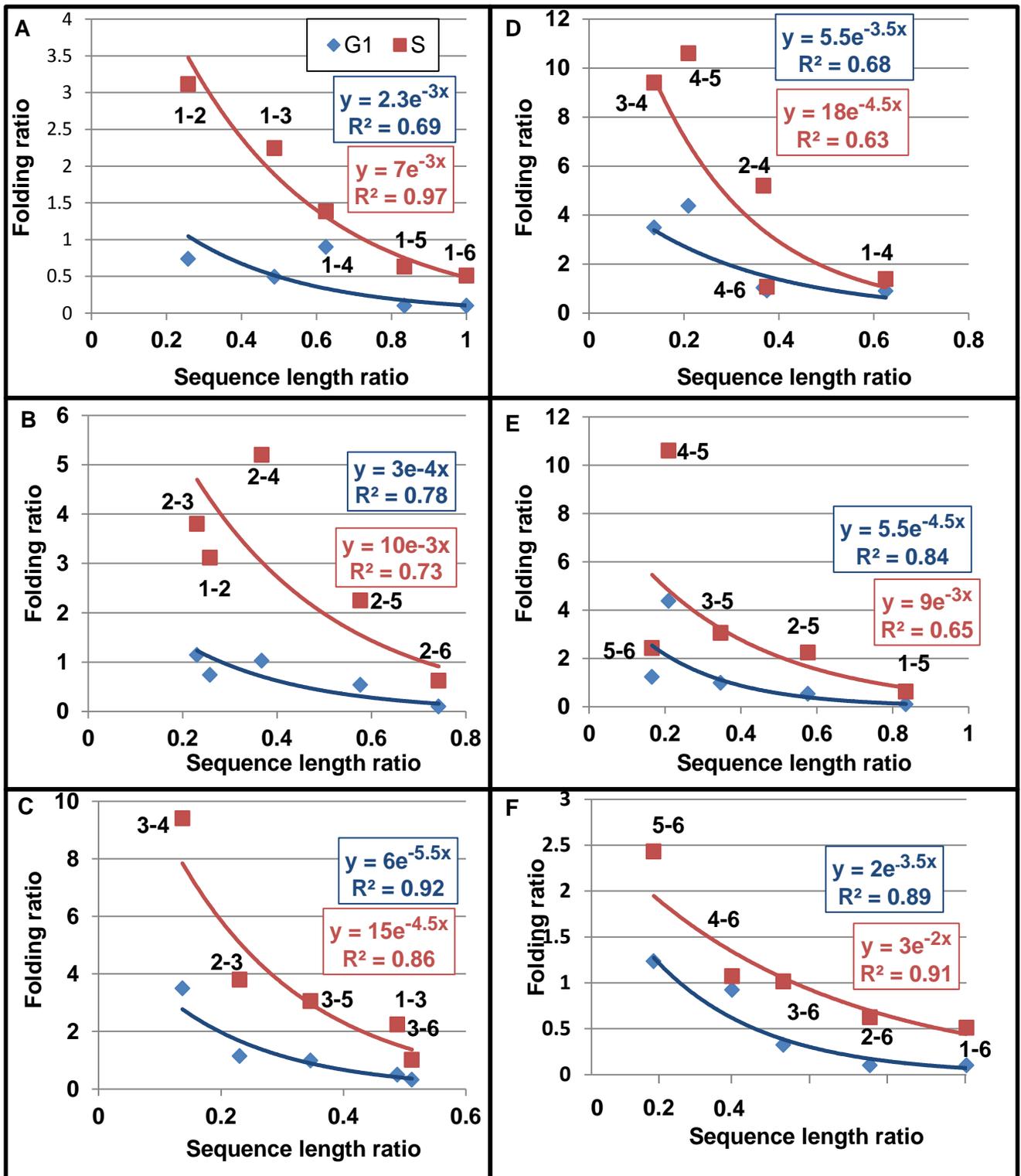


Figure S12. Variations in non-randomness across CT17. The folding ratio (FR) is defined as the spatial distance (microns) between any two given regions divided by their respective sequence length. A higher number indicates a greater distance per Mbp. Six points were randomly generated within the experimental CT space. The folding ratios for those randomly generated regions (FRr) were calculated. The experimental FRs (FRe) were then subtracted from these random FRs to determine the level of non-randomness across sequence lengths. The FRr-FRe values for all distances relative to position 1 (A), 2 (B), 3 (C), 4 (D), 5 (E), and 6 (F) are shown for CT17. Trendlines are exponential. Blue is G1 and red is S.

