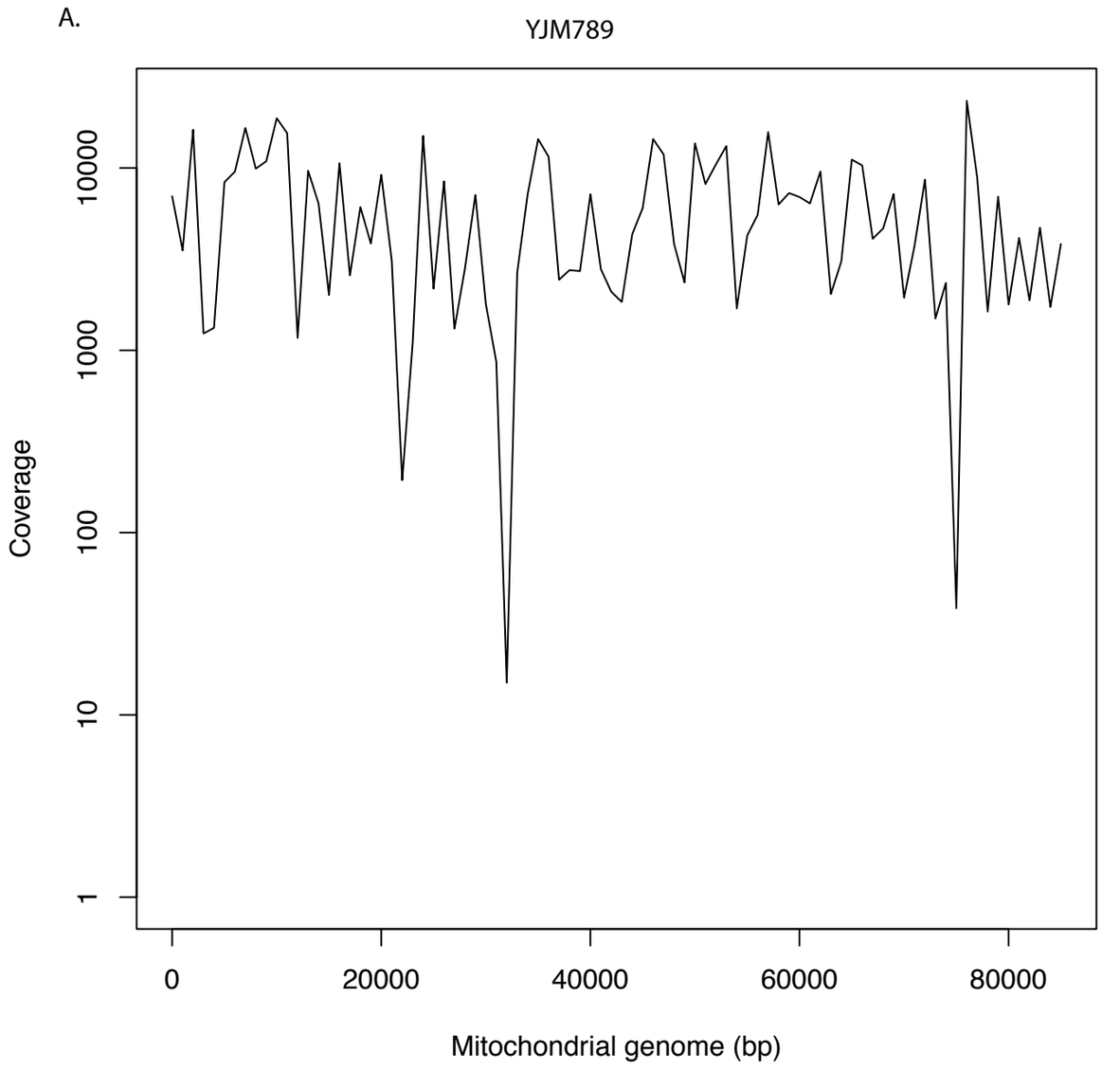
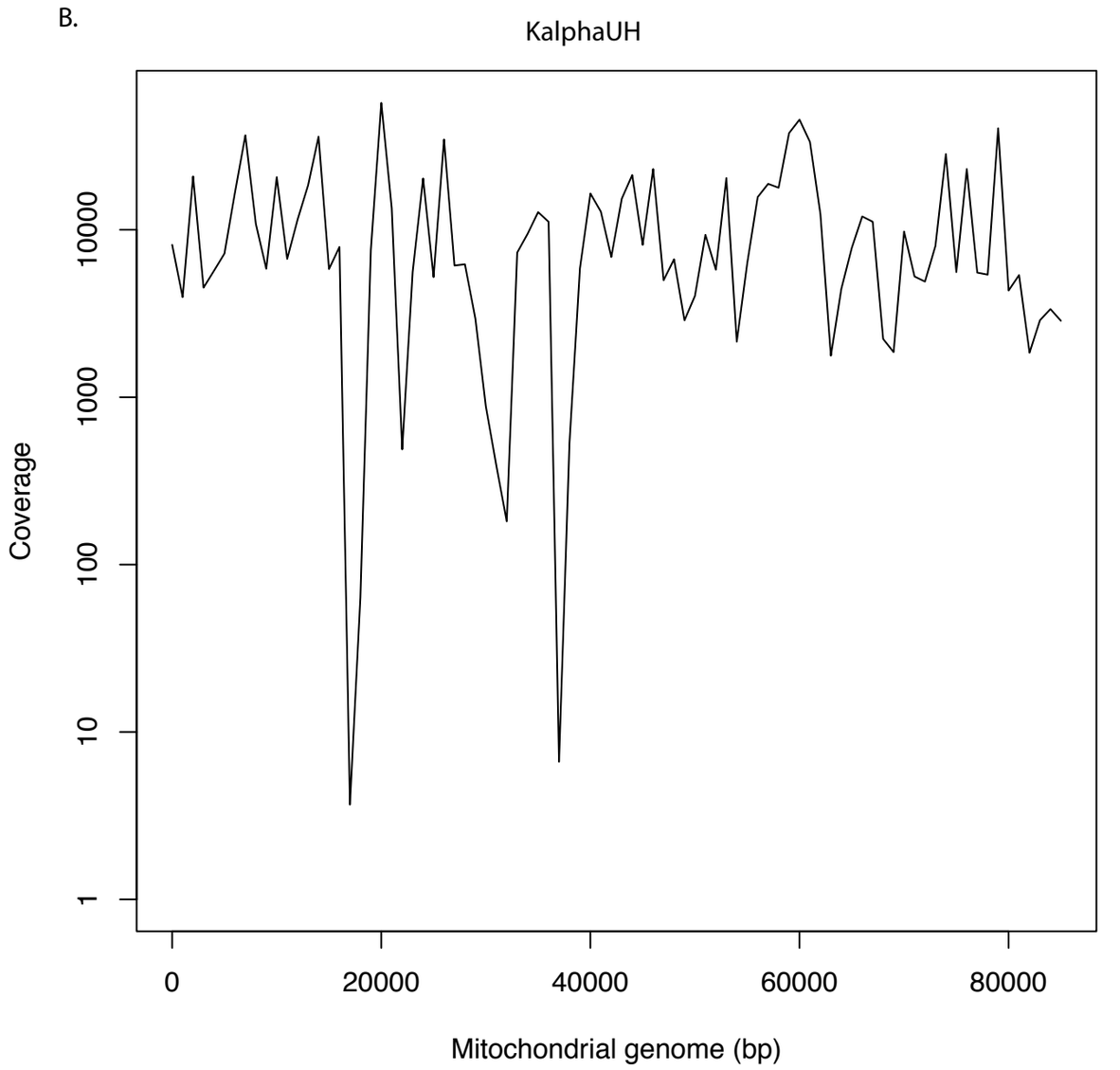
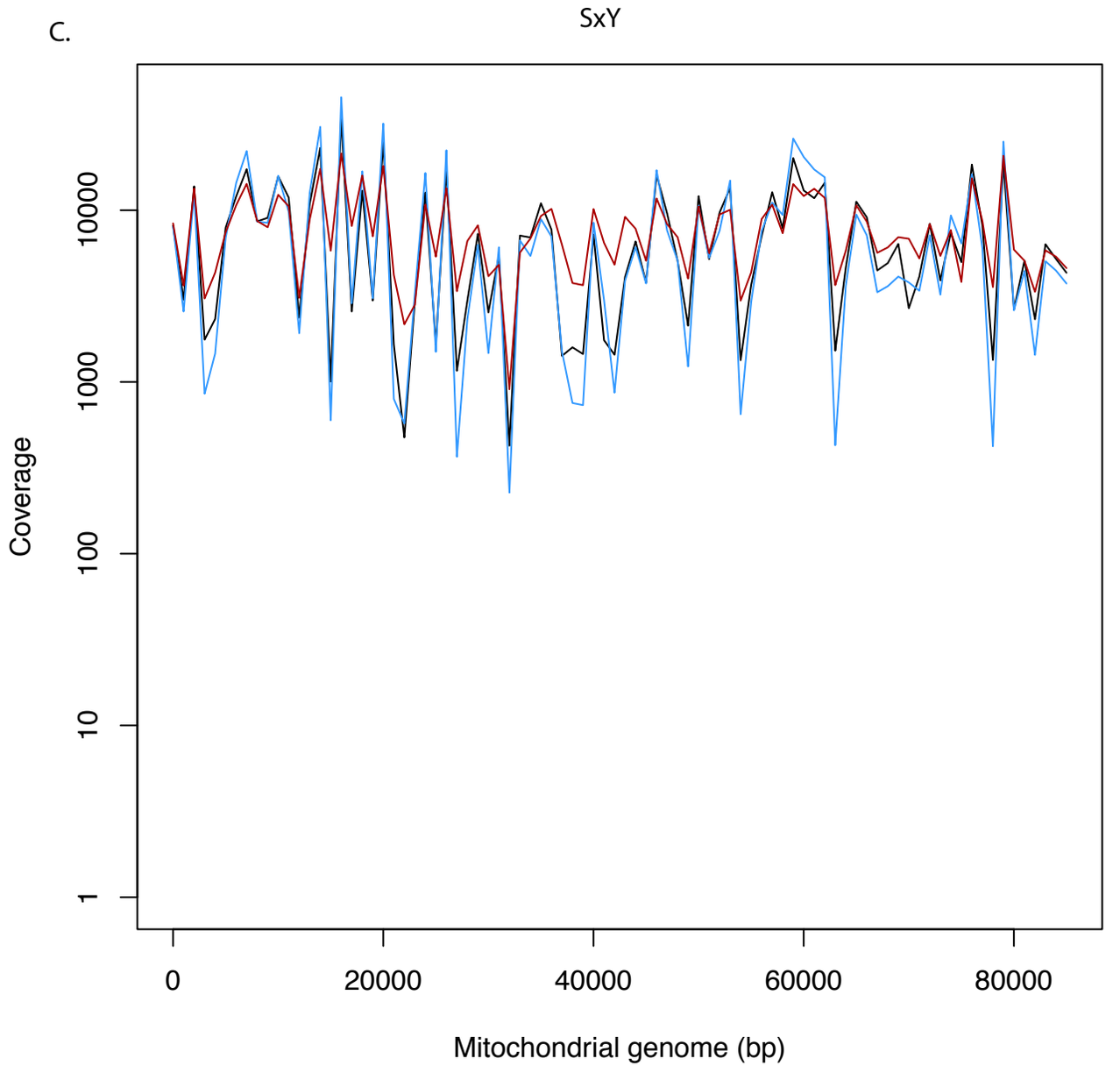
Supplementary Figure 1

