**SUPPLEMENTARY MATERIALS OF**

**"Evolution of the yeast recombination landscape"**

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**The supplementary materials include:**

**Table S1.** Summary statistics of the sequencing data.

**Table S2.** Correlation between local CO rate and heterozygosity and that between local NCO rate and heterozygosity at different scales.

**Fig. S1.** Distribution of markers in three hybrid yeast strains analyzed in this study. Marker density is measured by the number of markers per nucleotide in 20 kb windows. X-axis shows genomic positions on each chromosome (×100 kb).

**Fig. S2.** Correction of the number of NCO events per meiosis. (**A**) Mean number of markers per tract as a function of tract length. For each tract length from 100 bp to 3000 bp with a step size of 100 bp, 10,000 random NCO events are simulated and the mean number of markers converted among tracts with at least one marker is calculated and plotted against tract length. (**B**) Probability of detection of a tract in the simulation as a function of tract length. In the real data, an average NCO event converts 18 markers, corresponding to a tract length of 1500 bp in panel A; this tract length corresponds to a detection probability of 0.985 in panel B.

**Fig. S3.** Tract length distributions for NCO (**A**) and CO-GeneConv (**B**) events in *Spar*.

**Fig. S4.** Comparison of CO and NCO rates (number of events per Mb per meiosis) among different chromosomal regions.

**Fig. S5.** CO and NCO counts per meiosis in each chromosome, and CO and NCO rates per Mb per meiosis in each chromosome in *Scer* and *Spar*. Pearson's correlation coefficient and associated *P*-value are shown in each panel. (**A**) Relationship between CO count and chromosome length in *Scer*. (**B**) Relationship between NCO count and chromosome length in *Scer*. (**C**) Relationship between CO count and chromosome length in *Spar*. (**D**) Relationship between NCO count and chromosome length in *Spar*. (**E**) Relationship between CO rate and chromosome length in *Scer*. (**F**) Relationship between NCO rate and chromosome length in

*Scer*. (**G**) Relationship between CO rate and chromosome length in *Spar*. (**H**) Relationship between NCO rate and chromosome length in *Spar*.

**Fig. S6.** Variations of CO and NCO rates relative to DSB rates with respective to several factors in *Scer* and *Spar*. (**A**) The CO/DSB rate ratio in regions of various distances to centromere. (**B**) The CO/DSB rate ratio in regions of various GC contents. (**C**) The CO/DSB rate ratio in regions of various gene densities. (**D**) The NCO/DSB rate ratio in regions of various distances to centromere. (**E**) The NCO/DSB rate ratio in regions of various gene densities. On the X-axis of panels A and D, "1" indicates the 20 kb bin closest to centromere, "2" indicates the next closest 20 kb bin, and so on. In panel B, 20 kb windows are binned based on the GC content, which ranges from 35.5% to 42.5% with a step size of 1%. In (**C**) and (**E**), 20 kb windows are binned based on gene density (# of genes per 20 kb), which ranges from 5 to 18 with a step size of 2. In each bin, the data are presented as a bar plot; the lower and upper edges of a box represent the first ($qu_1$) and third quartiles ($qu_3$), respectively, the horizontal line inside the box indicates the median (md), the whiskers extend to the most extreme values inside inner fences, $md \pm 1.5(qu_3-qu_1)$, and the dots represent values outside the inner fences (outliers). Wilcoxon rank-sum tests are performed between each bin and all other bins combined, and the associated *P*-values are shown above each bin.

**Fig. S7.** Comparison of heterozygosity in 1 kb regions around COs, NCOs, and one million random sites. In each bin, data are presented as a bar plot. The lower and upper edges of a box represent the first ($qu_1$) and third quartiles ($qu_3$), respectively, the horizontal line inside the box indicates the median (md), the whiskers extend to the most extreme values inside inner fences, $md \pm 1.5(qu_3-qu_1)$, and the dots represent values outside the inner fences (outliers). Wilcoxon rank-sum tests are performed between COs (or NCOs) and random sites with *P*-values presented at the top.

Table S1. Summary statistics of the sequencing data. N17 and N44 are the parental *Spar* strains, whereas the rest are meiotic spores. Each tetrad has a unique number, and the four spores of the tetrad are marked with A, B, C, and D.