Figure S13. CT18

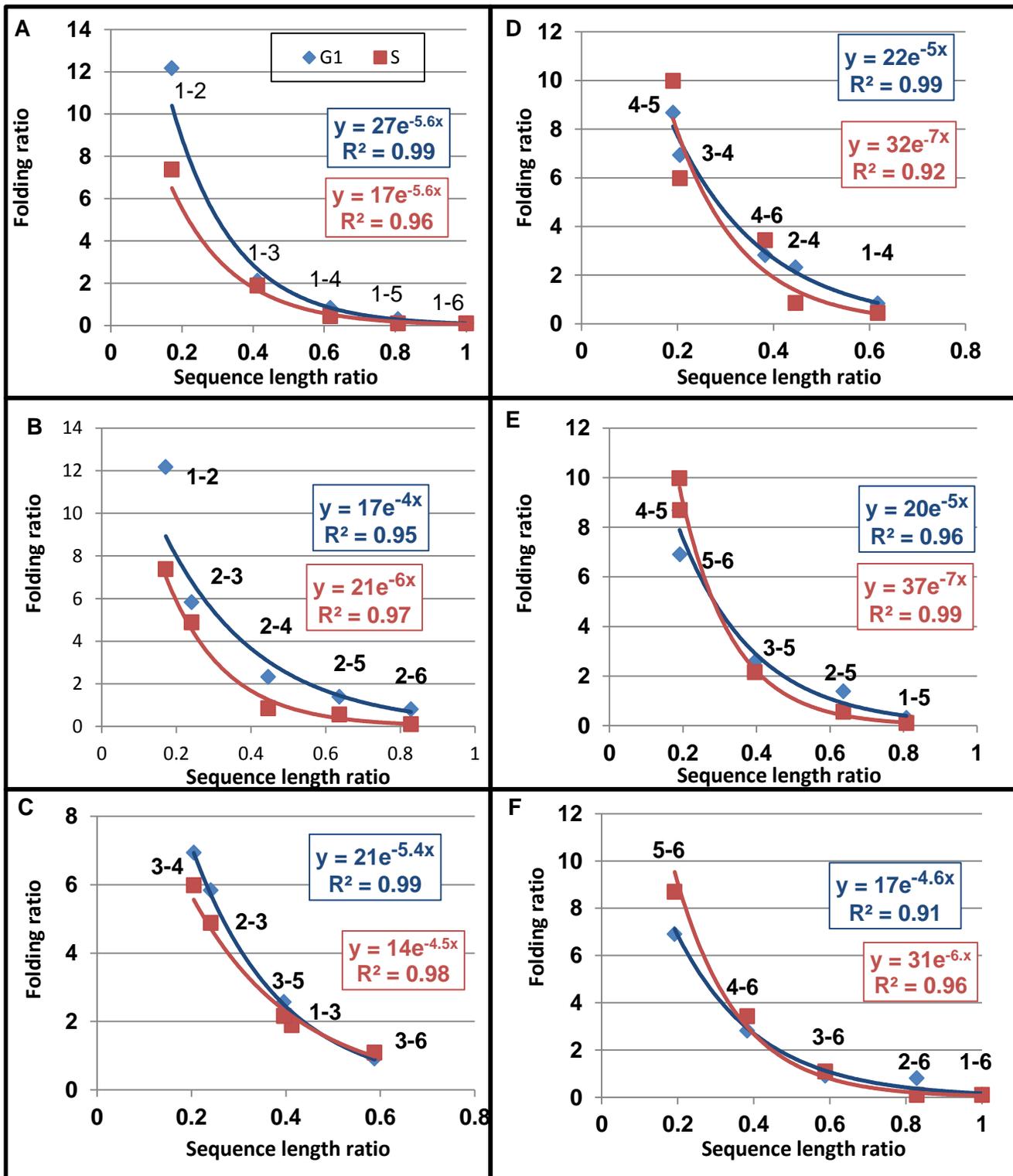


Figure S13. Variations in non-randomness across CT18. The folding ratio (FR) is defined as the spatial distance (microns) between any two given regions divided by their respective sequence length. A higher number indicates a greater distance per Mbp. Six points were randomly generated within the experimental CT space. The folding ratios for those randomly generated regions (FRr) were calculated. The experimental FRs (FR_e) were then subtracted from these random FRs to determine the level of non-randomness across sequence lengths. The FRr-FR_e values for all distances relative to position 1 (A), 2 (B), 3 (C), 4 (D), 5 (E), and 6 (F) are shown for CT18. Trendlines are exponential. Blue is G1 and red is S.

