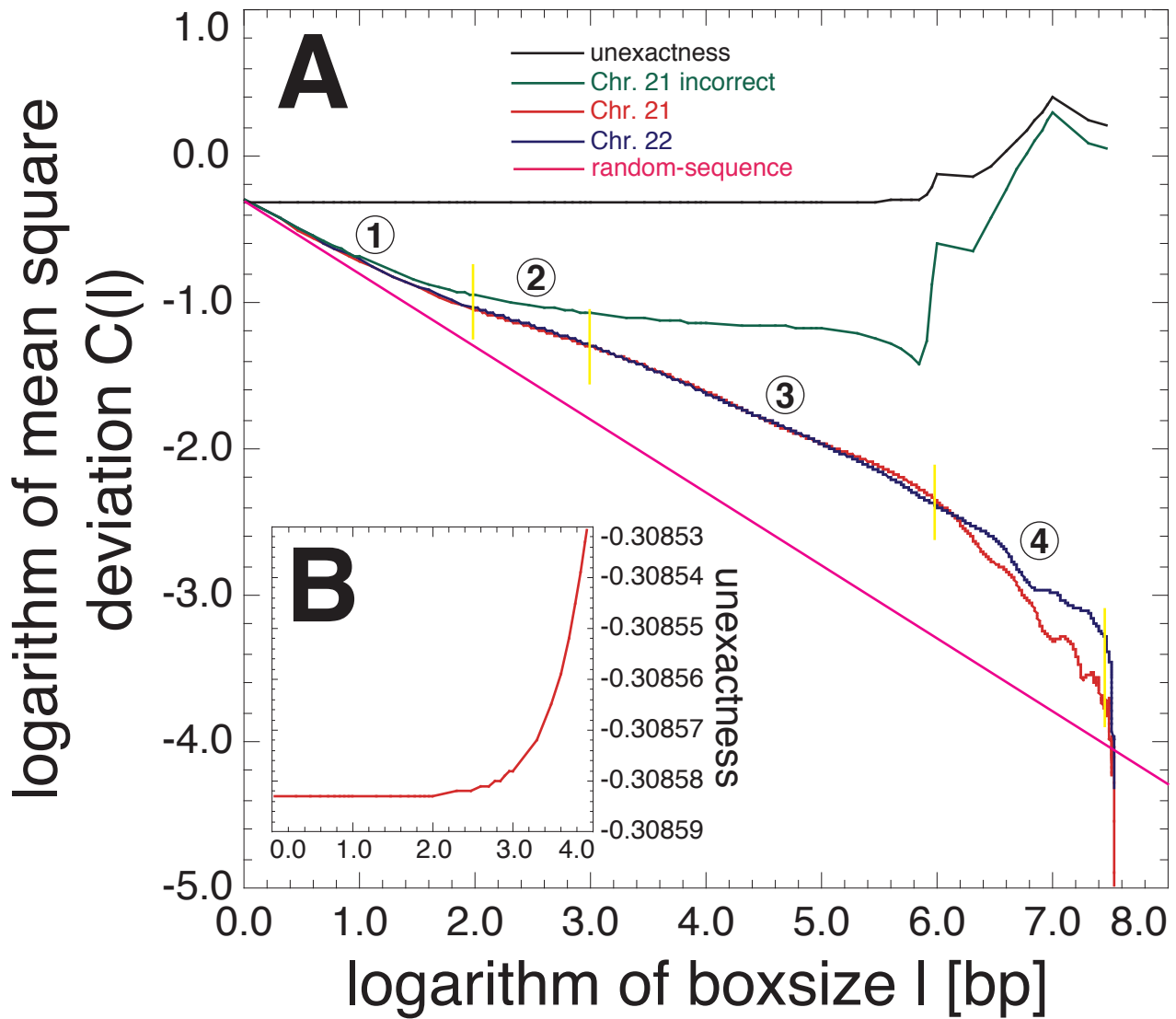


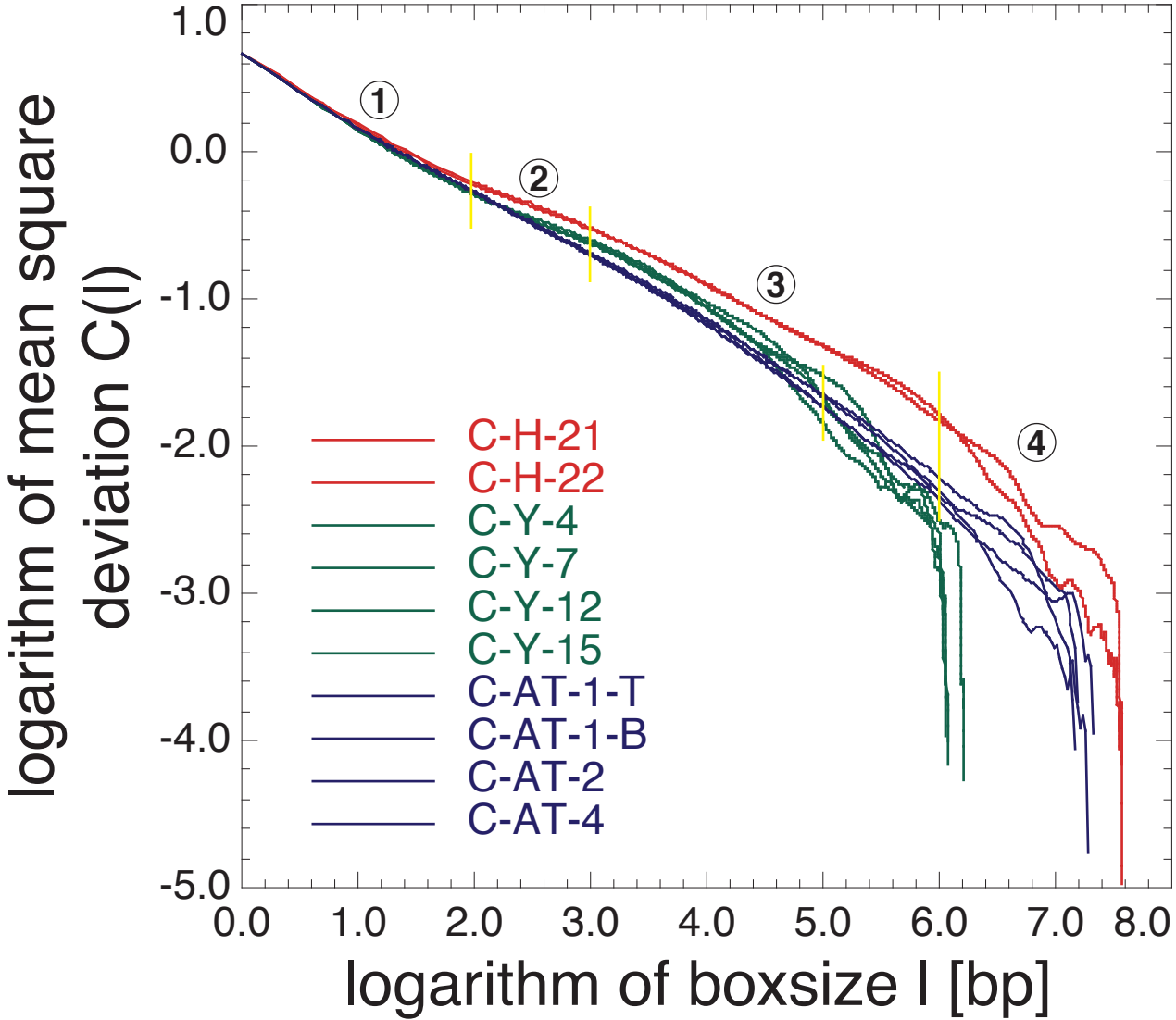
# Fractal analysis of the DNA sequence of human chromosomes

show non trivial long range correlations over  $10^6$  to  $7.5 \times 10^7$  base pairs, thus the genome seems to consist of full correlated sequences (FCS)



