**Table S6 Estimating the linear density of DNA in euchromatin, heterochromatin, and kinetochores by FISH[1]**

| Chromatin Type | Chr. # | Scaffold # | Scaffold Size Mb (Corrected Mb)[2] | SC Length - µm | Mb/µm |
|---|---|---|---|---|---|
| Euchromatin | 1 | SL2.40sc04323 | 17.0 (16.8) | 12.6 | 1.33 |
| | 2 | SL2.40sc03665 | 22.4 (21.8) | 15.3 | 1.43 |
| | 3 | SL2.40sc04439 | 2.5 (2.3) | 1.4 | 1.62 |
| | 3 | SL2.40sc03701 | 9.2 (8.7) | 6.2 | 1.40 |
| | 4 | SL2.40sc04135 | 8.8 (8.6) | 5.2 | 1.65 |
| | 6 | SL2.40sc05054 | 10.3 (9.8) | 6.2 | 1.58 |
| | 6 | SL2.40sc03622 | 1.8 (1.7) | 1.2 | 1.38 |
| | 7 | SL2.40sc04626 | 3.4 (3.2) | 2.0 | 1.58 |
| | 8 | SL2.40sc03923 | 7.5 (7.4) | 4.6 | 1.60 |
| | 10 | SL2.40sc04199 | 8.0 (7.7) | 4.5 | 1.70 |
| | 11 | SL2.40sc03876 | 8.2 (7.9) | 3.8 | 2.07 |
| | 12 | SL2.40sc05380 | 2.6 (2.3) | 1.4 | 1.66 |
| | **Total** | | **101.7 (98.0) Mb** | **64.4 µm** | **1.52 Mb/µm[3]** |
| Heterochromatin | 1 | SL2.40sc03594 | 6.3 (5.9) | 0.7 | 8.41 |
| | 7 | SL2.40sc05397 | 8.0 (7.8) | 0.9 | 8.69 |
| | 8 | SL2.40sc04701 | 7.0 (6.8) | 0.7 | 9.76 |
| | 10 | SL2.40sc03798 | 16.5 (16.3) | 1.9 | 8.58 |
| | **Total** | | **37.8 (36.8) Mb** | **4.2 µm** | **8.76 Mb/µm[3]** |
| Kinetochore | 10 | SL2.40sc04872 | 3.9 (3.6) | 1.1 | 3.27 |
| | **Total** | | **3.9 (3.6) Mb** | **1.1 µm** | **3.27 Mb/µm[3]** |

[1] Scaffold numbers, DNA amounts in scaffolds, lengths of scaffolds, and chromatin types were extracted from Table S1.

[2] The FISH signals at either end of a scaffold are not at the very ends of the scaffold but somewhat into the scaffold [see File S1, Additional Materials and Methods- Determining the amount of DNA per micrometer of SC (= linear DNA density) in kinetochores, euchromatin, and heterochromatin]. Because of this, scaffold DNA extending beyond the FISH signals must be subtracted from the length of the scaffold to yield the "Corrected Mb" between FISH signals that will be divided by SC length in micrometers to yield Mb/µm.

[3] = Total (corrected) Mb DNA ÷ total SC length (µm)