Figure S14. CTXa

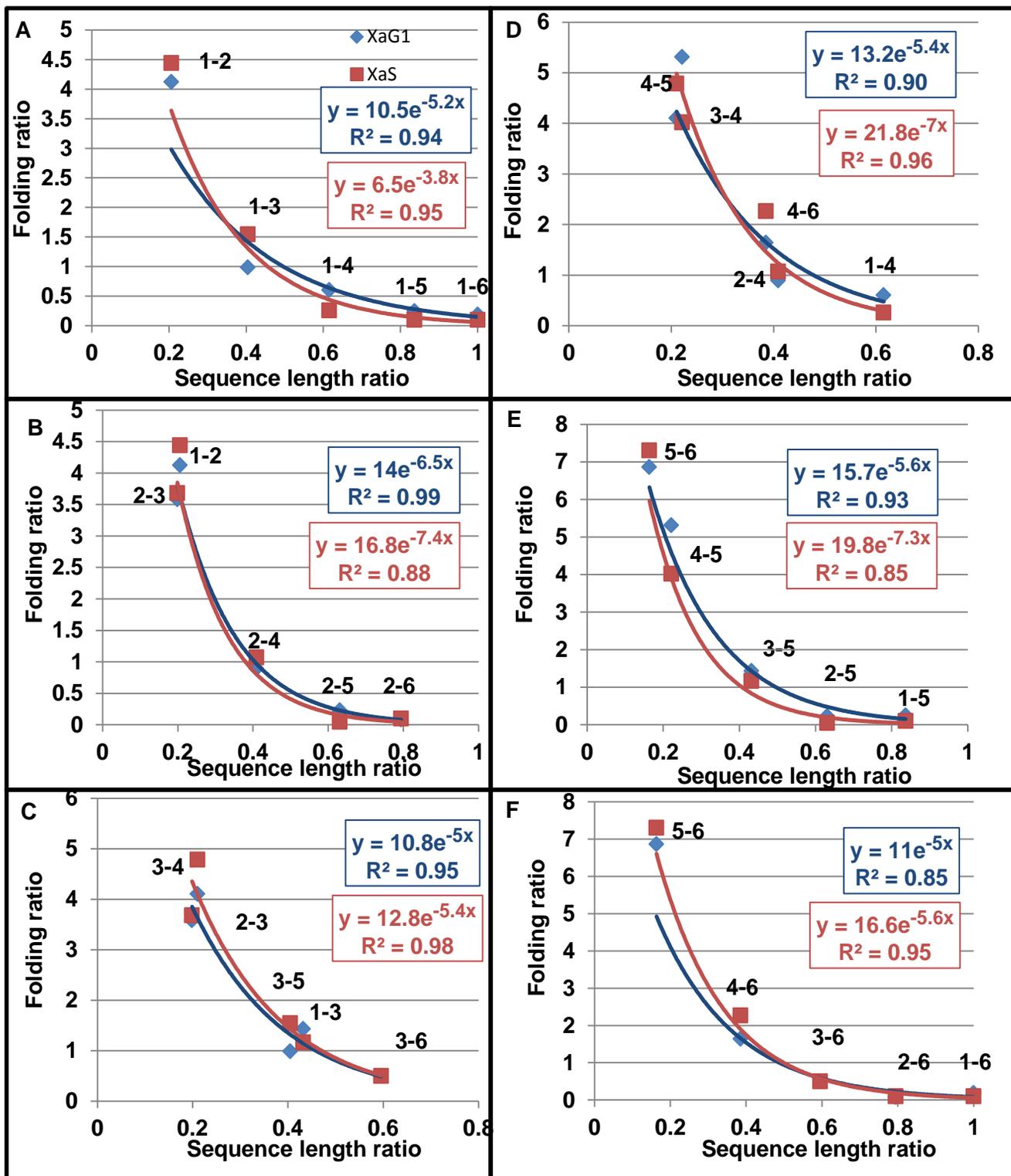


Figure S14. Variations in non-randomness across CTXa. The folding ratio (FR) is defined as the spatial distance (microns) between any two given regions divided by their respective sequence length. A higher number indicates a greater distance per Mbp. Six points were randomly generated within the experimental CT space. The folding ratios for those randomly generated regions (FRr) were calculated. The experimental FRs (FRe) were then subtracted from these random FRs to determine the level of non-randomness across sequence lengths. The FRr-FRe values for all distances relative to position 1 (A), 2 (B), 3 (C), 4 (D), 5 (E), and 6 (F) are shown for CTXa. Trendlines are exponential. Blue is G1 and red is S.