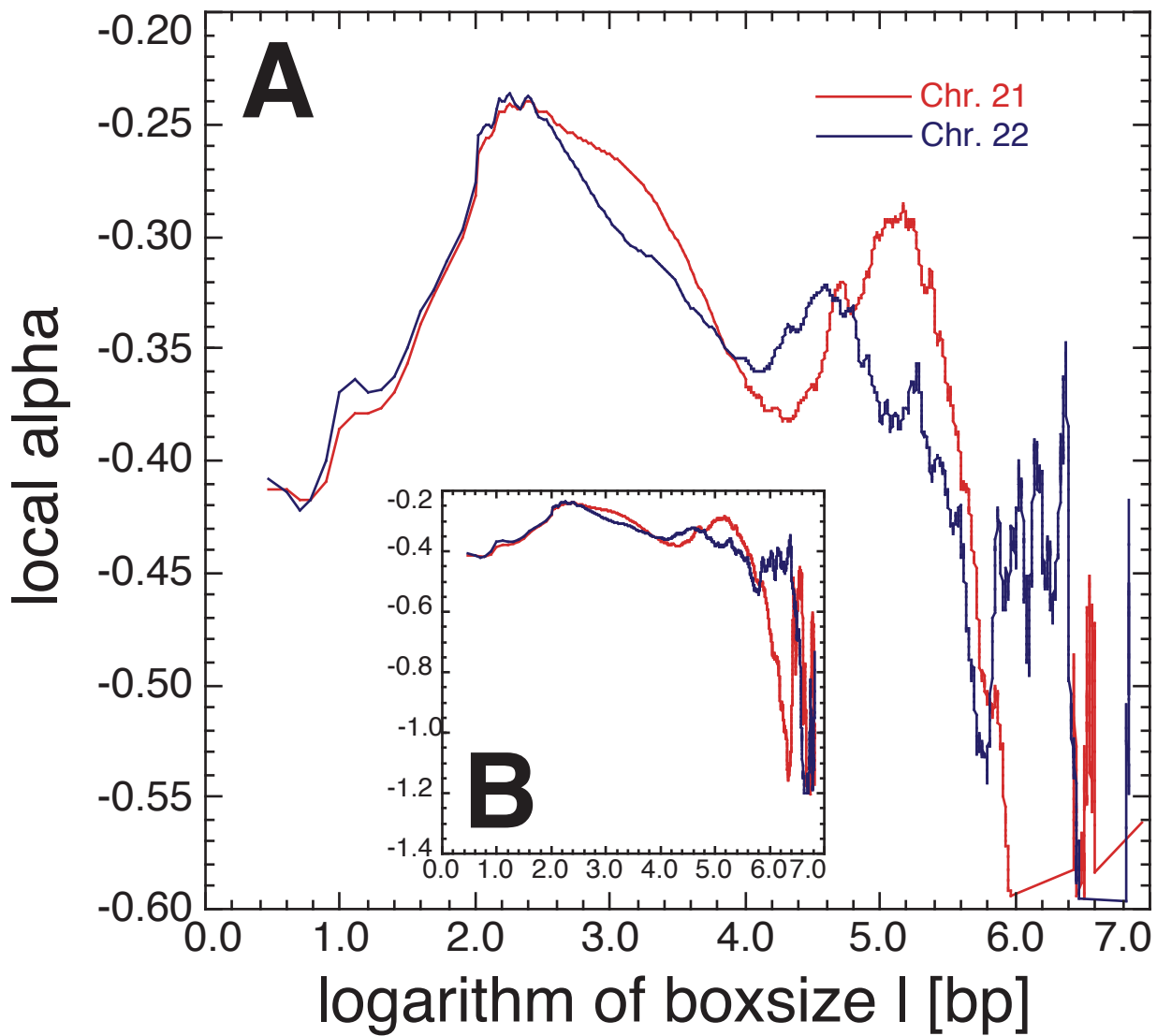
alpha	①	②	③	④
Chr. 21	-0.37084	-0.24881	-0.34588	-0.93132
Chr. 22	-0.36393	-0.25424	-0.36931	-0.63850

**Comparison of sequence correlations  
between different species  
Homo sapiens, Saccharomyces cerevisiae  
and Arabidopsis thaliana  
show differences in their full sequence correlations.**