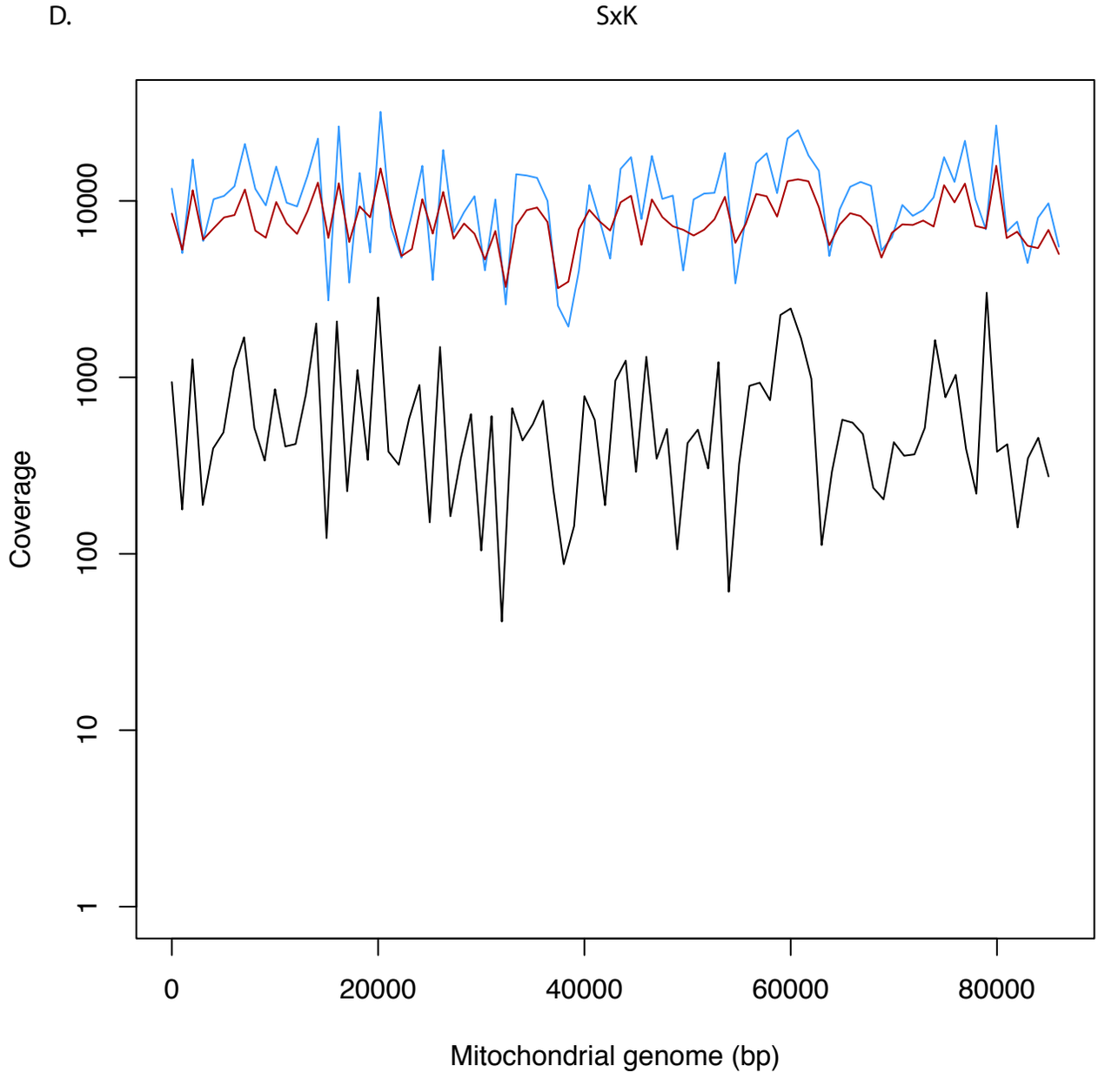


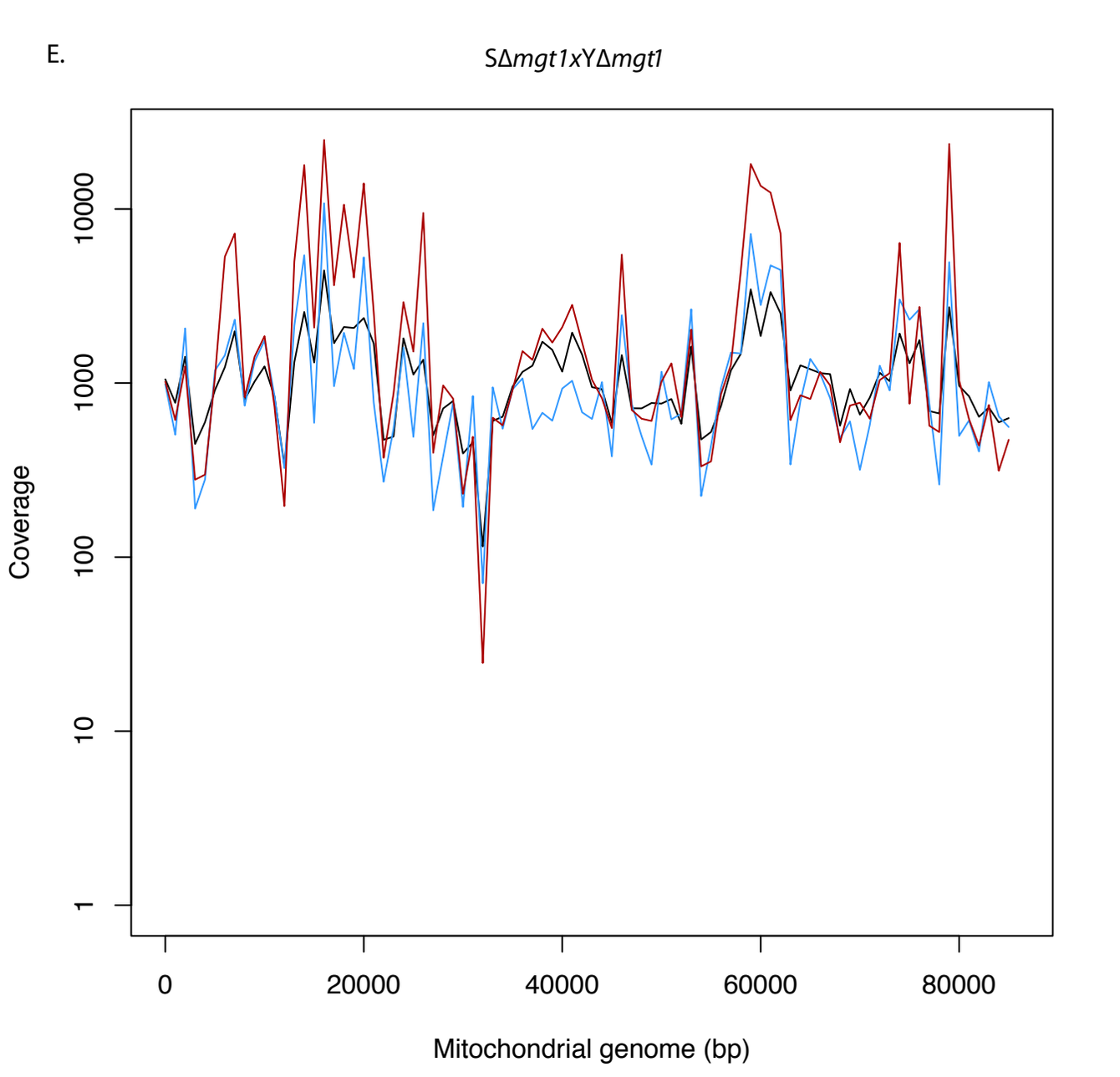


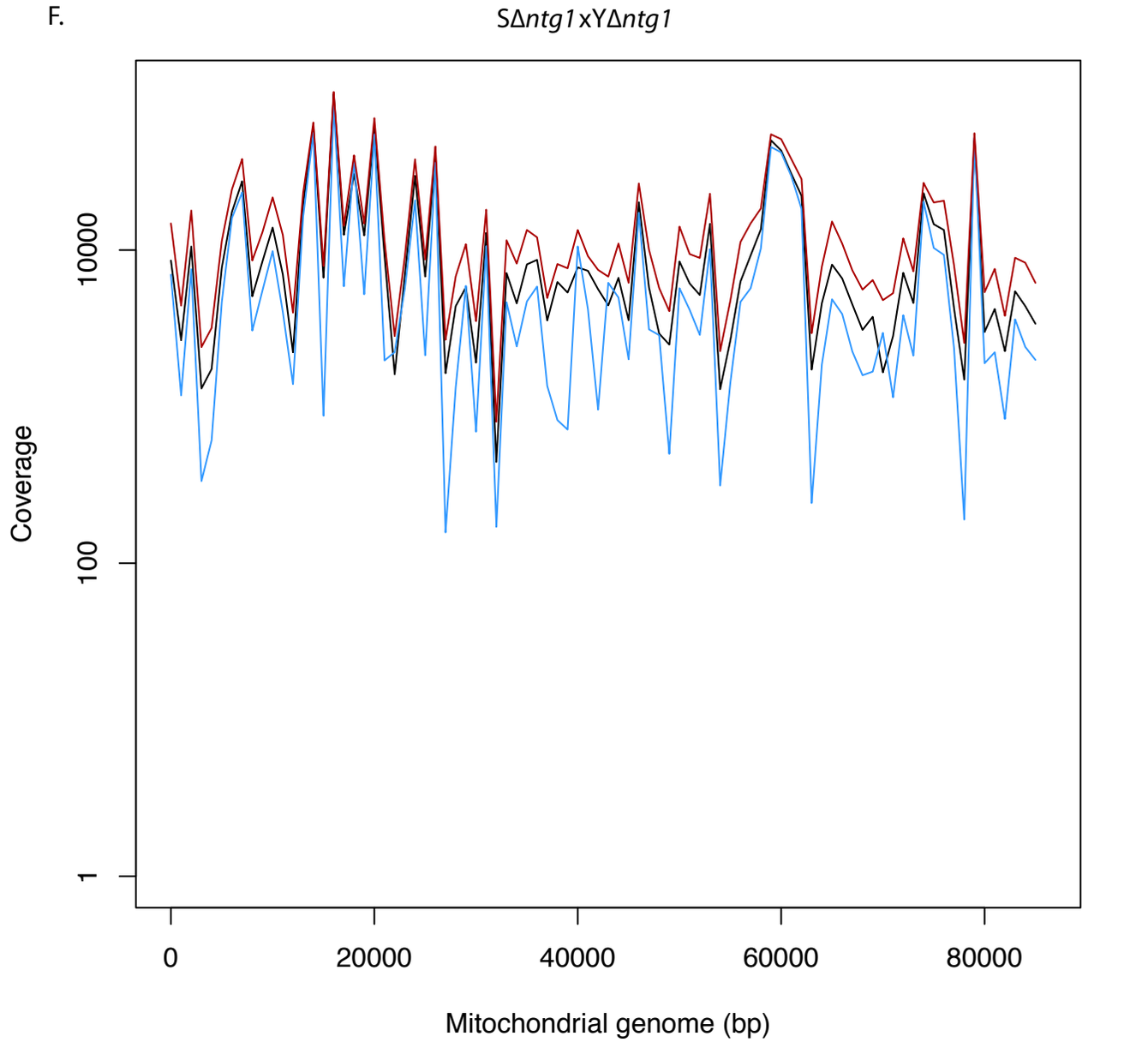
C.