Figure S15. CTXi

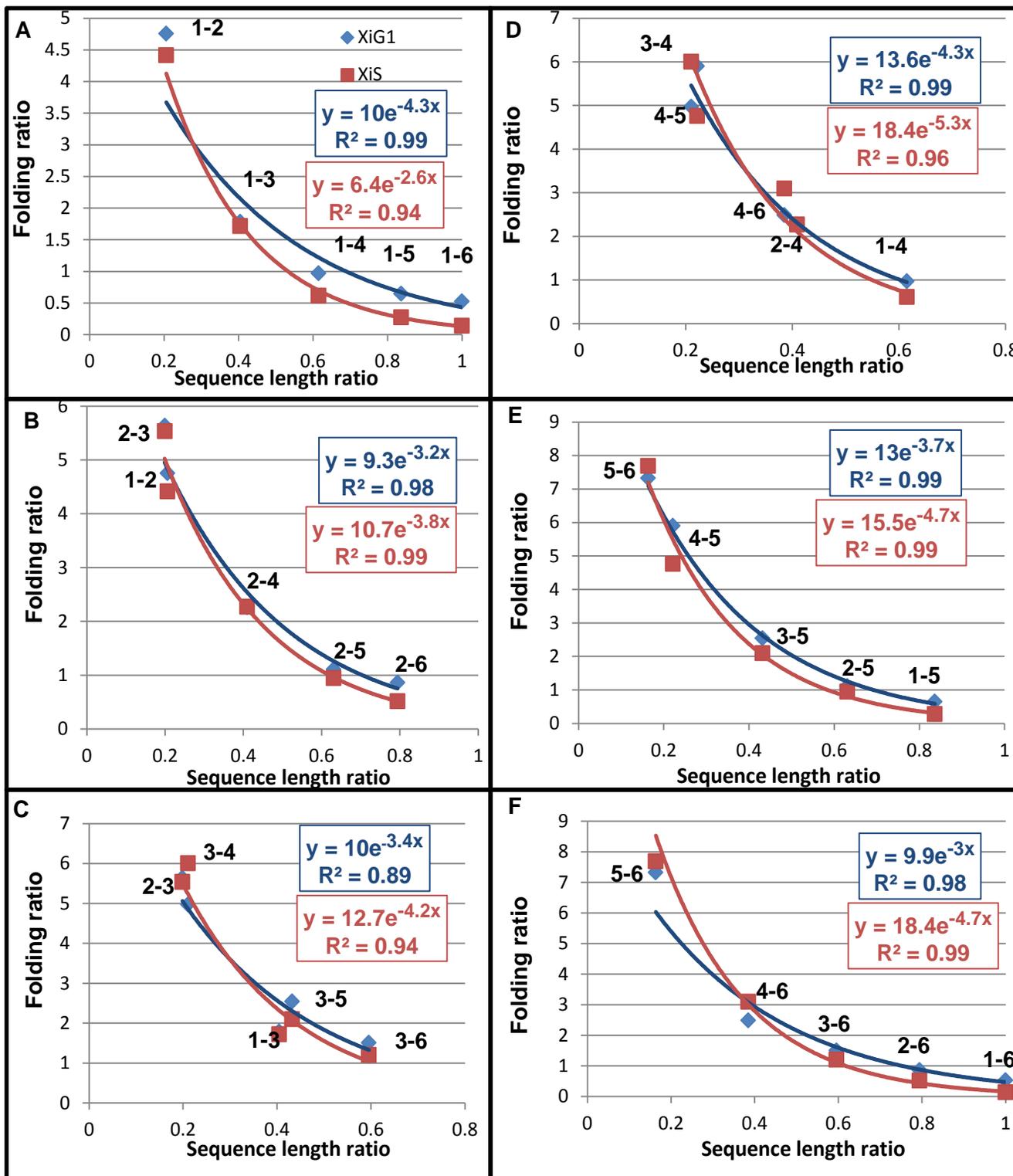


Figure S15. Variations in non-randomness across CTXi. The folding ratio (FR) is defined as the spatial distance (microns) between any two given regions divided by their respective sequence length. A higher number indicates a greater distance per Mbp. Six points were randomly generated within the experimental CT space. The folding ratios for those randomly generated regions (FRr) were calculated. The experimental FRs (FRe) were then subtracted from these random FRs to determine the level of non-randomness across sequence lengths. The FRr-FRe values for all distances relative to position 1 (A), 2 (B), 3 (C), 4 (D), 5 (E), and 6 (F) are shown for CTXi. Trendlines are exponential. Blue is G1 and red is S.

