

Supplementary Materials for **Three-dimensional positioning and structure of chromosomes in a human prophase nucleus**

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The PDF file includes:

- Legends for movies S1 and S2
- table S1. Volume statistics of all the broken chromosomes in the nucleus.
- table S2. Reassignment of all the intact chromosomes as a comparison with the assignment in the main text.
- fig. S1. SBFSEM slices of the measured (smaller) chromosomes.
- fig. S2. Second linear fitting of the chromatid volumes against their base pair numbers.

Other Supplementary Material for this manuscript includes the following:

(available at advances.sciencemag.org/cgi/content/full/3/7/e1602231/DC1)

- movie S1 (.mpg format). 3D rendering of the measured prophase nucleus.
- movie S2 (.mpg format). 3D rendering of the measured prophase nucleus from another orientation.

movie S1. 3D rendering of the measured prophase nucleus. 3D rendering of the spatial structure of the (partial) human prophase nucleus with the chromosomes inside obtained by serial block-face scanning electron microscopy (SBFSEM) measurement.

movie S2. 3D rendering of the measured prophase nucleus from another orientation. 3D rendering of the spatial structure of the (partial) human prophase nucleus with the chromosomes inside obtained by serial block-face scanning electron microscopy (SBFSEM) measurement. This rendering was shown from another orientation of the same nucleus data set of the Supplementary Video S1.

table S1. Volume statistics of all the broken chromosomes in the nucleus.

Broken Chromosome (Number)	Chromatid Volume* (μm^3)
1	1.233
2	1.182
3	1.138
4	0.863
5	0.789
6	0.783
7	0.765
8	0.681
9	0.628
10	0.546
11	0.467
12	0.326
13	0.262
14	0.261
15	0.244
16	0.201
17	0.130

* Here, the chromatid volume is half of the measured volume of the chromosomes without cavities, i.e. half of the volume of the black region only in the imaged chromosomes (with chromatid pairs) measured by Avizo.

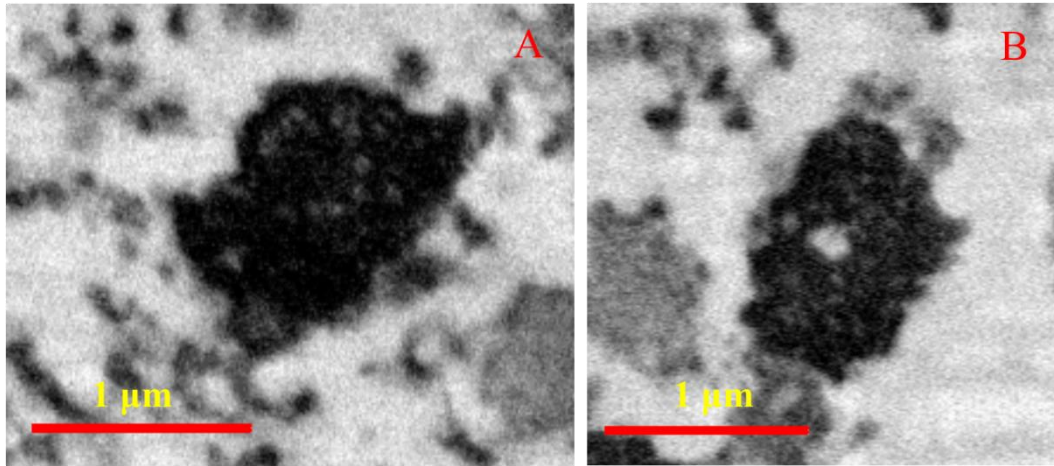


fig. S1. SBFSEM slices of the measured (smaller) chromosomes. SBFSEM slices of the measured (smaller) chromosomes D5 (A) and D6 (B).

table S2. Reassignment of all the intact chromosomes as a comparison with the assignment in the main text.