| Samples | Sequencing depth | Genomic coverage |
|---|---|---|
| N17 | 51.87 | 0.99 |
| N44 | 53.30 | 1 |
| 1A | 11.58 | 0.99 |
| 1B | 11.45 | 0.99 |
| 1C | 11.53 | 0.99 |
| 1D | 11.46 | 0.99 |
| 2A | 11.47 | 0.99 |
| 2B | 11.27 | 0.99 |
| 2C | 11.52 | 0.99 |
| 2D | 11.45 | 0.99 |
| 3A | 11.55 | 0.99 |
| 3B | 11.41 | 0.99 |
| 3C | 11.48 | 0.99 |
| 3D | 11.41 | 0.99 |
| 4A | 11.49 | 0.99 |
| 4B | 11.42 | 0.99 |
| 4C | 11.46 | 0.99 |
| 4D | 11.52 | 0.99 |
| 5A | 11.64 | 0.99 |
| 5B | 11.51 | 0.99 |
| 5C | 11.53 | 0.99 |
| 5D | 11.36 | 0.99 |
| 6A | 11.47 | 0.99 |
| 6B | 11.41 | 0.99 |
| 6C | 11.36 | 0.99 |
| 6D | 11.49 | 0.99 |
| 7A | 11.16 | 0.99 |
| 7B | 11.39 | 0.99 |
| 7C | 11.59 | 0.99 |
| 7D | 11.71 | 0.99 |
| 8A | 11.24 | 0.99 |
| 8B | 11.54 | 0.99 |
| 8C | 11.41 | 0.99 |
| 8D | 13.81 | 1 |
| 9A | 11.68 | 0.99 |
| 9B | 13.90 | 0.99 |
| 9C | 11.45 | 0.99 |
| 9D | 11.59 | 0.99 |
| 10A | 11.46 | 0.99 |
| 10B | 12.64 | 0.99 |
| 10C | 10.79 | 0.99 |
| 10D | 11.41 | 0.99 |

| | | |
|---|---|---|
| 11A | 11.37 | 0.99 |
| 11B | 11.47 | 0.99 |
| 11C | 11.52 | 0.99 |
| 11D | 13.84 | 0.99 |
| 12A | 11.38 | 0.99 |
| 12B | 11.48 | 0.99 |
| 12C | 11.51 | 0.99 |
| 12D | 11.49 | 0.99 |
| 13A | 11.46 | 0.99 |
| 13B | 11.49 | 0.99 |
| 13C | 11.65 | 0.99 |
| 13D | 11.61 | 0.99 |
| 14A | 11.55 | 0.99 |
| 14B | 11.21 | 0.99 |
| 14C | 11.52 | 0.99 |
| 14D | 11.36 | 0.99 |
| 15A | 11.48 | 0.99 |
| 15B | 11.44 | 0.99 |
| 15C | 11.45 | 0.99 |
| 15D | 11.58 | 0.99 |
| 16A | 11.45 | 0.99 |
| 16B | 11.45 | 0.99 |
| 16C | 11.56 | 0.99 |
| 16D | 11.45 | 0.99 |
| 17A | 11.61 | 0.99 |
| 17B | 11.50 | 0.99 |
| 17C | 11.43 | 0.99 |
| 17D | 11.52 | 0.99 |
| 18A | 11.51 | 0.99 |
| 18B | 11.48 | 0.99 |
| 18C | 11.47 | 0.99 |
| 18D | 11.48 | 0.99 |
| 19A | 13.51 | 0.99 |
| 19B | 11.43 | 0.99 |
| 19C | 11.39 | 0.99 |
| 19D | 11.49 | 0.99 |
| 20A | 14.84 | 0.99 |
| 20B | 11.52 | 0.99 |
| 20C | 11.45 | 0.99 |
| 20D | 11.46 | 0.99 |
| 21A | 11.44 | 0.99 |
| 21B | 11.50 | 0.99 |
| 21C | 11.45 | 0.99 |
| 21D | 11.39 | 0.99 |
| 22A | 11.46 | 0.99 |
| 22B | 11.33 | 0.99 |
| 22C | 11.44 | 0.99 |

