

CONTENIDO EN GC EN EL GENOMA HUMANO

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Laboratorio Genómica Evolutiva

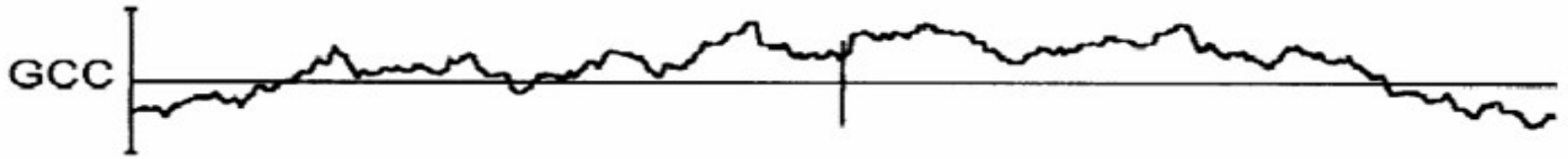
Departamento Biología Celular y Molecular

Facultad de Ciencias

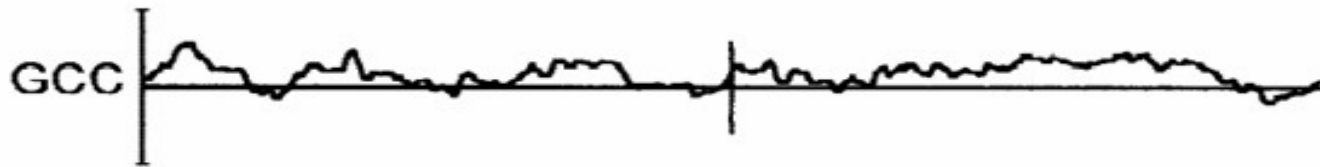
Uruguay

hmusto@gmail.com

Variación en el contenido en GC% en procariontas



E. coli



Synechocystis sp.