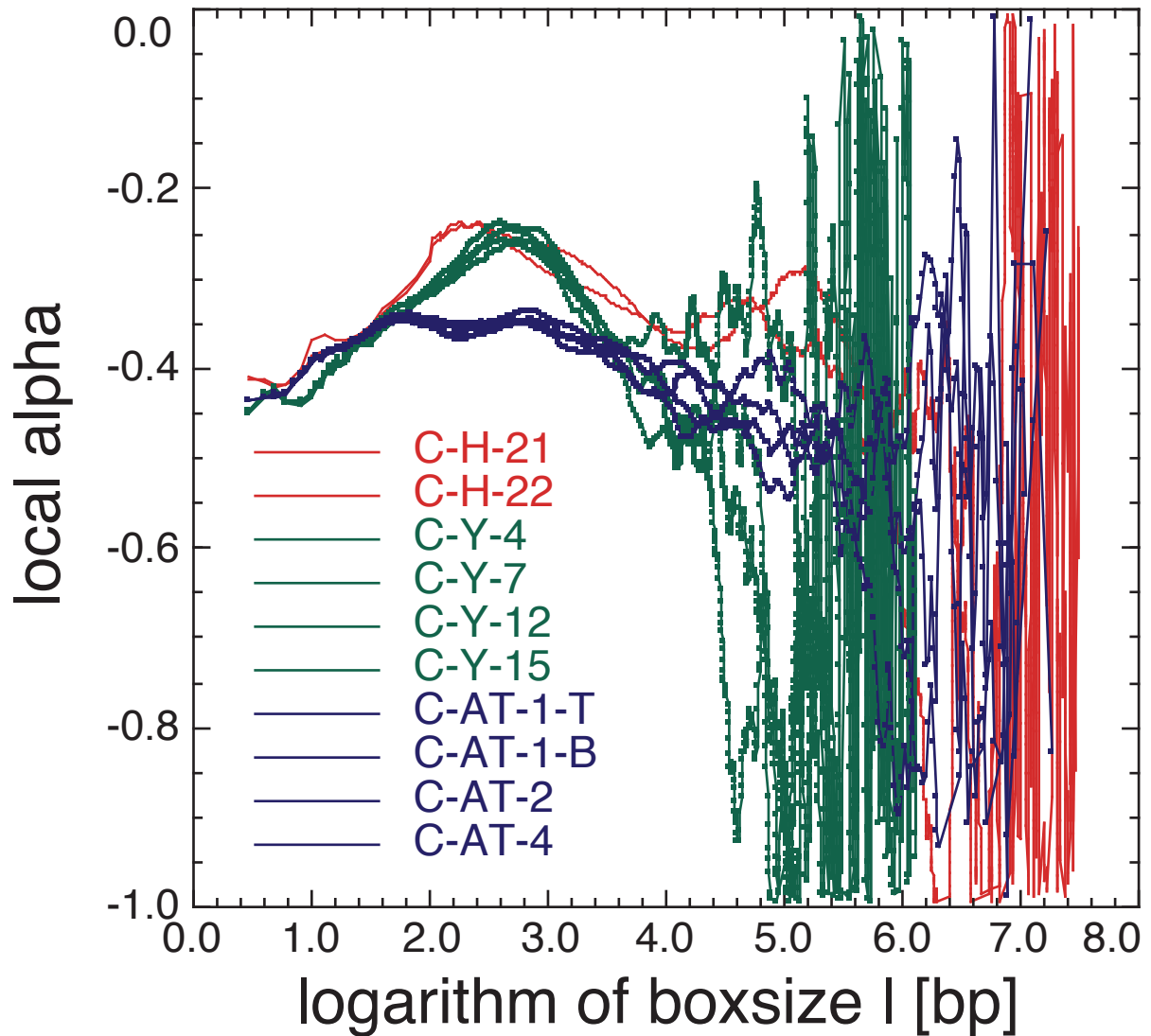
alpha	①	②	③
C-H-21	-0.37084	-0.24881	-0.34757
C-H-22	-0.36393	-0.25424	-0.37079
C-Y-4	-0.38630	-0.25659	-0.48930
C-Y-7	-0.38951	-0.27689	-0.49458
C-Y-12	-0.39239	-0.26320	-0.48487
C-Y-15	-0.39217	-0.27180	-0.53428
C-AT-1-T	-0.38014	-0.35539	-0.43333
C-AT-1-B	-0.38285	-0.35880	-0.44201
C-AT-2	-0.38075	-0.34596	-0.42440
C-AT-4	-0.38195	-0.35161	-0.44370

**A more accurate fractal analysis of full correlated sequences is achieved by the local determination of the correlation parameter alpha, through taking the derivative of C(l). Consequently alpha is a measure for the correlation on a scale of the respective boxsize.**