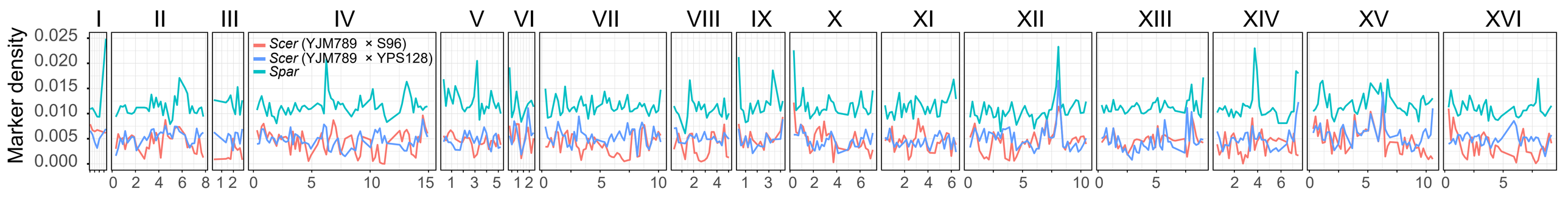
| | | |
|---|---|---|
| 22D | 11.48 | 0.99 |
| 23A | 11.55 | 0.99 |
| 23B | 11.38 | 0.99 |
| 23C | 11.47 | 0.99 |
| 23D | 11.43 | 0.99 |
| 24A | 11.52 | 0.99 |
| 24B | 11.37 | 0.99 |
| 24C | 11.46 | 0.99 |
| 24D | 13.04 | 0.99 |
| 25A | 12.08 | 0.99 |
| 25B | 10.19 | 0.99 |
| 25C | 11.15 | 0.99 |
| 25D | 11.18 | 0.99 |
| 26A | 10.30 | 0.99 |
| 26B | 9.85 | 0.99 |
| 26C | 10.06 | 0.99 |
| 26D | 10.49 | 0.99 |
| 27A | 12.17 | 0.99 |
| 27B | 11.62 | 0.99 |
| 27C | 11.42 | 0.99 |
| 27D | 12.52 | 0.99 |
| 28A | 11.58 | 0.99 |
| 28B | 10.66 | 0.99 |
| 28C | 12.89 | 0.99 |
| 28D | 11.21 | 0.99 |
| 30A | 13.71 | 0.99 |
| 30B | 13.43 | 0.99 |
| 30C | 12.25 | 0.99 |
| 30D | 14.11 | 1 |
| 31A | 12.30 | 1 |
| 31B | 13.13 | 0.99 |
| 31C | 11.88 | 0.99 |
| 31D | 12.75 | 0.99 |
| 32A | 13.96 | 0.99 |
| 32B | 13.49 | 0.99 |
| 32C | 12.95 | 0.99 |
| 32D | 12.77 | 1 |
| 33A | 10.81 | 0.99 |
| 33B | 11.99 | 0.99 |
| 33C | 11.17 | 0.99 |
| 33D | 11.99 | 0.99 |
| 34A | 13.12 | 0.99 |
| 34B | 11.15 | 0.99 |
| 34C | 12.82 | 0.99 |
| 34D | 13.49 | 0.99 |
| 35A | 12.54 | 0.99 |
| 35B | 11.33 | 1 |

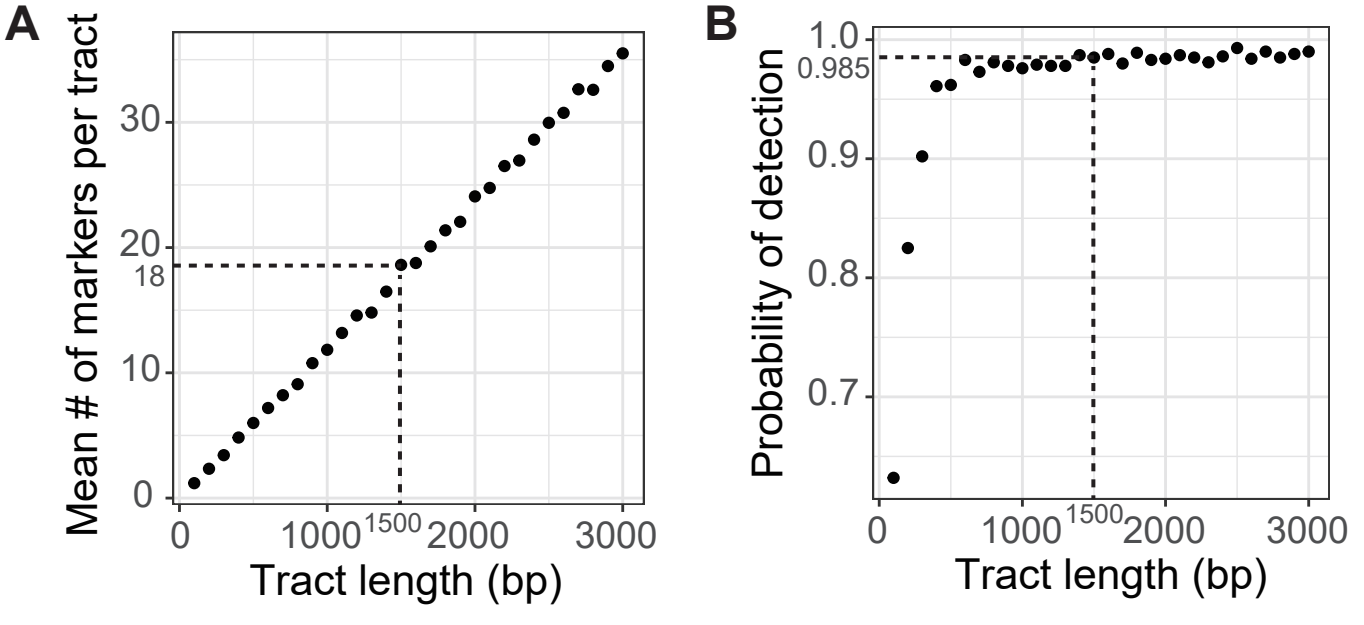
| | | |
|---|---|---|
| 35C | 11.70 | 0.99 |
| 35D | 11.79 | 1 |
| 36A | 13.20 | 0.99 |
| 36B | 11.94 | 0.99 |
| 36C | 12.89 | 0.99 |
| 36D | 13.14 | 0.99 |
| 37A | 14.92 | 0.99 |
| 37B | 11.87 | 0.99 |
| 37C | 12.27 | 0.99 |
| 37D | 12.62 | 0.99 |
| 38A | 10.77 | 0.99 |
| 38B | 12.64 | 0.99 |
| 38C | 12.89 | 0.99 |
| 38D | 11.18 | 0.99 |
| 39A | 10.18 | 0.99 |
| 39B | 11.44 | 0.99 |
| 39C | 11.86 | 0.99 |
| 39D | 11.10 | 0.99 |
| 40A | 11.64 | 0.99 |
| 40B | 12.22 | 0.99 |
| 40C | 10.19 | 0.99 |
| 40D | 12.78 | 0.99 |
| 41A | 13.55 | 0.99 |
| 41B | 11.17 | 0.99 |
| 41C | 12.84 | 0.99 |
| 41D | 12.15 | 0.99 |
| 42A | 11.84 | 0.99 |
| 42B | 14.04 | 1 |
| 42C | 12.54 | 0.99 |
| 42D | 12.49 | 0.99 |
| 43A | 13.63 | 0.99 |
| 43B | 14.43 | 0.99 |
| 43C | 13.50 | 0.99 |
| 43D | 11.39 | 0.99 |
| 44A | 11.75 | 0.99 |
| 44B | 12.43 | 0.99 |
| 44C | 13.34 | 0.99 |
| 44D | 11.77 | 0.99 |
| 45A | 11.04 | 0.99 |
| 45B | 12.11 | 0.99 |
| 45C | 13.20 | 0.99 |
| 45D | 11.28 | 0.99 |
| 46A | 13.67 | 1 |
| 46B | 12.84 | 0.99 |
| 46C | 11.50 | 0.99 |
| 46D | 11.39 | 0.99 |
| 47A | 11.37 | 0.99 |