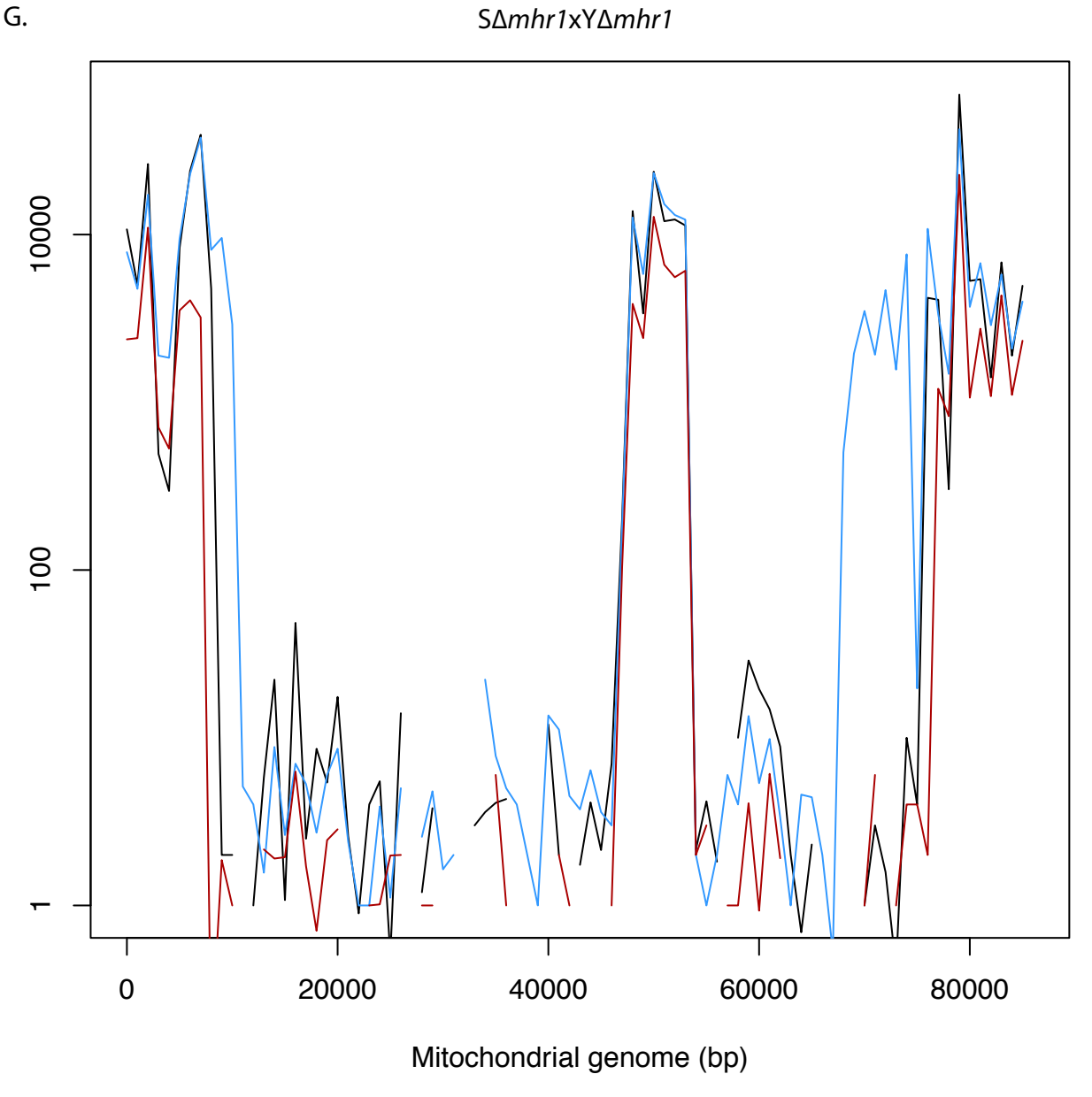

SxY
Coverage
10000
1000
100
10
1
0
20000
40000
60000
80000
Mitochondrial genome (bp)

D.