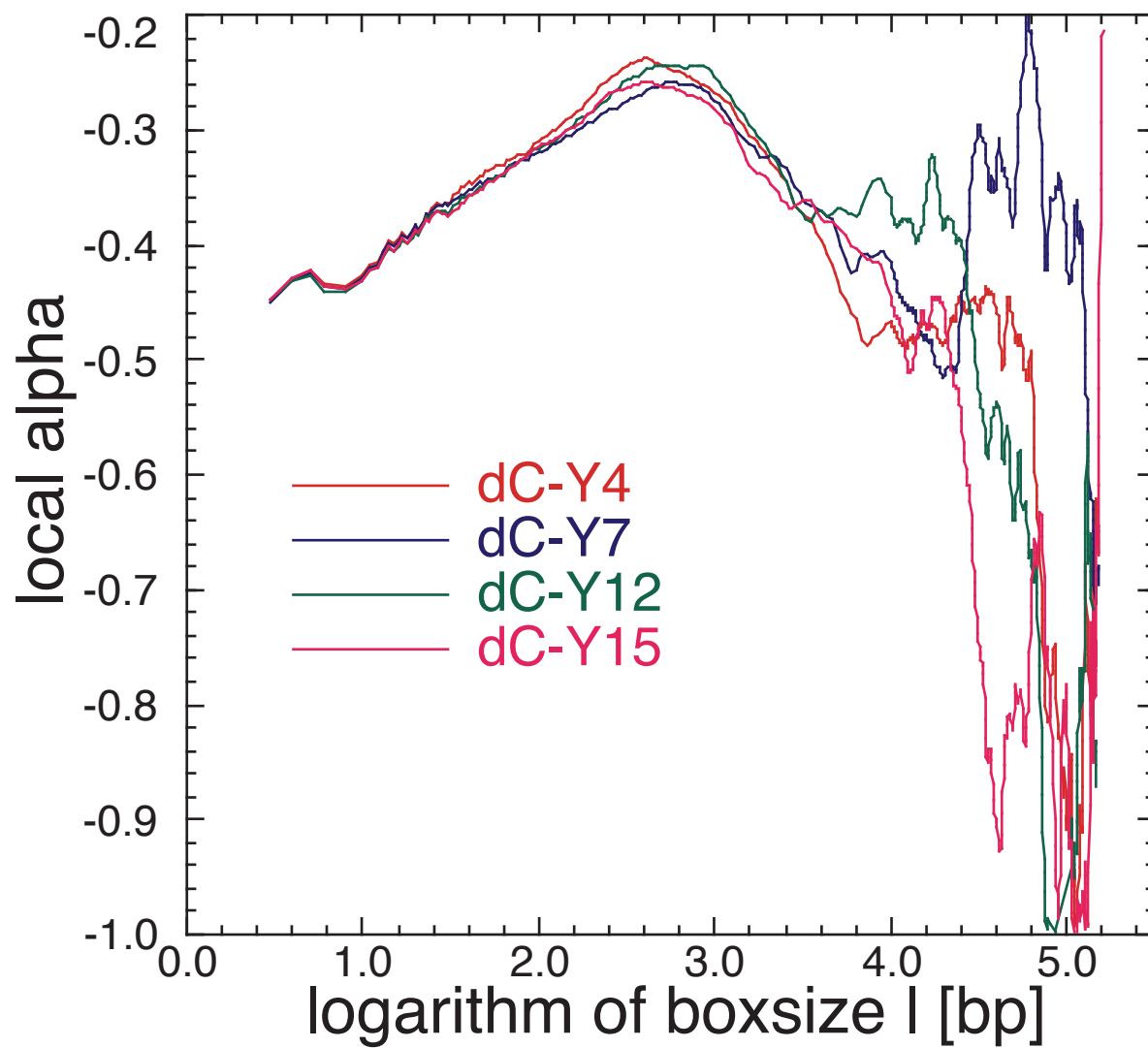
alpha	①	②	③	④
Chr. 21	-0.37084	-0.24881	-0.34588	-0.93132
Chr. 22	-0.36393	-0.25424	-0.36931	-0.63850

**Comparison of the local alpha for  
Homo sapiens, Saccharomyces cerevisiae  
and Arabidopsis thaliana  
reveals the predicted differences  
from C(I).**