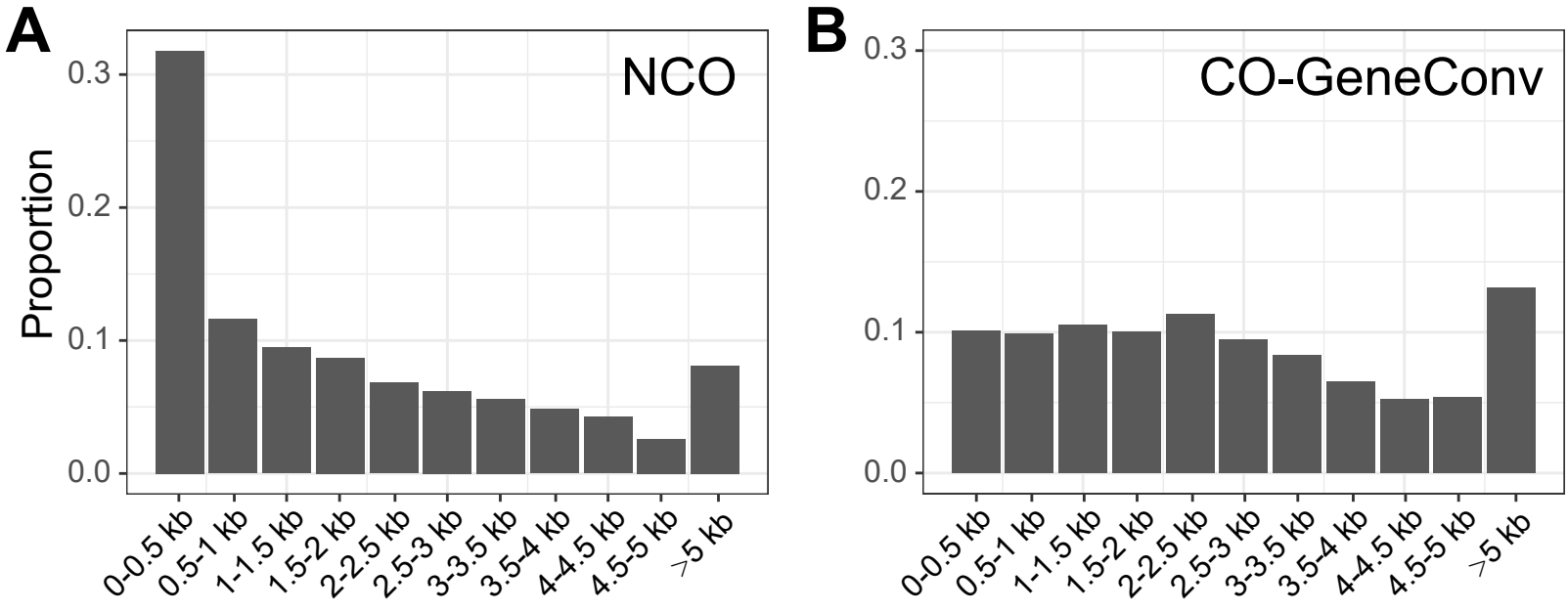
| | | |
|---|---|---|
| 47B | 11.50 | 0.99 |
| 47C | 11.45 | 0.99 |
| 47D | 11.42 | 0.99 |
| 48A | 11.55 | 0.99 |
| 48B | 11.40 | 0.99 |
| 48C | 11.35 | 0.99 |
| 48D | 11.34 | 0.99 |
| 49A | 11.23 | 0.99 |
| 49B | 11.28 | 0.99 |
| 49C | 11.35 | 0.99 |
| 49D | 11.23 | 0.99 |
| 50A | 11.28 | 0.99 |
| 50B | 11.21 | 0.99 |
| 50C | 11.21 | 0.99 |
| 50D | 11.24 | 0.99 |
| 51A | 11.18 | 0.99 |
| 51B | 11.37 | 0.99 |
| 51C | 11.29 | 0.99 |
| 51D | 11.34 | 0.99 |
| Average | 12.22 | 0.99 |