Figure S16

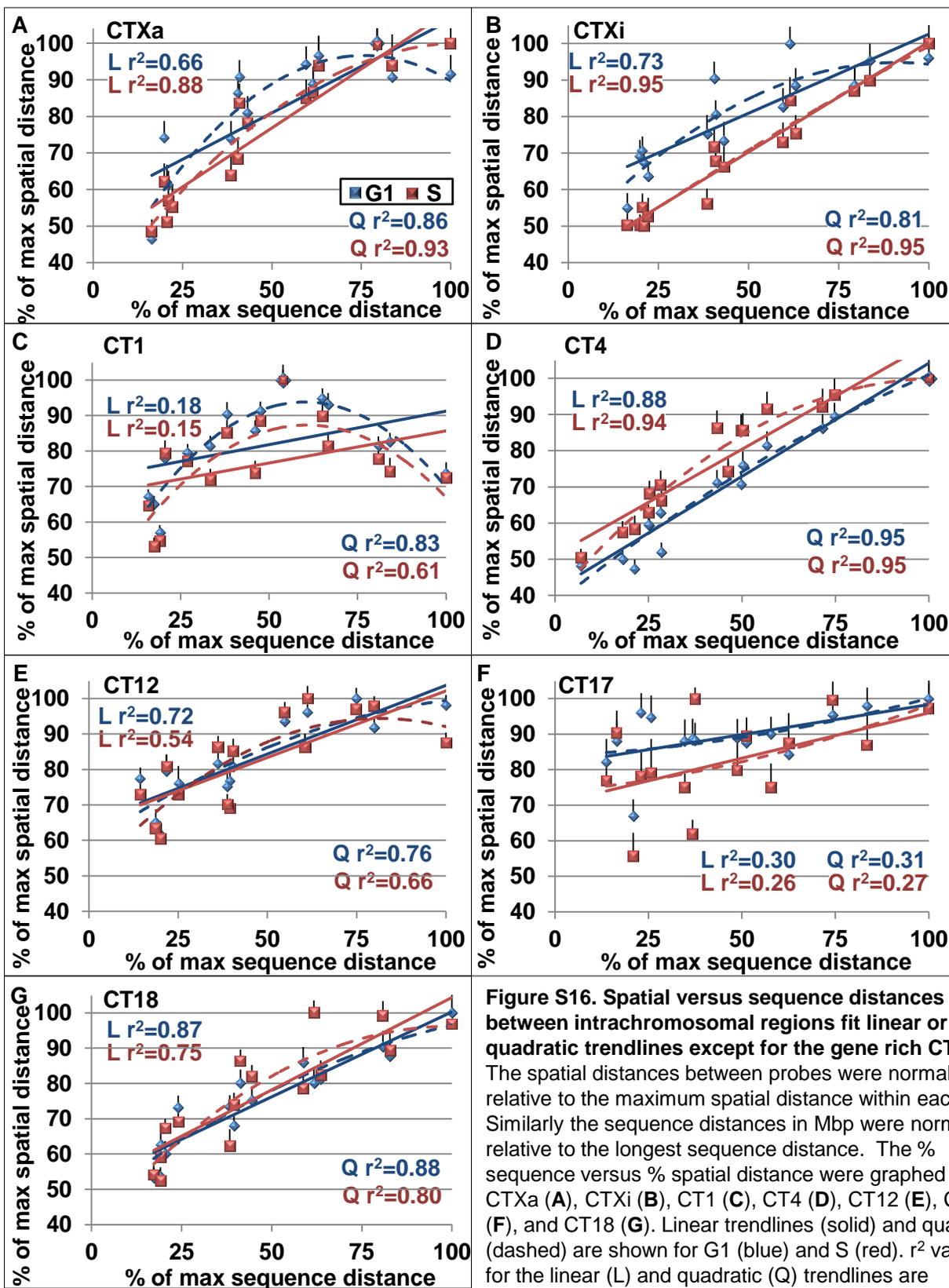


Figure S16. Spatial versus sequence distances between intrachromosomal regions fit linear or quadratic trendlines except for the gene rich CT17. The spatial distances between probes were normalized relative to the maximum spatial distance within each CT. Similarly the sequence distances in Mbp were normalized relative to the longest sequence distance. The % sequence versus % spatial distance were graphed for CTXa (A), CTXi (B), CT1 (C), CT4 (D), CT12 (E), CT17 (F), and CT18 (G). Linear trendlines (solid) and quadratic (dashed) are shown for G1 (blue) and S (red). r^2 values for the linear (L) and quadratic (Q) trendlines are displayed on the graphs.