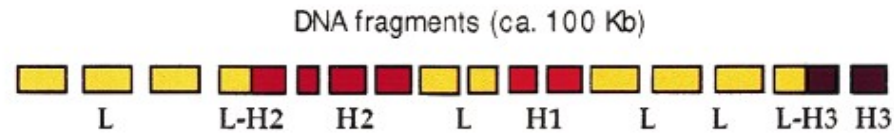


M. jannaschii

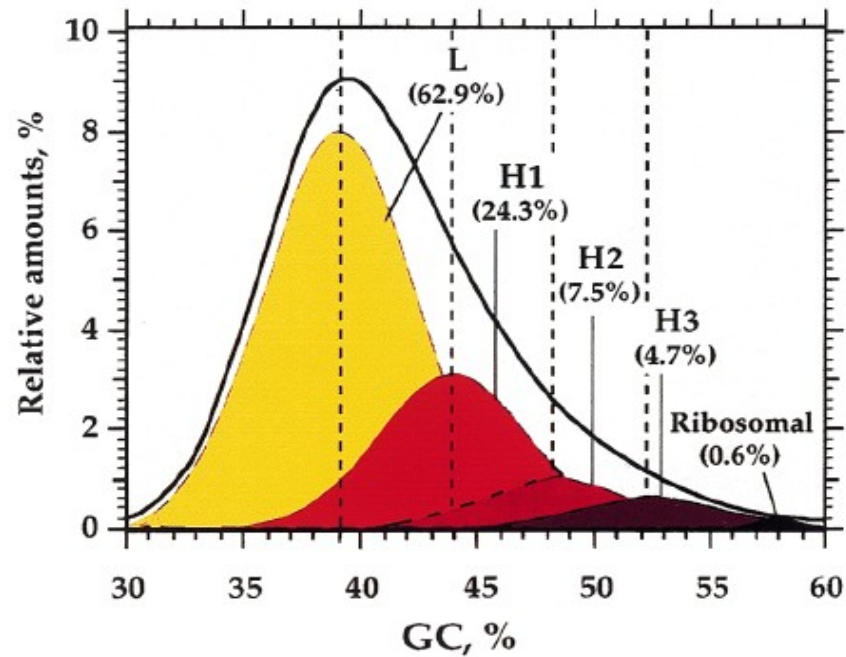
ISOCHORES >300 Kb

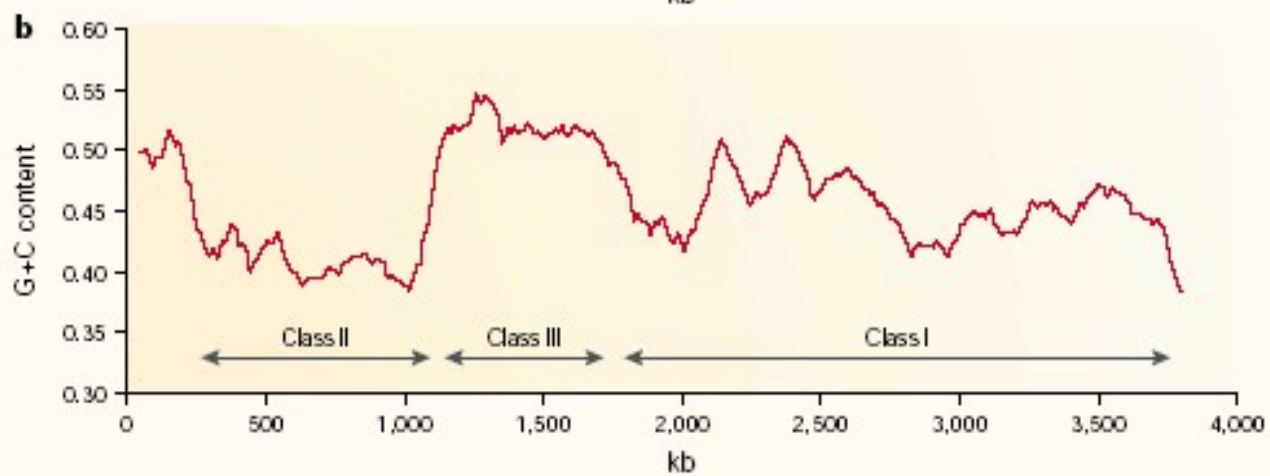
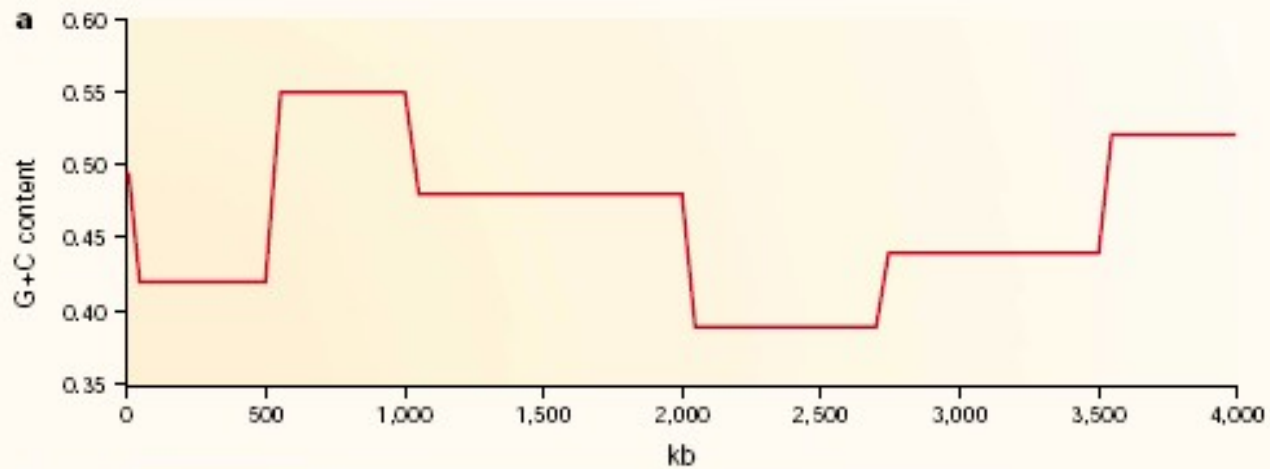