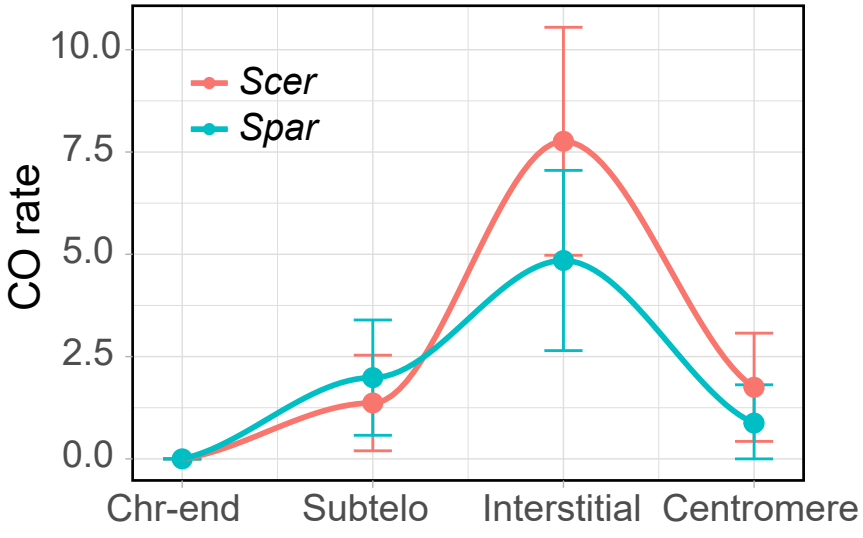
Table S2. Correlation between local CO rate and heterozygosity and that between local NCO rate and heterozygosity at different scales.

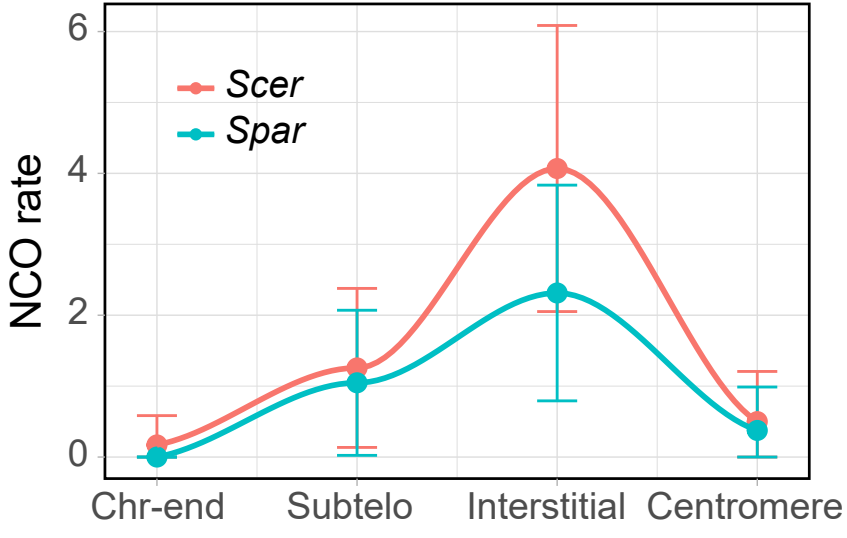
| Variables | Window size | *Scer* (YJM789 × S96) | | *Scer* (YJM789 × YPS128) | | *Spar* (N44 × N17) | |
|---|---|---|---|---|---|---|---|
| | | Spearman's ρ | *P*-value | Spearman's ρ | *P*-value | Spearman's ρ | *P*-value |
| CO rate and heterozygosity | | | | | | | |
| | 5 kb | 0.0992 | 1.1e-5 | 0.0177 | 0.43 | -0.0367 | 0.10 |
| | 10 kb | 0.0987 | 0.0020 | 0.0108 | 0.74 | -0.0658 | 0.039 |
| | 20 kb | 0.129 | 0.0041 | 0.0225 | 0.62 | -0.0308 | 0.50 |
| | 40 kb | 0.116 | 0.081 | 0.0201 | 0.76 | 0.00415 | 0.95 |
| NCO rate and heterozygosity | | | | | | | |
| | 5 kb | 0.244 | 5.7e-28 | 0.0454 | 0.044 | 0.00865 | 0.70 |
| | 10 kb | 0.283 | 1.8e-19 | 0.0753 | 0.018 | -0.00672 | 0.83 |
| | 20 kb | 0.329 | 6.8e-14 | 0.0700 | 0.12 | -0.0268 | 0.55 |
| | 40 kb | 0.347 | 9.2e-8 | 0.107 | 0.11 | -0.0213 | 0.75 |