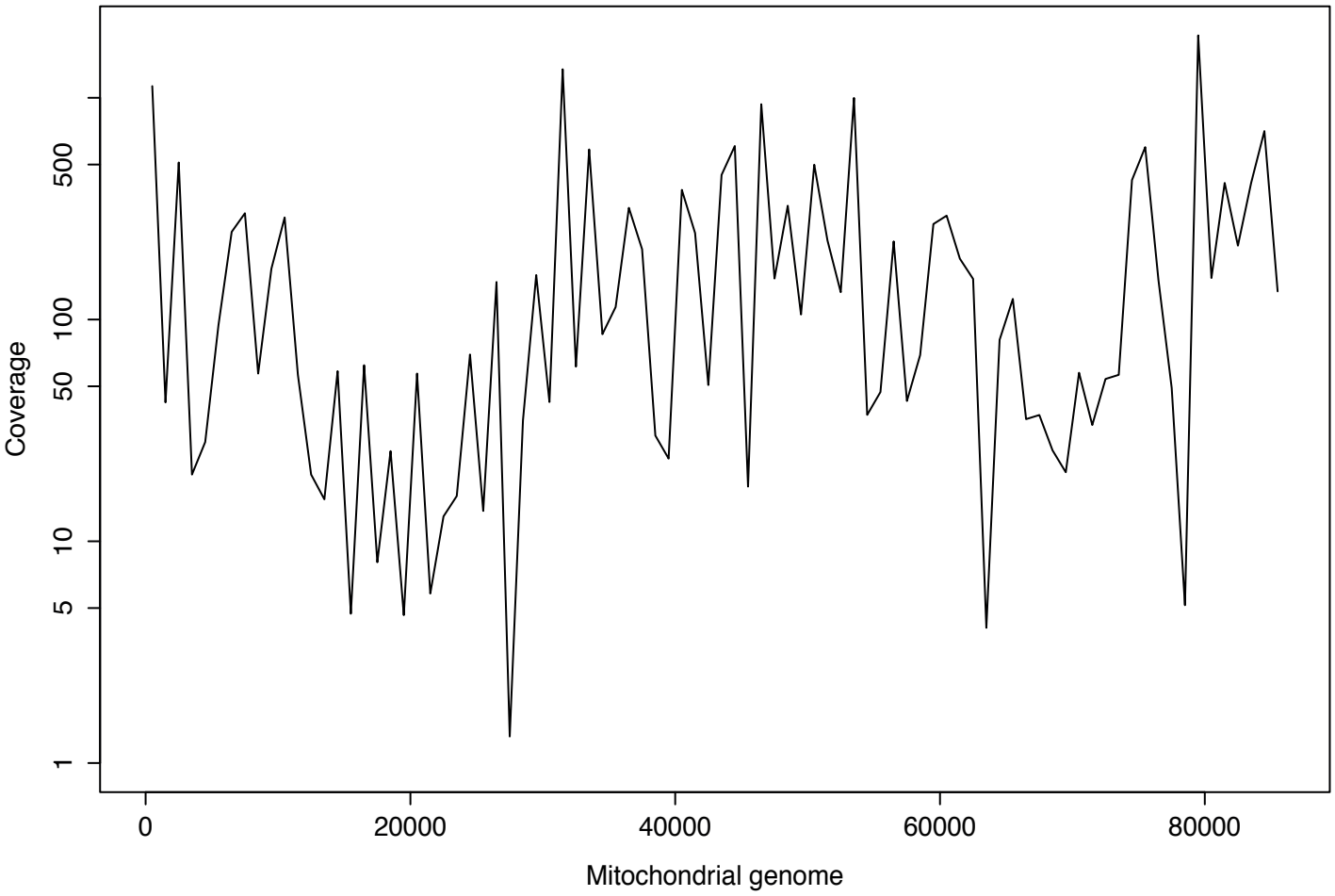

SxK
Coverage
10000
1000
100
10
1
0
20000
40000
60000
80000
Mitochondrial genome (bp)


E.
SΔmgt1xYΔmgt1
Coverage
10000
1000
100
10
1
0
20000
40000
60000
80000
Mitochondrial genome (bp)


F.
SΔntg1xYΔntg1
Coverage
10000
100
1
0
20000
40000
60000
80000
Mitochondrial genome (bp)


G.
SΔmhr1xYΔmhr1
Coverage
10000
100
1
0
20000
40000
60000
80000
Mitochondrial genome (bp)

H. SΔ*mhr1*



I. YΔ*mhr1*

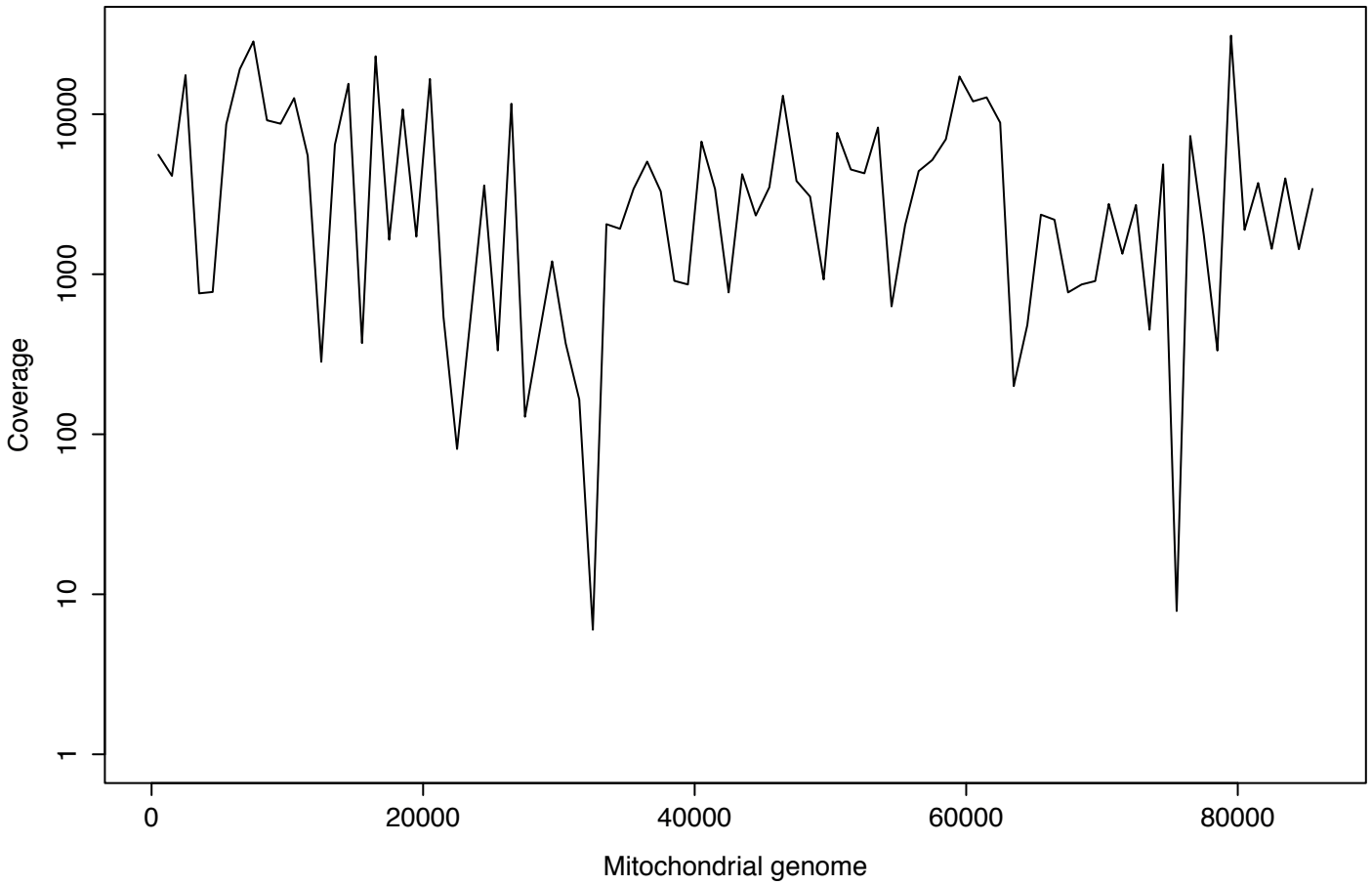
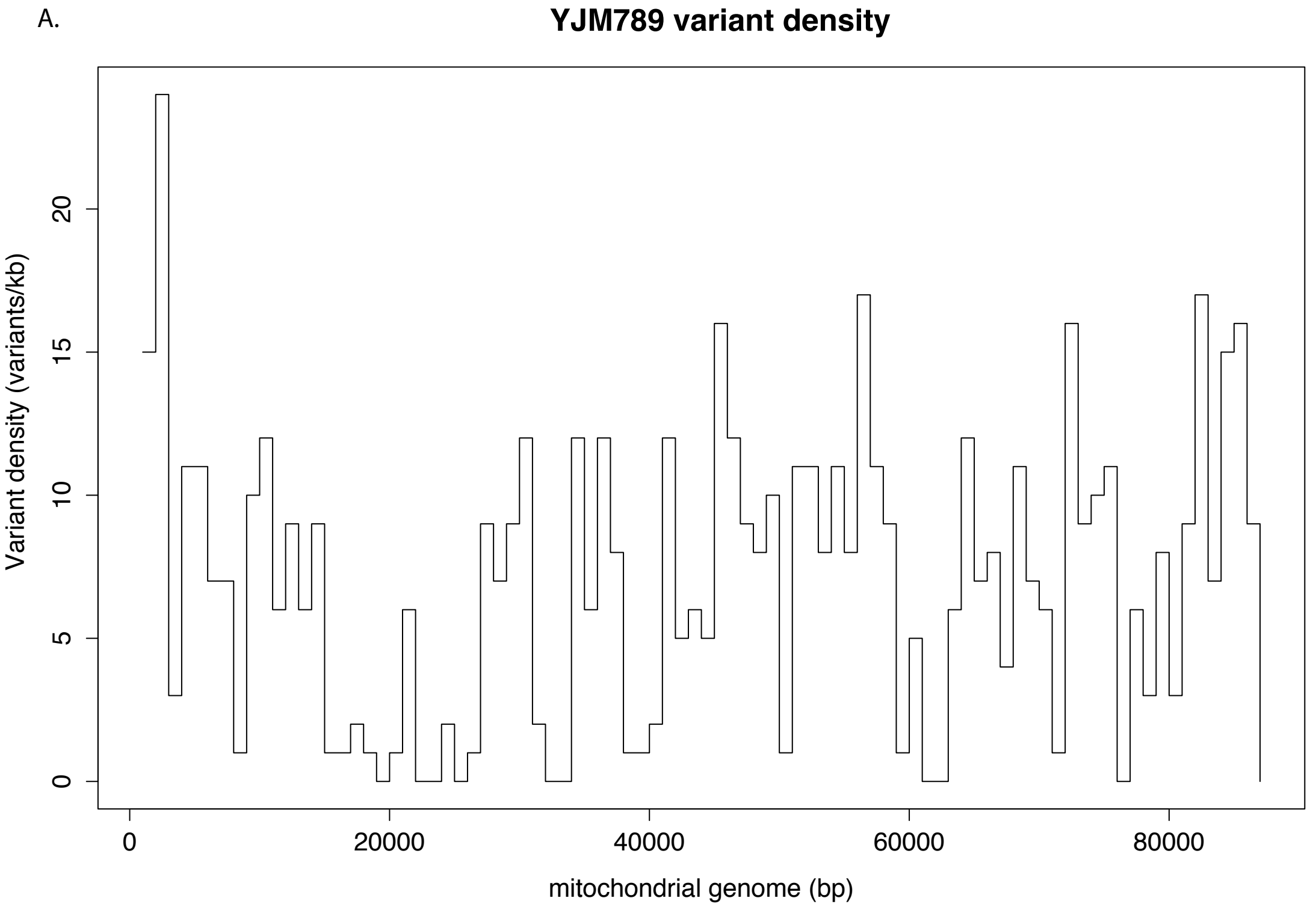