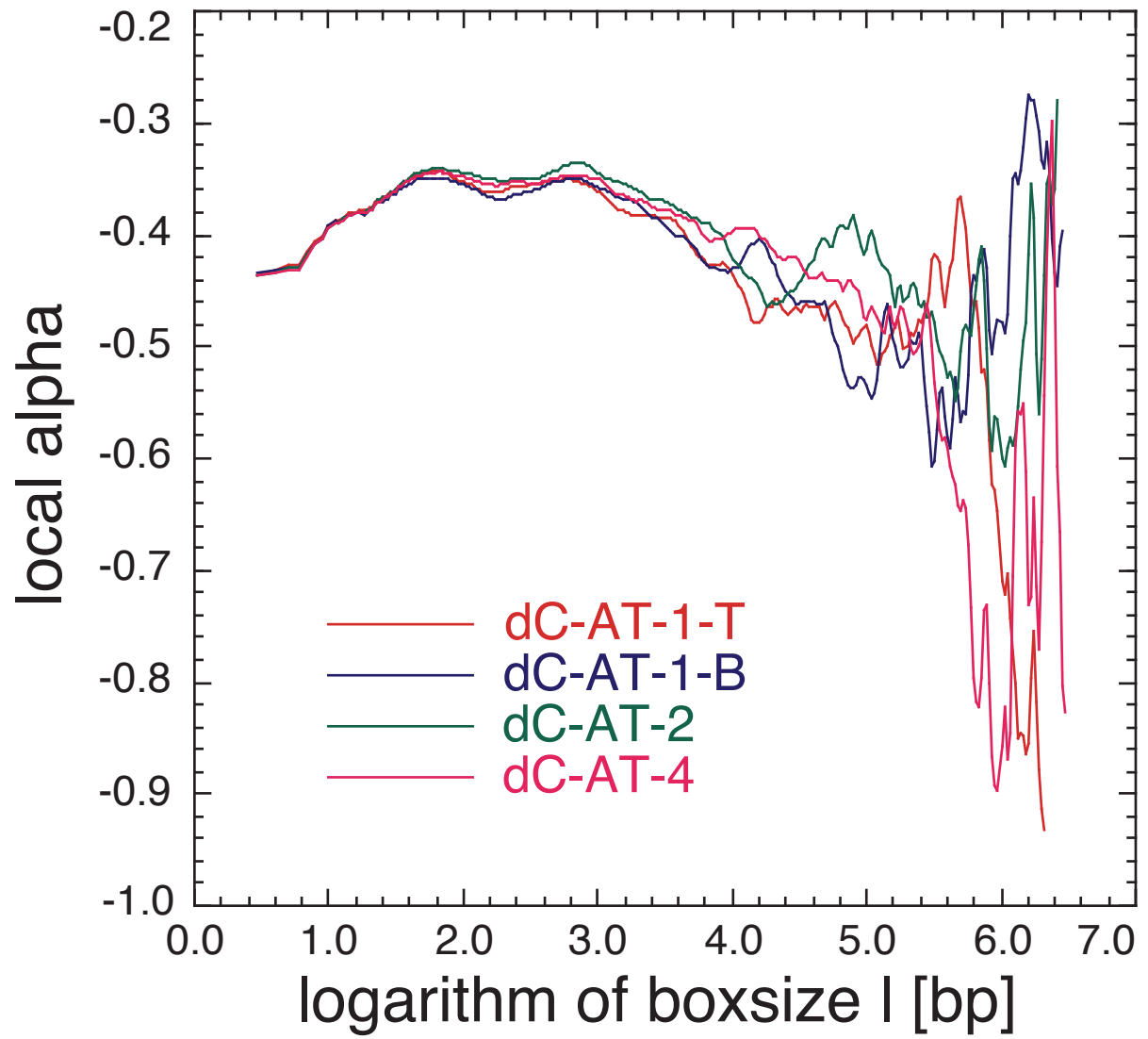


alpha	①	②	③
C-H-21	-0.37084	-0.24881	-0.34757
C-H-22	-0.36393	-0.25424	-0.37079
C-Y-4	-0.38630	-0.25659	-0.48930
C-Y-7	-0.38951	-0.27689	-0.49458
C-Y-12	-0.39239	-0.26320	-0.48487
C-Y-15	-0.39217	-0.27180	-0.53428
C-AT-1-T	-0.38014	-0.35539	-0.43333
C-AT-1-B	-0.38285	-0.35880	-0.44201
C-AT-2	-0.38075	-0.34596	-0.42440
C-AT-4	-0.38195	-0.35161	-0.44370