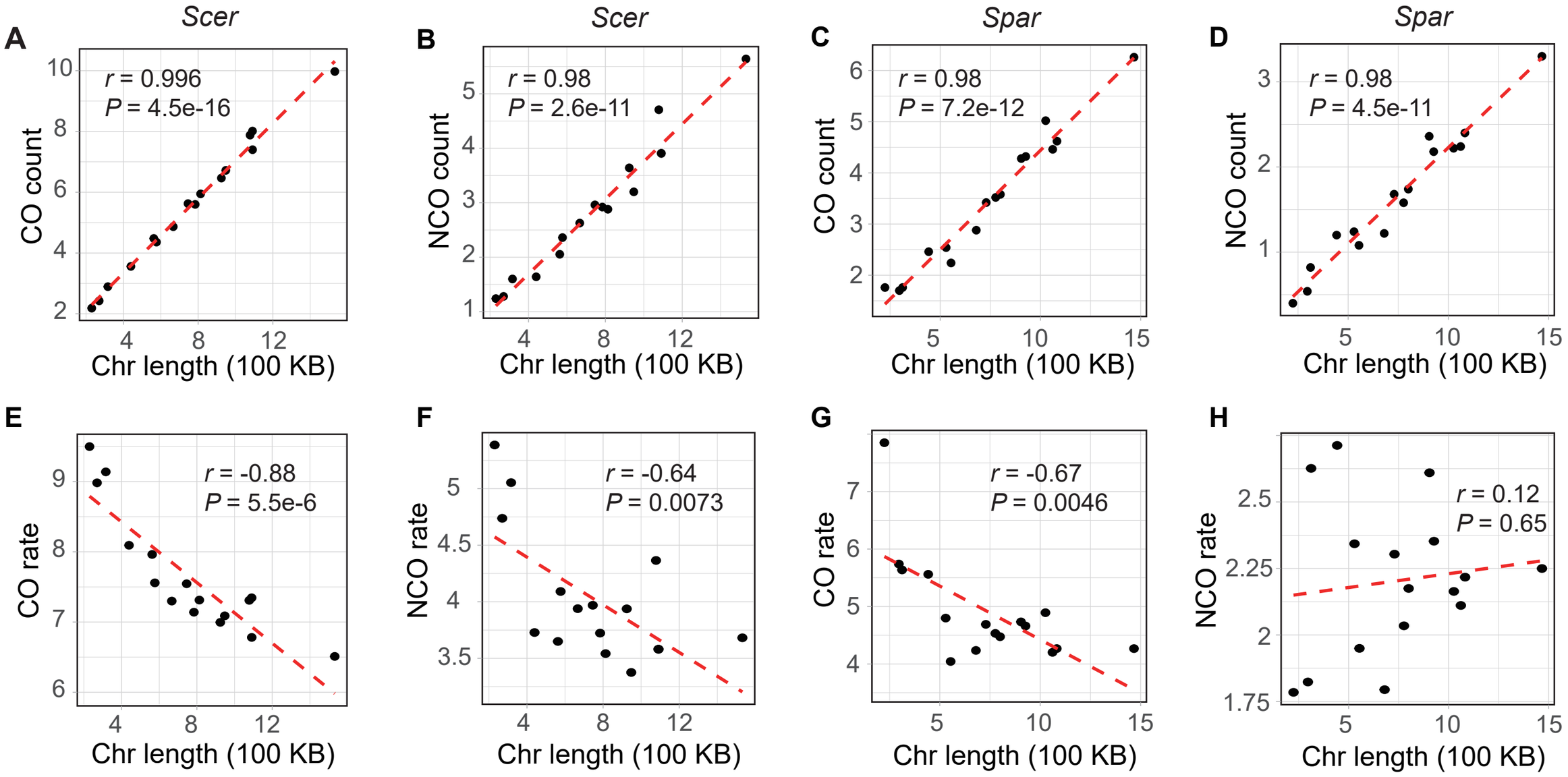

Marker density
0.025
0.020
0.015
0.010
0.005
0.000
I
II
III
IV
V
VI
VII
VIII
IX
X
XI
XII
XIII
XIV
XV
XVI
Scer (YJM789 × S96)
Scer (YJM789 × YPS128)
Spar