Figure S1 Coverage over the mitochondrial genome.
The mitochondrial genome was binned into consecutive 1kb windows. For each window, we determined the sum of the proportions of read pairs falling within the window. The values were then plotted over the mitochondrial genome. For the crosses, the coverage is represented for all three biological replicates.
A. Coverage for the parental YJM789 strain
B. Coverage for the parental KalphaUH strain
C. Coverage for the SxY cross
D. Coverage for the SxK cross
E. Coverage for the SΔ*mgt1*xYΔ*mgt1* cross
F. Coverage for the SΔ*ntg1*xYΔ*ntg1* cross
G. Coverage for the SΔ*mhr1*xYΔ*mhr1* cross
H. Coverage for the SΔ*mhr1* strain
I. Coverage for the YΔ*mhr1* strain

A.


YJM789 variant density
Variant density (variants/kb)
0
5
10
15
20
0
20000
40000
60000
80000
mitochondrial genome (bp)

B.

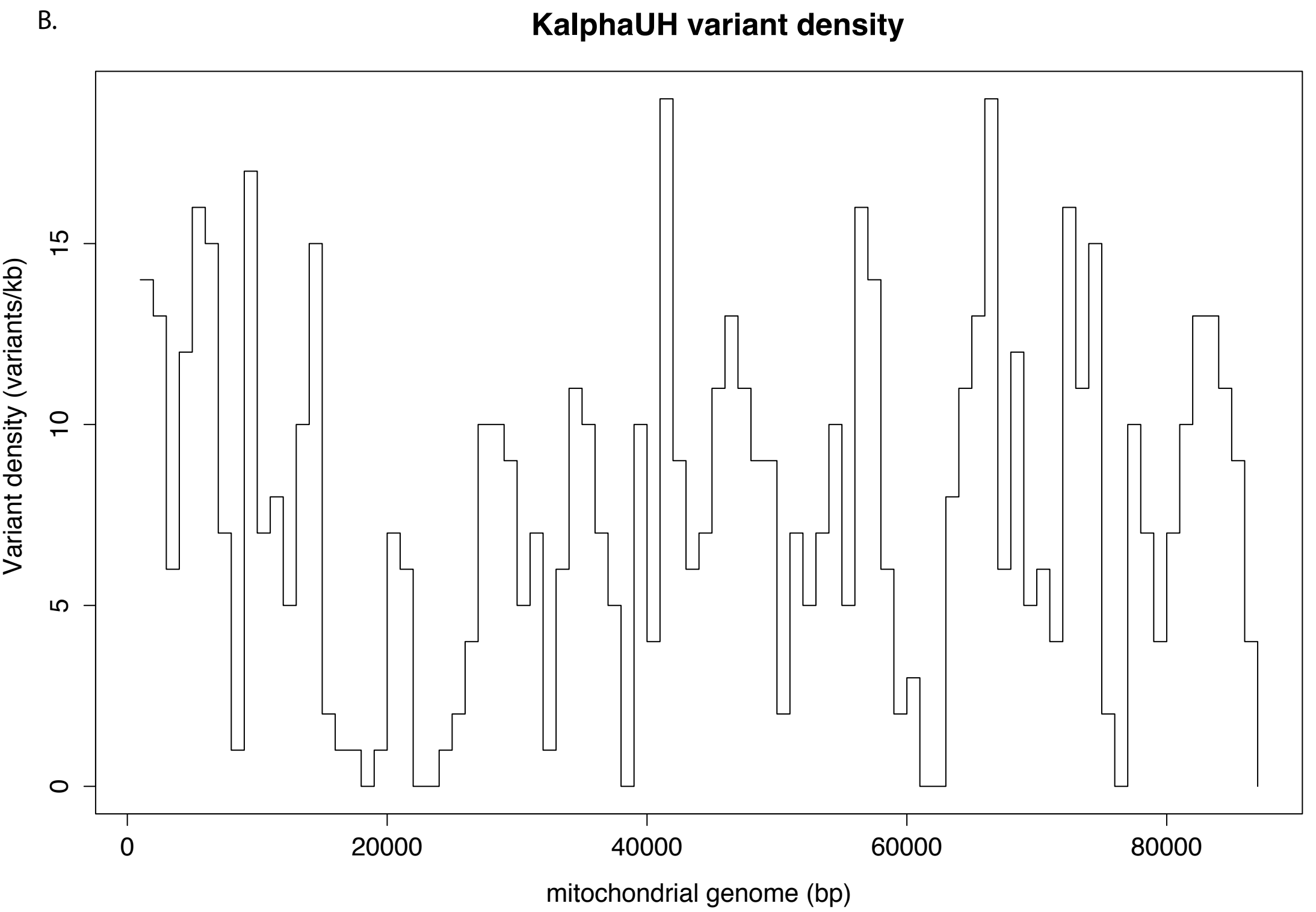
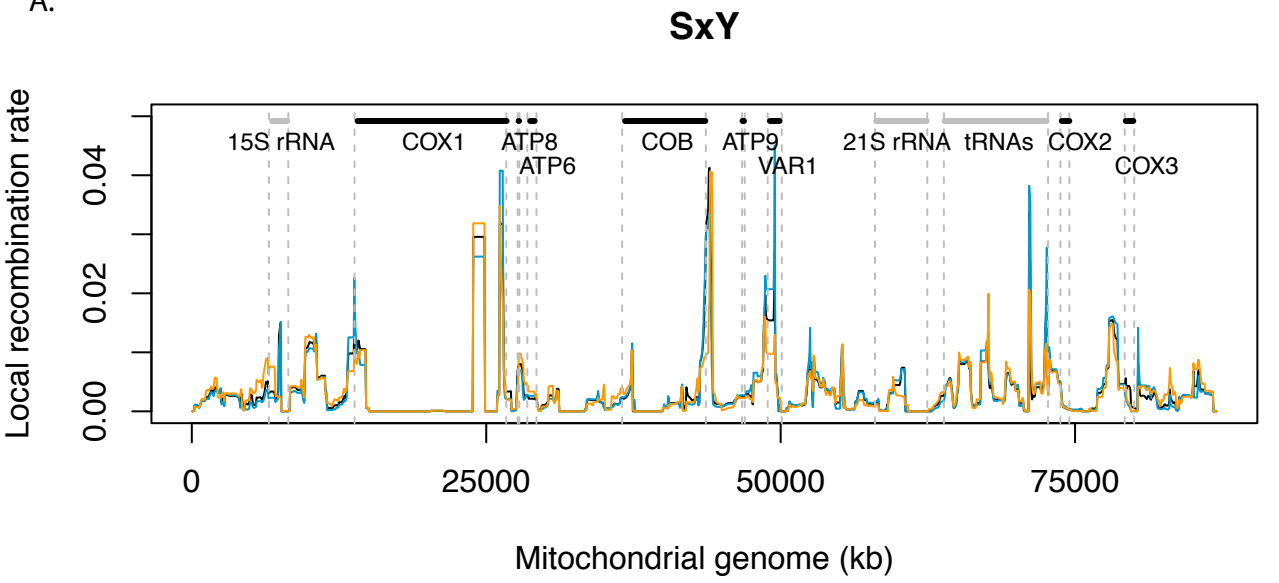
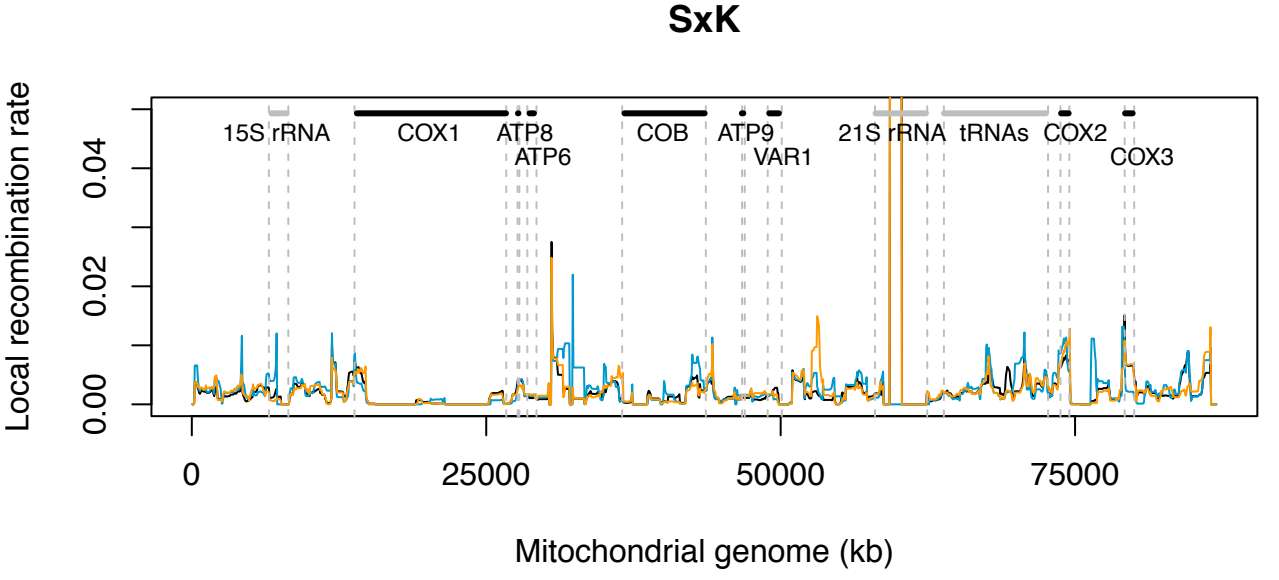