Degradation during DNA preparation

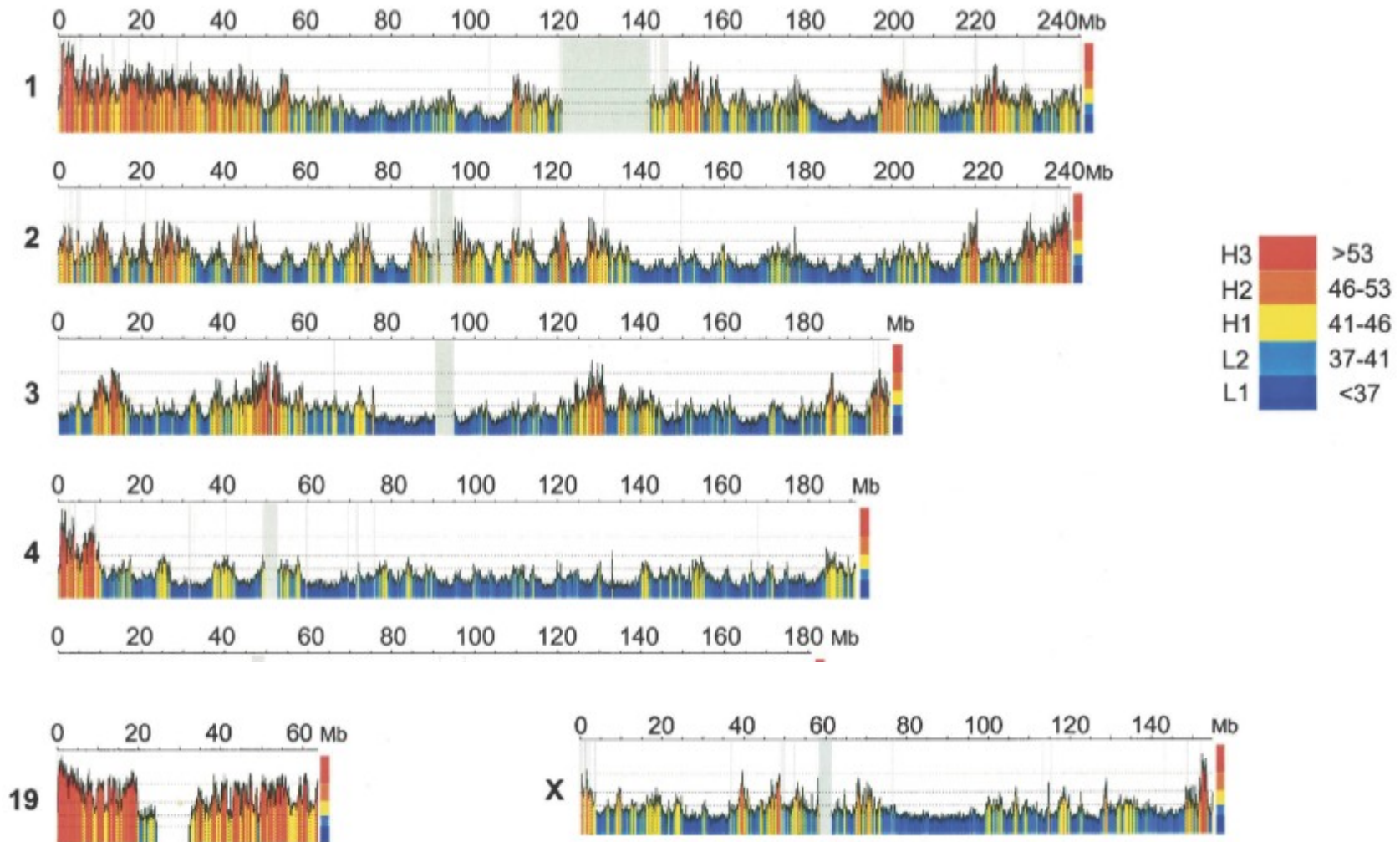


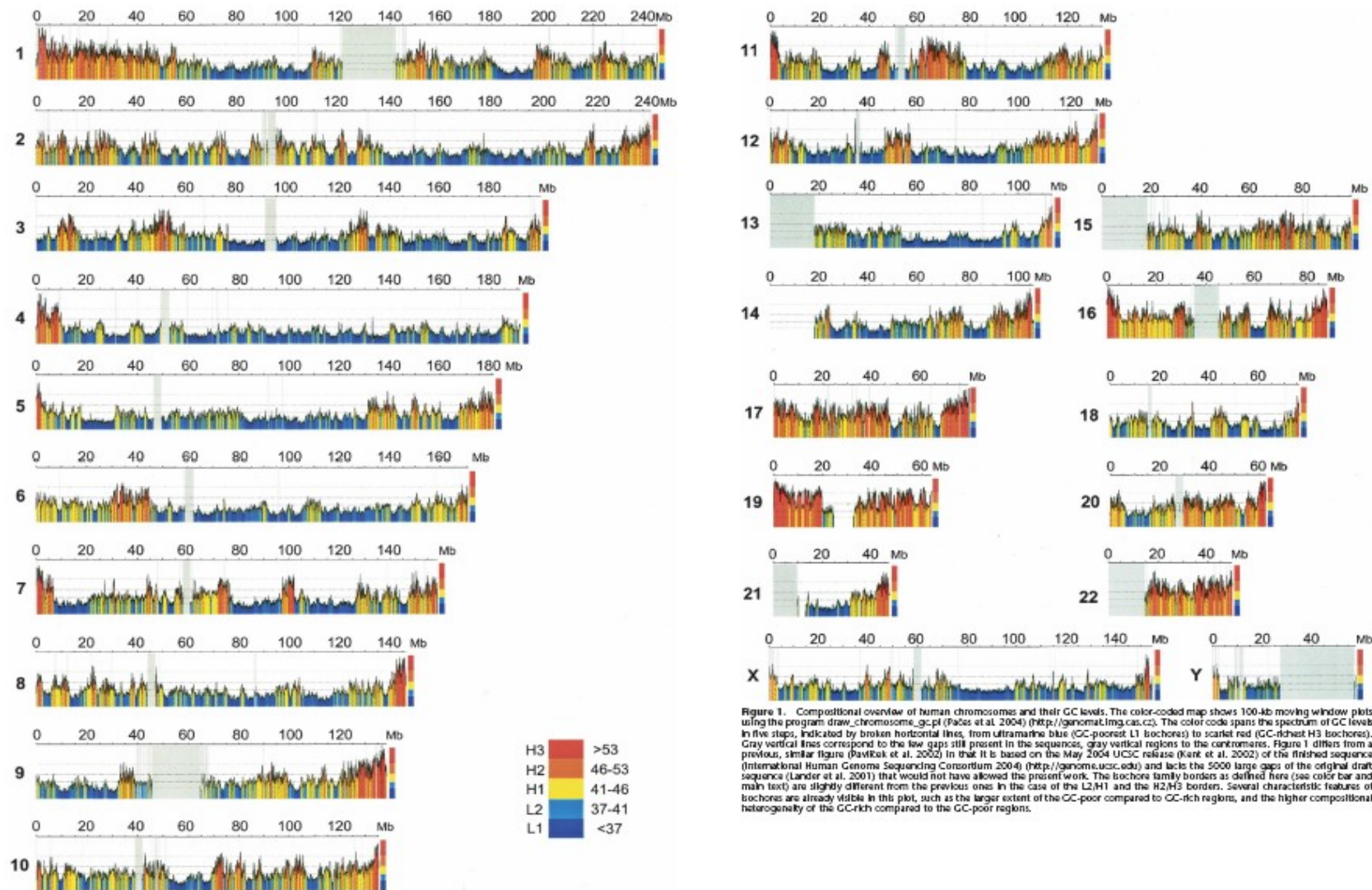
GC range 30-60%