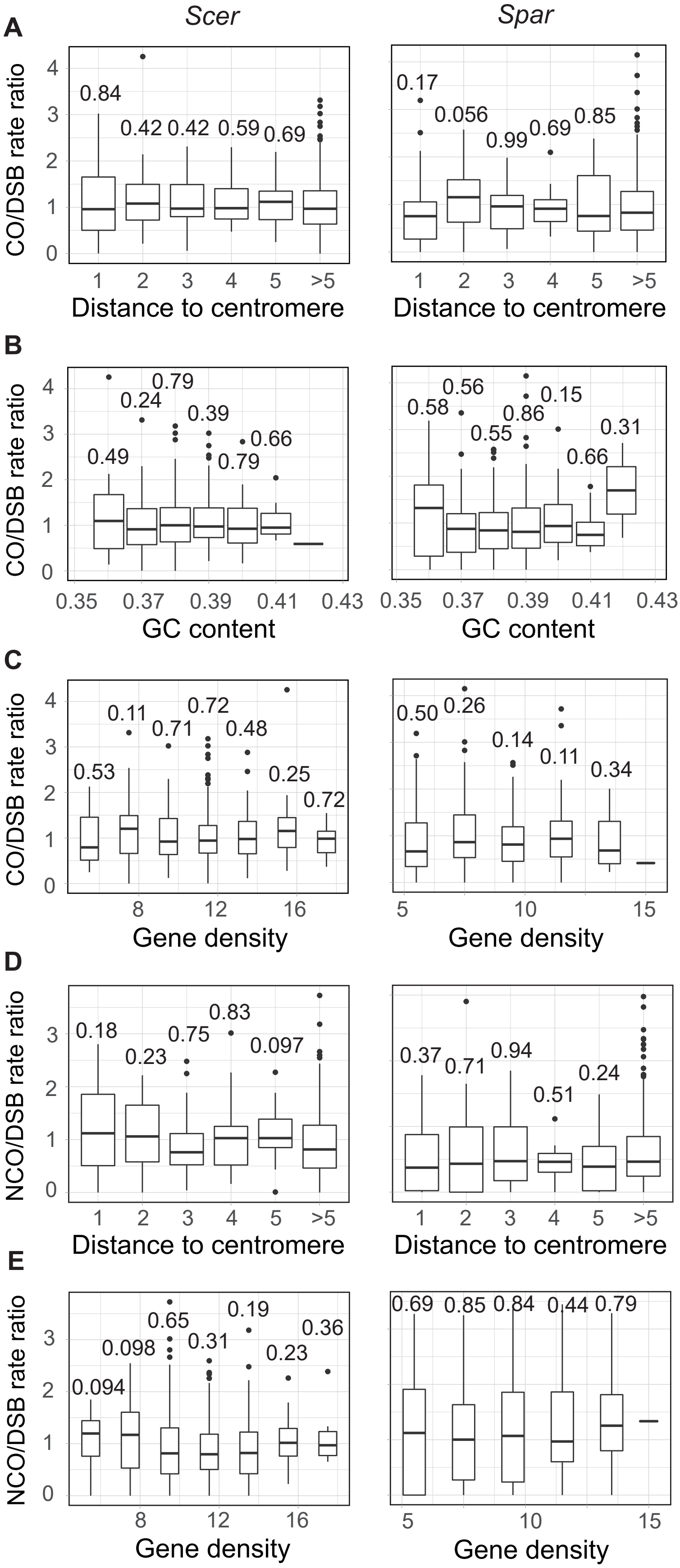

A
Mean # of markers per tract
30
20
18
10
0
0
1000
1500
2000
3000
Tract length (bp)
B
Probability of detection
1.0
0.985
0.9
0.8
0.7
0
1000
1500
2000
3000
Tract length (bp)