Figure S17

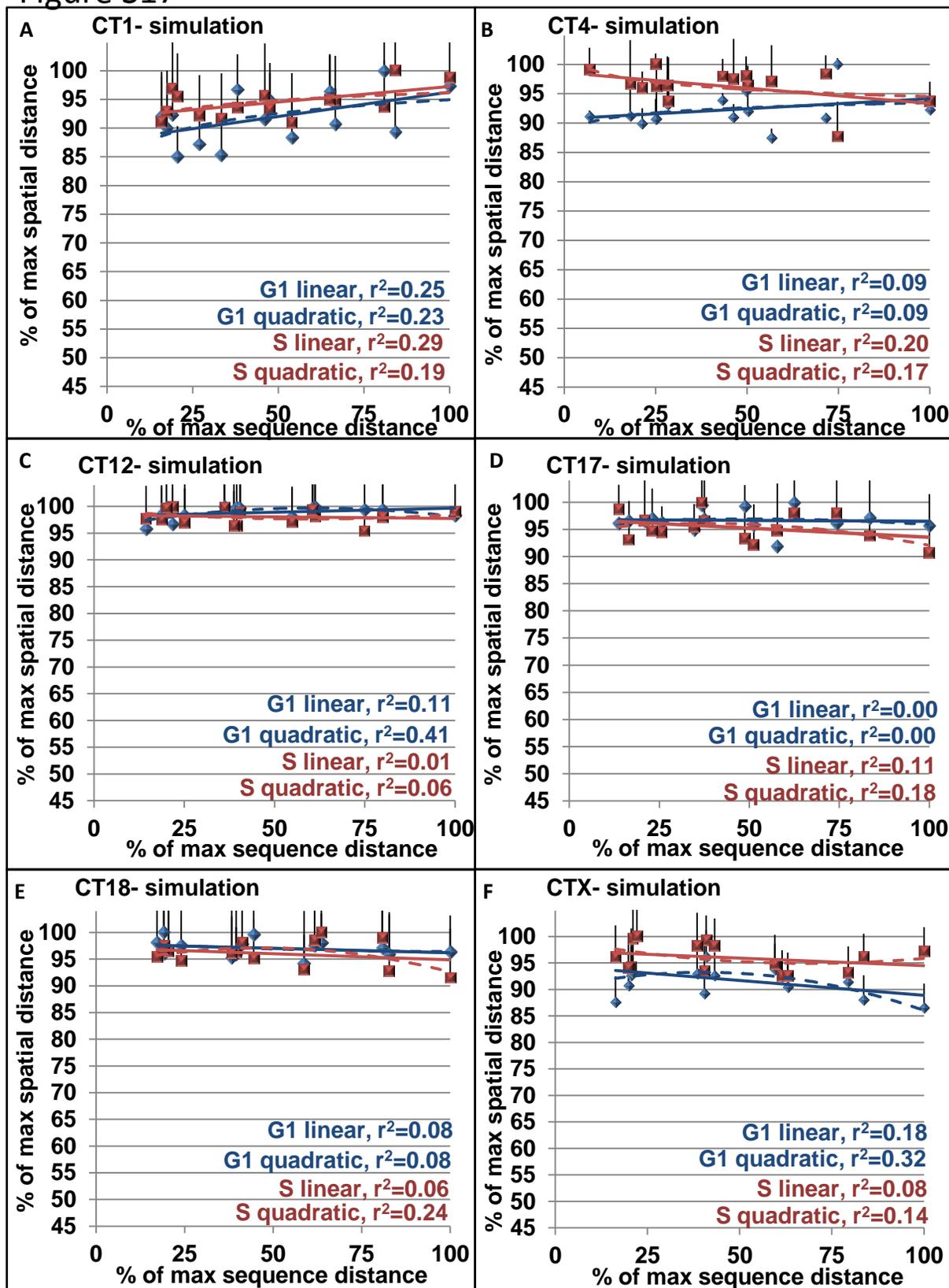


Figure S17. Spatial versus sequence distances in random simulations of CT. The spatial distance between probes was normalized relative to the maximum spatial distance within each random simulation of CT. Similarly the sequence distance in Mbp was normalized relative to the longest sequence distance. The % sequence versus % spatial distance were graphed for constrained random simulations of CT1 (A), CT4 (B), CT12 (C), CT17 (D), and CT18 (E) and CTX (F). Linear trendlines (solid) and quadratic (dashed) are shown for G1 (blue) and S (red). r^2 values for the linear (L) and quadratic (Q) trendlines are displayed on the graphs.