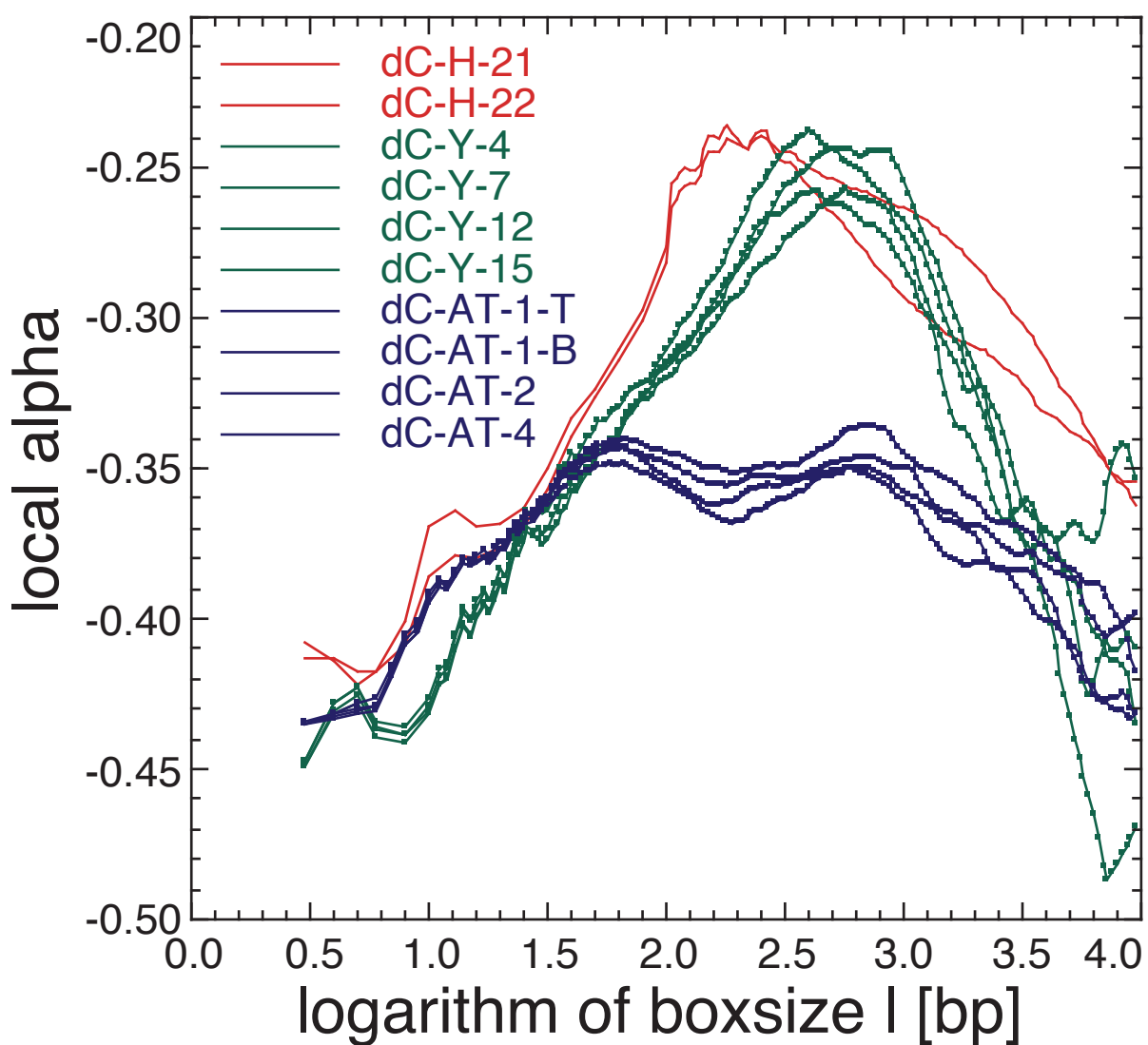
## Local alpha of *Saccharomyces cerevisiae*.



## Local alpha of *Arabidopsis thaliana*.



**The local alpha reveals distinct structures  
in the full correlated sequences.**







# Fractal Analysis of the DNA Sequence of Different Species

**Knoch, T. A.**

*Biophysics of Macromolecules Seminar, German Cancer Research Centre (DKFZ),  
Heidelberg, Germany, Oktober, 2001.*

Corresponding author email contact: TA.Knoch@taknoch.org

## Keywords:

Genome, genomics, genome organization, genome architecture, structural sequencing, architectural sequencing, systems genomics, coevolution, holistic genetics, genome mechanics, genome function, genetics, gene regulation, replication, transcription, repair, homologous recombination, simultaneous co-transfection, cell division, mitosis, metaphase, interphase, cell nucleus, nuclear structure, nuclear organization, chromatin density distribution, nuclear morphology, chromosome territories, subchromosomal domains, chromatin loop aggregates, chromatin rosettes, chromatin loops, chromatin fibre, chromatin density, persistence length, spatial distance measurement, histones, H1.0, H2A, H2B, H3, H4, mH2A1.2, DNA sequence, complete sequenced genomes, molecular transport, obstructed diffusion, anomalous diffusion, percolation, long-range correlations, fractal analysis, scaling analysis, exact yard-stick dimension, box-counting dimension, lacunarity dimension, local nuclear dimension, nuclear diffuseness, parallel super computing, grid computing, volunteer computing, Brownian Dynamics, Monte Carlo, fluorescence in situ hybridization, confocal laser scanning microscopy, fluorescence correlation spectroscopy, super resolution microscopy, spatial precision distance microscopy, autofluorescent proteins, CFP, GFP, YFP, DsRed, fusionprotein, in vivo labelling.