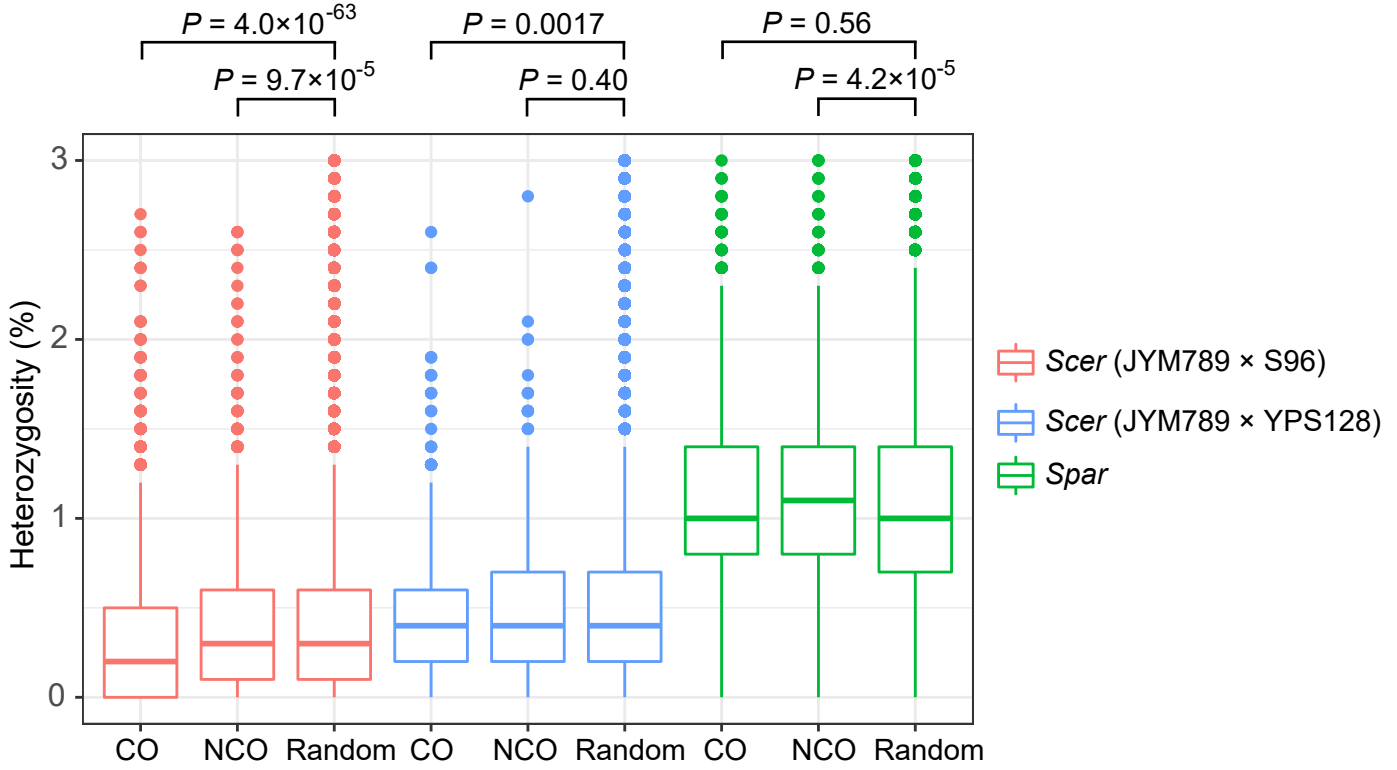

A
NCO
Proportion
0.3
0.2
0.1
0.0
0-0.5 kb
0.5-1 kb
1-1.5 kb
1.5-2 kb
2-2.5 kb
2.5-3 kb
3-3.5 kb
3.5-4 kb
4-4.5 kb
4.5-5 kb
>5 kb
B
CO-GeneConv
0.3
0.2
0.1
0.0
0-0.5 kb
0.5-1 kb
1-1.5 kb
1.5-2 kb
2-2.5 kb
2.5-3 kb
3-3.5 kb
3.5-4 kb
4-4.5 kb
4.5-5 kb
>5 kb


CO rate
10.0
7.5
5.0
2.5
0.0
Scer
Spar
Chr-end
Subtelo
Interstitial
Centromere


NCO rate
6
4
2
0
Scer
Spar
Chr-end
Subtelo
Interstitial
Centromere


A
Scer
r = 0.996
P = 4.5e-16
CO count
Chr length (100 KB)
B
Scer
r = 0.98
P = 2.6e-11
NCO count
Chr length (100 KB)
C
Spar
r = 0.98
P = 7.2e-12
CO count
Chr length (100 KB)
D
Spar
r = 0.98
P = 4.5e-11
NCO count
Chr length (100 KB)
E
r = -0.88
P = 5.5e-6
CO rate
Chr length (100 KB)
F
r = -0.64
P = 0.0073
NCO rate
Chr length (100 KB)
G
r = -0.67
P = 0.0046
CO rate
Chr length (100 KB)
H
r = 0.12
P = 0.65
NCO rate
Chr length (100 KB)


A
Scer
Spar
CO/DSB rate ratio
0.84
0.42
0.42
0.59
0.69
0.17
0.056
0.99
0.69
0.85
1
2
3
4
5
>5
Distance to centromere
B
CO/DSB rate ratio
0.49
0.24
0.79
0.39
0.79
0.66
0.58
0.56
0.55
0.86
0.15
0.66
0.31
0.35
0.37
0.39
0.41
0.43
GC content
C
CO/DSB rate ratio
0.53
0.11
0.71
0.72
0.48
0.25
0.72
0.50
0.26
0.14
0.11
0.34
8
12
16
5
10
15
Gene density
D
NCO/DSB rate ratio
0.18
0.23
0.75
0.83
0.097
0.37
0.71
0.94
0.51
0.24
Distance to centromere
E
NCO/DSB rate ratio
0.094
0.098
0.65
0.31
0.19
0.23
0.36
0.69
0.85
0.84
0.44
0.79
Gene density


P = 4.0×10-63
P = 0.0017
P = 0.56
P = 9.7×10-5
P = 0.40
P = 4.2×10-5
Heterozygosity (%)
3
2
1
0
CO
NCO
Random
CO
NCO
Random
CO
NCO
Random
Scer (JYM789 × S96)
Scer (JYM789 × YPS128)
Spar