Figure S18

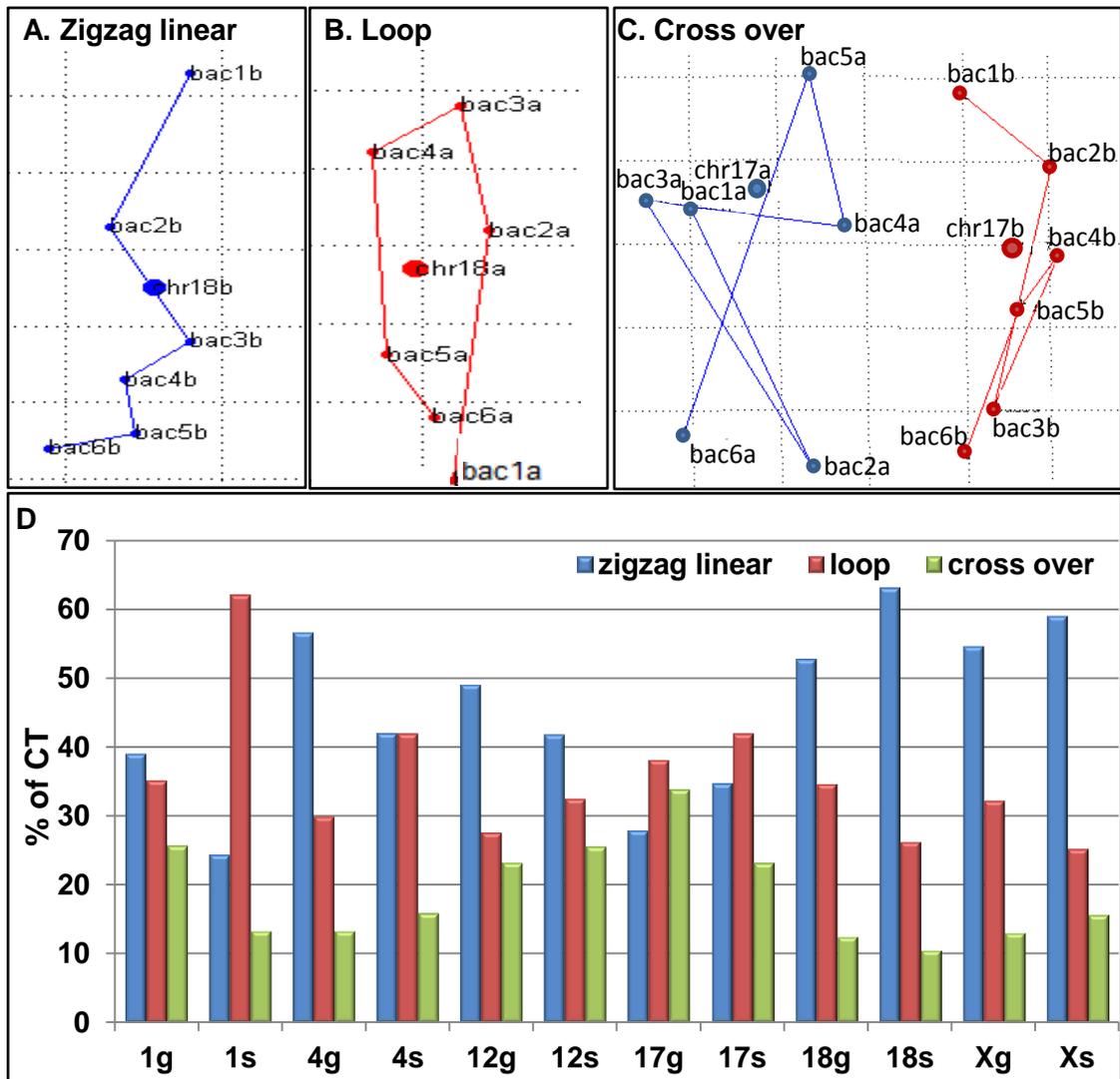


Figure S18. Visual categorization of CT 3-D topology. The eFISHent program outputs graphs for each CT in the population of the 3-D coordinates of the probes within the CT which are connected by lines between consecutive positions (A-C). These were then visually categorized as: (A) **zigzag linear**: consecutive regions arranged in a zigzag line); (B) **loops**: at least one of the consecutive regions bends back on itself, forming a loop); or (C) **crossing over**: consecutive regions are arranged in a crisscross fashion. The percent distributions of these categorizations are shown for all CT in G1 and S (D).