KalphaUH variant density
Variant density (variants/kb)
0
5
10
15
0
20000
40000
60000
80000
mitochondrial genome (bp)

Figure S2 Variant density over the mitochondrial genome.
The mitochondrial genome was binned into consecutive 1kb windows and the number of variants falling within each window was subsequently plotted over the mitochondrial genome.
A. YJM789 variant density
B. KalphaUH variant density

A.

Supplementary Figure 3





B.

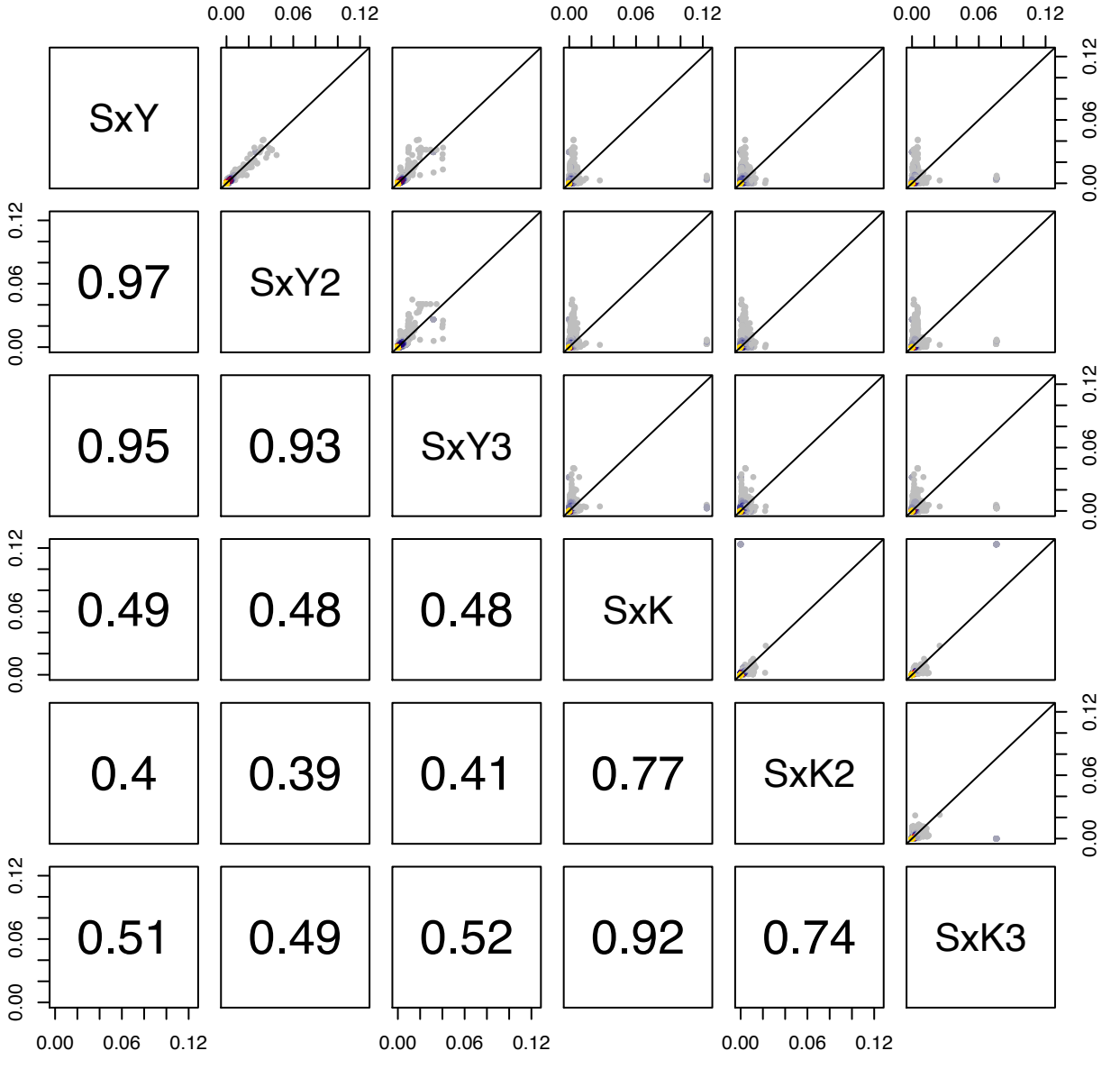

Local recombination rate
SxY
SxY2
SxY3
SxK
SxK2
SxK3
0.97
0.95
0.93
0.49
0.48
0.48
0.4
0.39
0.41
0.77
0.51
0.49
0.52
0.92
0.74
0.00
0.06
0.12

Figure S3 Local recombination of the SxY and SxK crosses.
A. Local recombination profiles for the SxY and SxK crosses.
The local recombination rate was calculated for 1kb windows shifted by 50bp. The recombination profiles for three replicates of each cross are represented over the mitochondrial genome. The mitochondrial features are also indicated with protein coding genes as black bars and non protein coding genes as grey bars.
B. Pairwise scatterplots of the local recombination rates for the SxY and SxK crosses. The Spearman correlation coefficient is indicated for each pairwise comparison.