## *Literature References*

- Knoch, T. A.** Dreidimensionale Organisation von Chromosomen-Domänen in Simulation und Experiment. (Three-dimensional organization of chromosome domains in simulation and experiment.) *Diploma Thesis*, Faculty for Physics and Astronomy, Ruperto-Carola University, Heidelberg, Germany, 1998, and TAK Press, Tobias A. Knoch, Mannheim, Germany, ISBN 3-00-010685-5 and ISBN 978-3-00-010685-9 (soft cover, 2nd ed.), ISBN 3-00-035857-9 and ISBN 978-3-00-0358857-0 (hard cover, 2nd ed.), ISBN 3-00-035858-7, and ISBN 978-3-00-035858-6 (DVD, 2nd ed.), 1998.
- Knoch, T. A.,** Münkkel, C. & Langowski, J. Three-dimensional organization of chromosome territories and the human cell nucleus - about the structure of a self replicating nano fabrication site. *Foresight Institute - Article Archive*, Foresight Institute, Palo Alto, CA, USA, <http://www.foresight.org>, 1- 6, 1998.

- Knoch, T. A.**, Münkkel, C. & Langowski, J. Three-Dimensional Organization of Chromosome Territories and the Human Interphase Nucleus. *High Performance Scientific Supercomputing*, editor Wilfried Juling, Scientific Supercomputing Center (SSC) Karlsruhe, University of Karlsruhe (TH), 27- 29, 1999.
- Knoch, T. A.**, Münkkel, C. & Langowski, J. Three-dimensional organization of chromosome territories in the human interphase nucleus. *High Performance Computing in Science and Engineering 1999*, editors Krause, E. & Jäger, W., High-Performance Computing Center (HLRS) Stuttgart, University of Stuttgart, Springer Berlin-Heidelberg-New York, ISBN 3-540-66504-8, 229-238, 2000.
- Bestvater, F., **Knoch, T. A.**, Langowski, J. & Spiess, E. GFP-Walking: Artificial construct conversions caused by simultaneous cotransfection. *BioTechniques* 32(4), 844-854, 2002.
- Knoch, T. A. (editor)**, Backes, M., Baumgärtner, V., Eysel, G., Fehrenbach, H., Göker, M., Hampl, J., Hampl, U., Hartmann, D., Hitzelberger, H., Nambena, J., Rehberg, U., Schmidt, S., Weber, A., & Weidemann, T. Humanökologische Perspektiven Wechsel - Festschrift zu Ehren des 70. Geburtstags von Prof. Dr. Kurt Egger. Human Ecology Working Group, Ruperto-Carola University of Heidelberg, Heidelberg, Germany, 2002.
- Knoch, T. A.** Approaching the three-dimensional organization of the human genome: structural-, scaling- and dynamic properties in the simulation of interphase chromosomes and cell nuclei, long- range correlations in complete genomes, *in vivo* quantification of the chromatin distribution, construct conversions in simultaneous co-transfections. *Dissertation*, Ruperto-Carola University, Heidelberg, Germany, and TAK†Press, Tobias A. Knoch, Mannheim, Germany, ISBN 3-00-009959-X and ISBN 978-3-00-009959-5 (soft cover, 3rd ed.), ISBN 3-00-009960-3 and ISBN 978-3-00-009960-1 (hard cover, 3rd ed.), ISBN 3-00-035856-9 and ISBN 978-3-00-010685-9 (DVD, 3rd ed.) 2002.
- Knoch, T. A.** Towards a holistic understanding of the human genome by determination and integration of its sequential and three-dimensional organization. *High Performance Computing in Science and Engineering 2003*, editors Krause, E., Jäger, W. & Resch, M., High-Performance Computing Center (HLRS) Stuttgart, University of Stuttgart, Springer Berlin-Heidelberg-New York, ISBN 3- 540-40850-9, 421-440, 2003.
- Wachsmuth, M., Weidemann, T., Müller, G., Urs W. Hoffmann-Rohrer, **Knoch, T. A.**, Waldeck, W. & Langowski, J. Analyzing intracellular binding and diffusion with continuous fluorescence photobleaching. *Biophys. J.* 84(5), 3353-3363, 2003.
- Weidemann, T., Wachsmuth, M., **Knoch, T. A.**, Müller, G., Waldeck, W. & Langowski, J. Counting nucleosomes in living cells with a combination of fluorescence correlation spectroscopy and confocal imaging. *J. Mol. Biol.* 334(2), 229-240, 2003.