Chromosome (Number)	Chromatid Volume [†] /V1 (μm^3)	Assigned Chromosome (Number)	Calculated Chromatid Volume [‡] (μm^3)
A1	1.655	2	1.411
A2	1.650	3	1.148
A3	1.328	4	1.109
A4	1.263	4	1.109
BC1	1.124	6	0.992
BC2	1.092	7 (or X)	0.923
BC3	1.056	8	0.849
C1	0.993	9	0.819
C2	0.972	10	0.786
C3	0.963	11	0.783
C4	0.955	12	0.777
C5	0.895	13	0.668
D1	0.776	14	0.622
D2	0.625	17	0.471
D3	0.603	18	0.453
D4	0.572	19	0.343
D5	0.509	22	0.298
D6	0.435	22	0.298
D7	0.213	21	0.279

[†] Here, the chromatid volume is half of the measured volume of the chromosomes without cavities, i.e. half of the volume of the black region only in the imaged chromosomes (with chromatid pairs) measured by Avizo;

[‡] Here, the calculated chromatid volumes were obtained by multiplying the sequence length of the assigned human chromosomes (in MBp) from the database by 5.80 nm^3 . The volume per base pair, 5.80 nm^3 , was obtained by theoretical calculation which is explained in the main text.

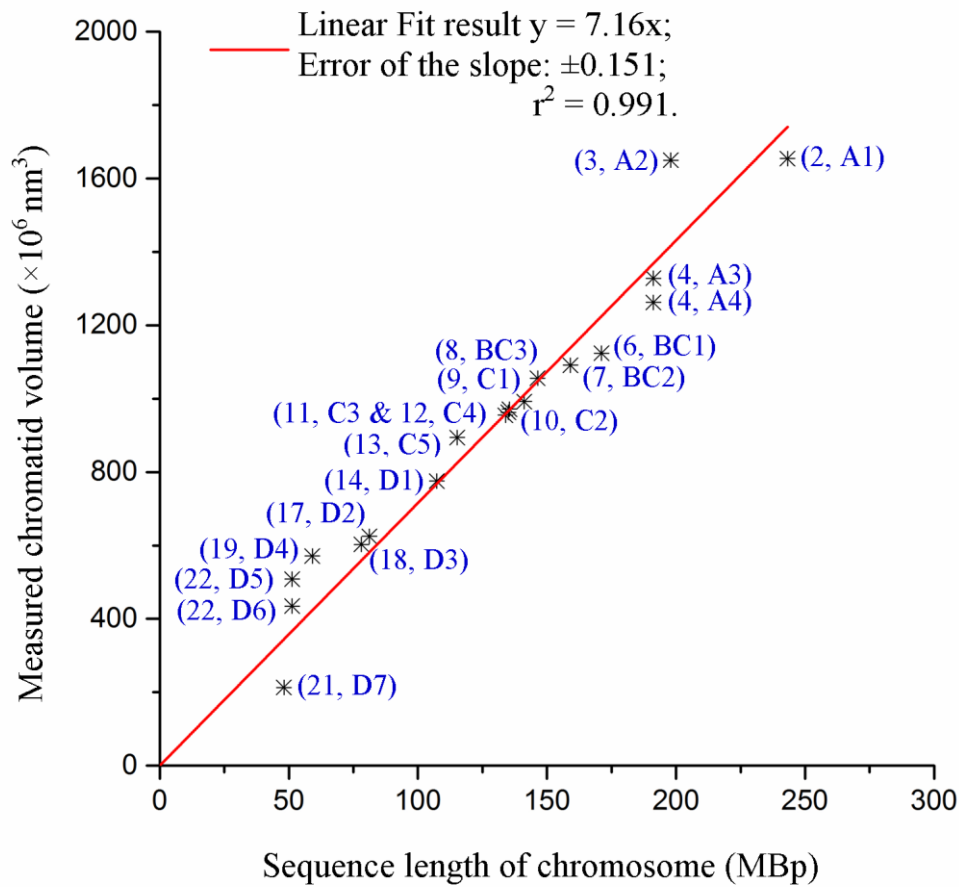


fig. S2. Second linear fitting of the chromatid volumes against their base pair numbers. Linear fitting of the measured (intact) chromatid volumes against the number of base pairs of the accordingly assigned chromosomes from the human genome sequence. In this case, the largest measured chromosome was assigned as chromosome 2, and the others were assigned accordingly as shown in Supplementary table S2.