Supplementary Figure 4

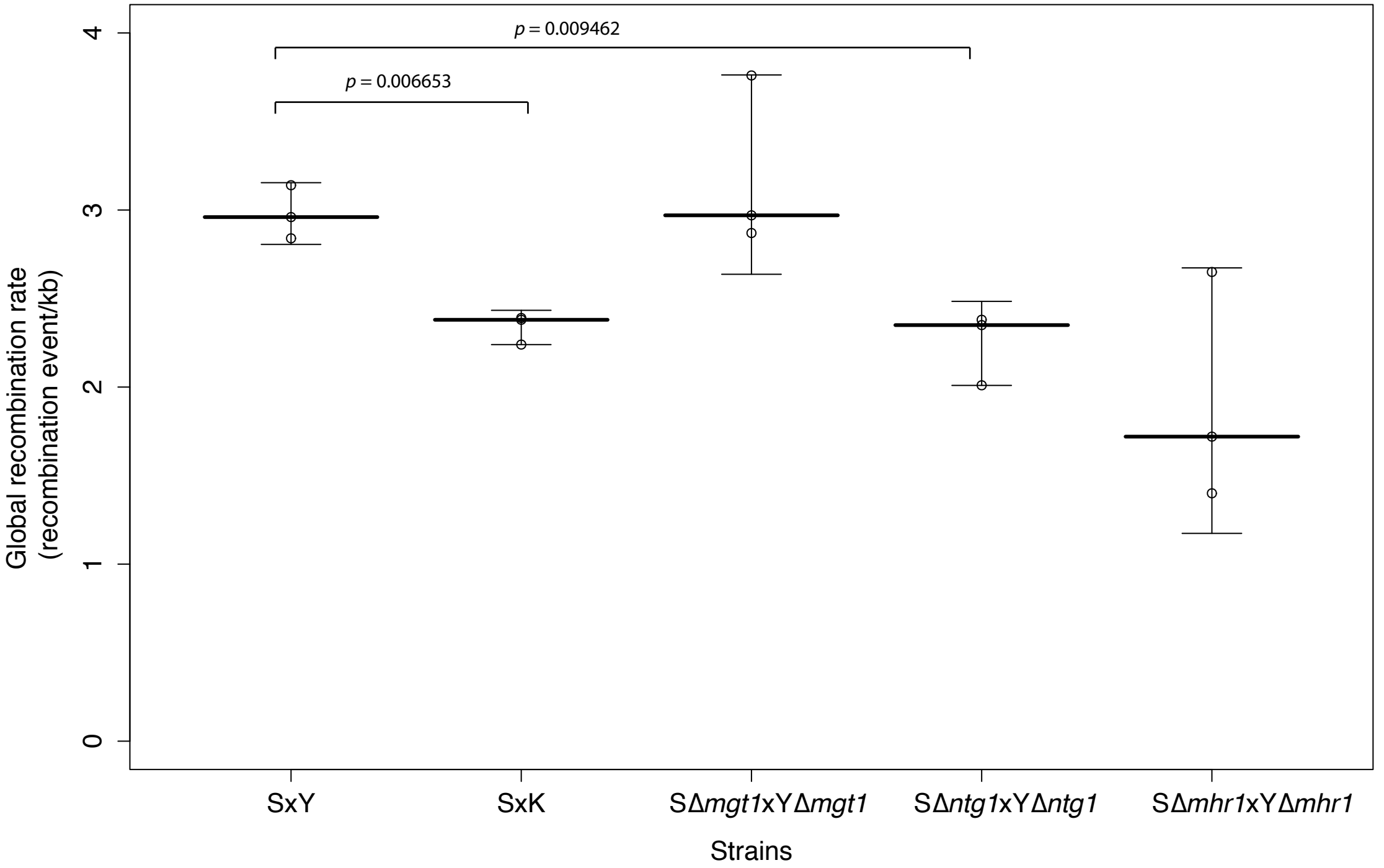
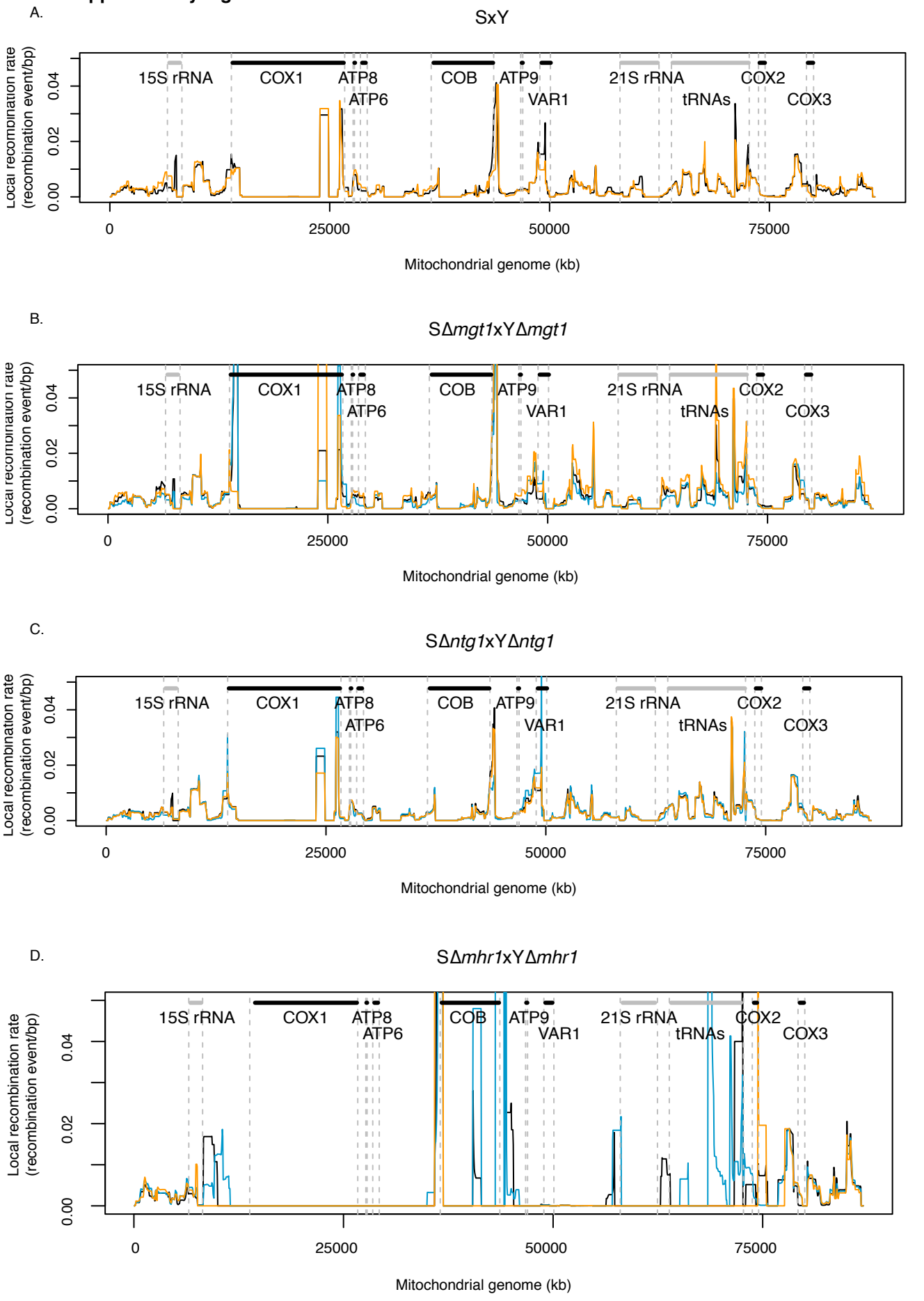
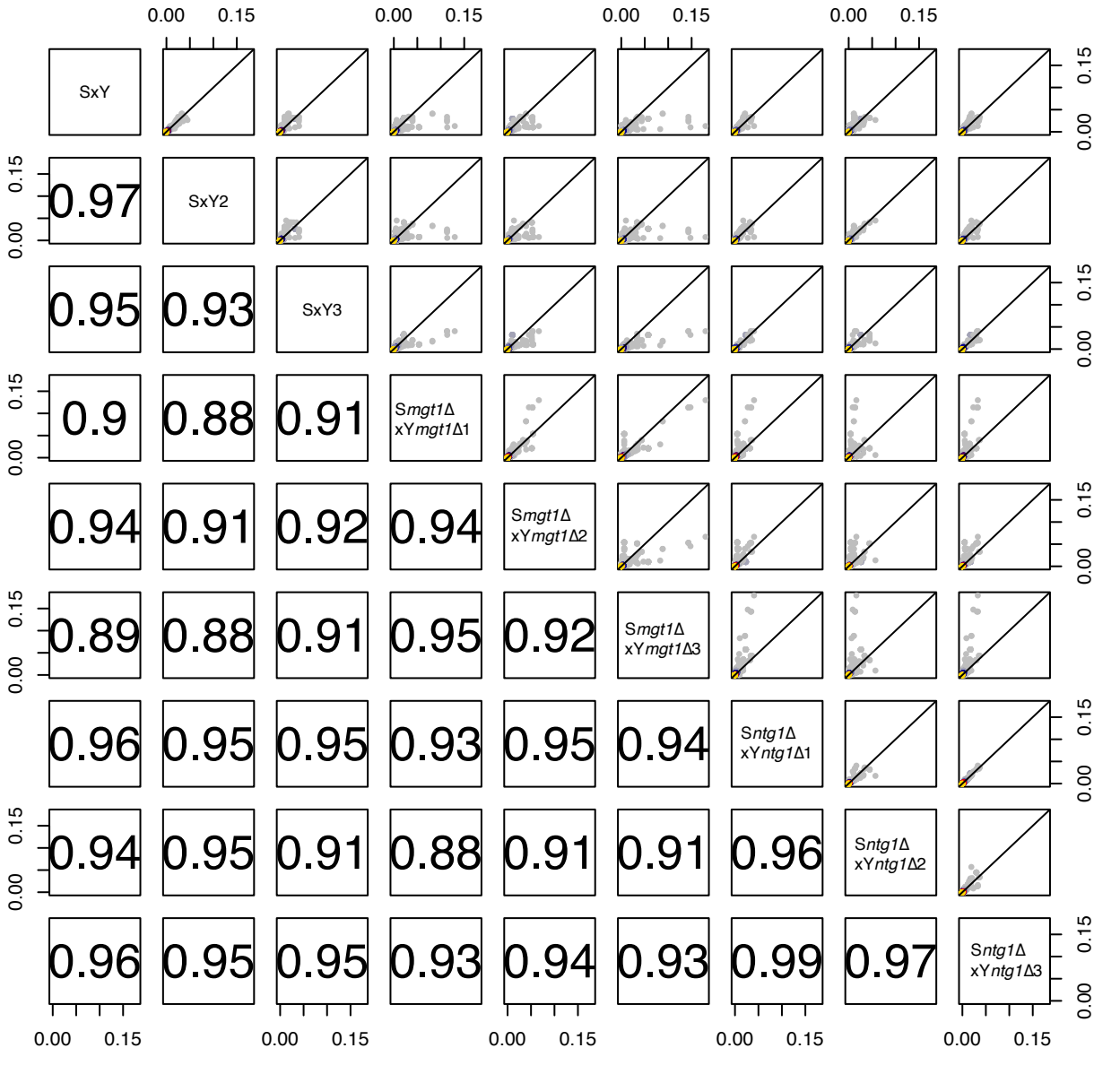


Figure S4 Global recombination rate for the different backgrounds.
The estimated mean value of the global recombination rates for the three replicates is plotted, as well as the standard errors. An ANOVA test was performed and a p-value of 0.01 was obtained. The p-value for the samples showing a statistically different rate is indicated.

Supplementary Figure 5



E.


Local recombination rate
SxY
SxY2
SxY3
S*mgt1Δ* x Y*mgt1Δ1*
S*mgt1Δ* x Y*mgt1Δ2*
S*mgt1Δ* x Y*mgt1Δ3*
S*ntg1Δ* x Y*ntg1Δ1*
S*ntg1Δ* x Y*ntg1Δ2*
S*ntg1Δ* x Y*ntg1Δ3*
0.97
0.95 0.93
0.9 0.88 0.91
0.94 0.91 0.92 0.94
0.89 0.88 0.91 0.95 0.92
0.96 0.95 0.95 0.93 0.95 0.94
0.94 0.95 0.91 0.88 0.91 0.91 0.96
0.96 0.95 0.95 0.93 0.94 0.93 0.99 0.97
0.00 0.15

F.

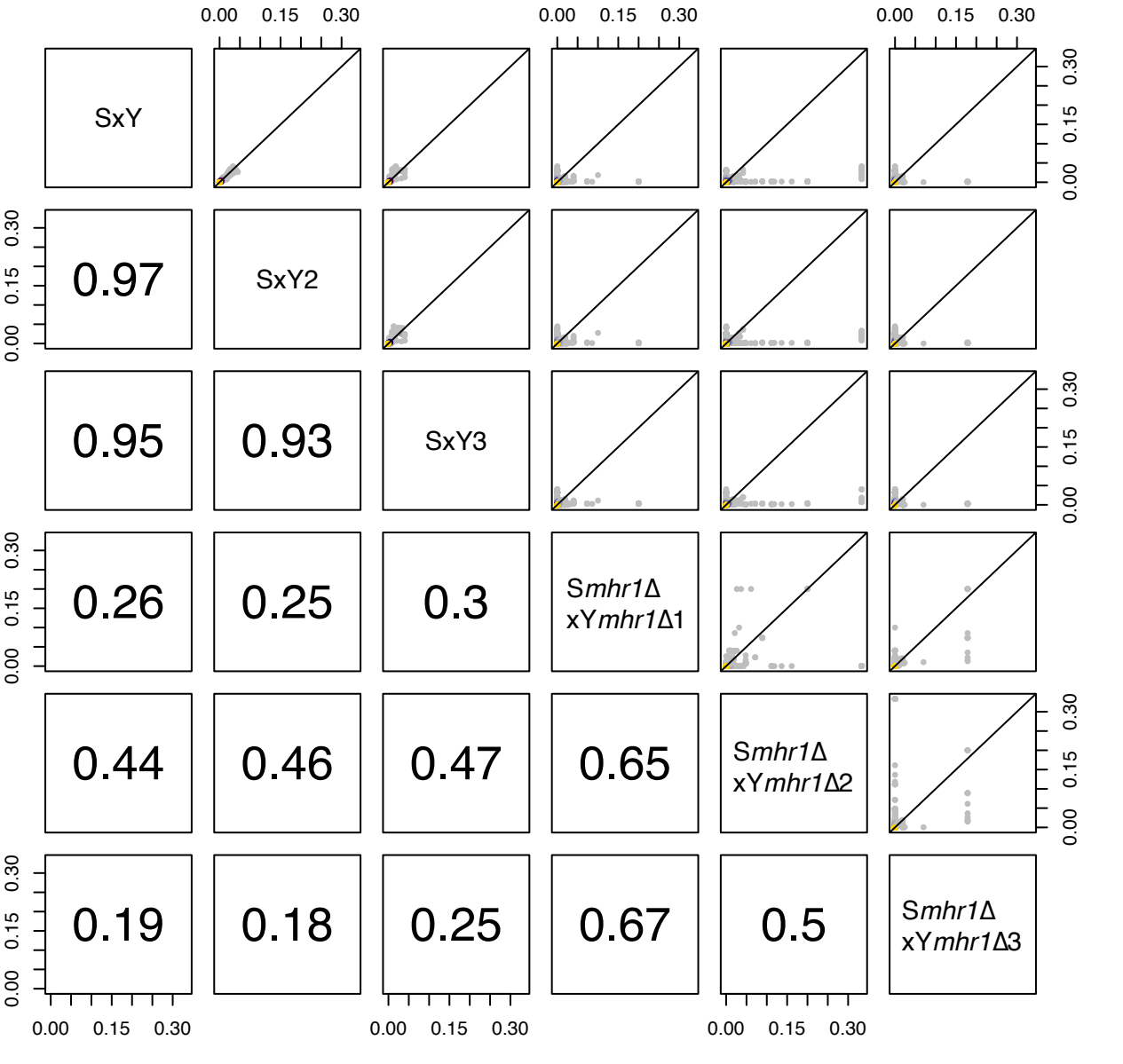

Local recombination rate
SxY
SxY2
SxY3
S*mhr1*Δ xY*mhr1*Δ1
S*mhr1*Δ xY*mhr1*Δ2
S*mhr1*Δ xY*mhr1*Δ3
0.97
0.95
0.93
0.26
0.25
0.3
0.44
0.46
0.47
0.65
0.19
0.18
0.25
0.67
0.5
0.00
0.15
0.30

Figure S5 Local recombination of the deletion backgrounds.
The local recombination rate was calculated for 1kb windows shifted by 50bp. The recombination profiles for three replicates of each cross are represented over the mitochondrial genome. The mitochondrial features are also indicated with protein coding genes as black bars and non protein coding genes as grey bars.
A. Local recombination profile for the reference SxY cross
B. Local recombination rate for the SΔ*mgt1*xYΔ*mgt1* cross
C. Local recombination rate for the SΔ*ntg1*xYΔ*ntg1* cross
D. Local recombination rate for the SΔ*mhr1*xYΔ*mhr1* cross
E. Pairwise scatterplots of the local recombination rates for the SxY and mutant Δ*mgt1* and Δ*ntg1* crosses. The Spearman correlation coefficient is indicated for each pairwise comparison.
F. Pairwise scatterplots of the local recombination rates for the SxY and the Δ*mhr1* cross. The Spearman correlation coefficient is indicated for each pairwise comparison.

Tables S1-S8

Available for download at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.166637/-/DC1

Table S1 Strains table

This table recapitulates the strains name, their genetic background and genotypes as well as their origin.

Table S2 Reads after filtering

Summary of the number of usable reads after filtering for the different strains used in this study. For the cross, the three replicates are indicated. The table contains the initial number of reads pairs, the number of read pairs aligned on the mitochondrial genome after filtering, the percentage of usable reads and an approximation of the coverage.

Table S3 Mutation/Sequencing error and global recombination rate

For each replicate of each strain, the global recombination rate, the global mutation rate and the mitochondrial and nuclear specific mutation rates are indicated.

Table S4 List of variants for SaUH

For each variant, the position on the S288c mitochondrial genome, the S288c sequences (reference) as well as the variant sequences for the SaUH strain (alternative) are indicated.

Table S5 List of variants for YJM789

For each variant, the position on the S288c mitochondrial genome, the S288c sequences (reference) as well as the variant sequences for the YJM789 strain (alternative) are indicated.

Table S6 List of variants for SaUK

For each variant, the position on the S288c mitochondrial genome, the S288c sequences (reference) as well as the variant sequences for the SaUK strain (alternative) are indicated.

Table S7 List of variants for KalphaUH

For each variant, the position on the S288c mitochondrial genome, the S288c sequences (reference) as well as the variant sequences for the KalphaUH strain (alternative) are indicated.

Table S8 Summary of the standard deviations

For each replicate of each cross, the minimum, maximum, median, third quantile and mean of the standard deviations for the local recombination rates are indicated.