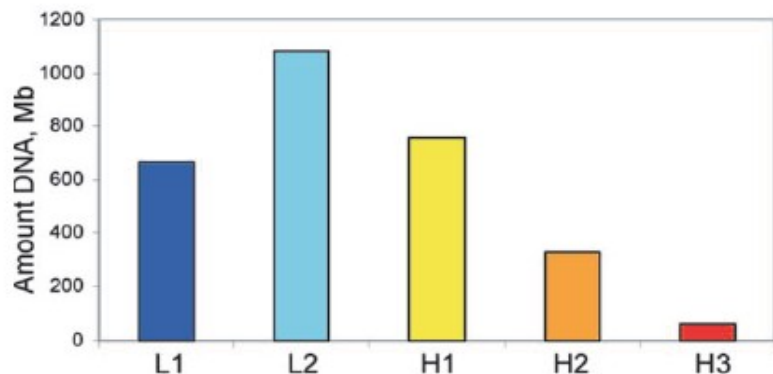


Visualización de los isocoros por métodos computacionales

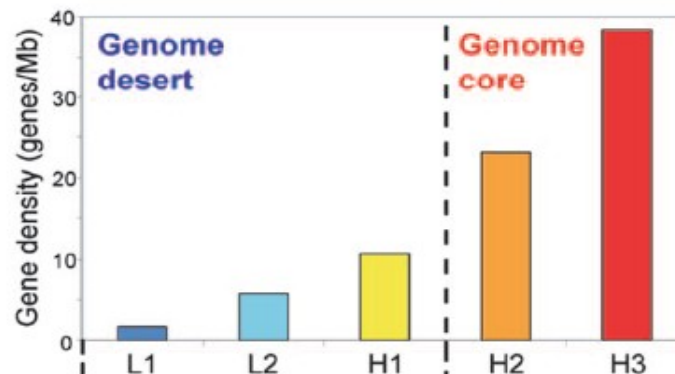




Isochore families



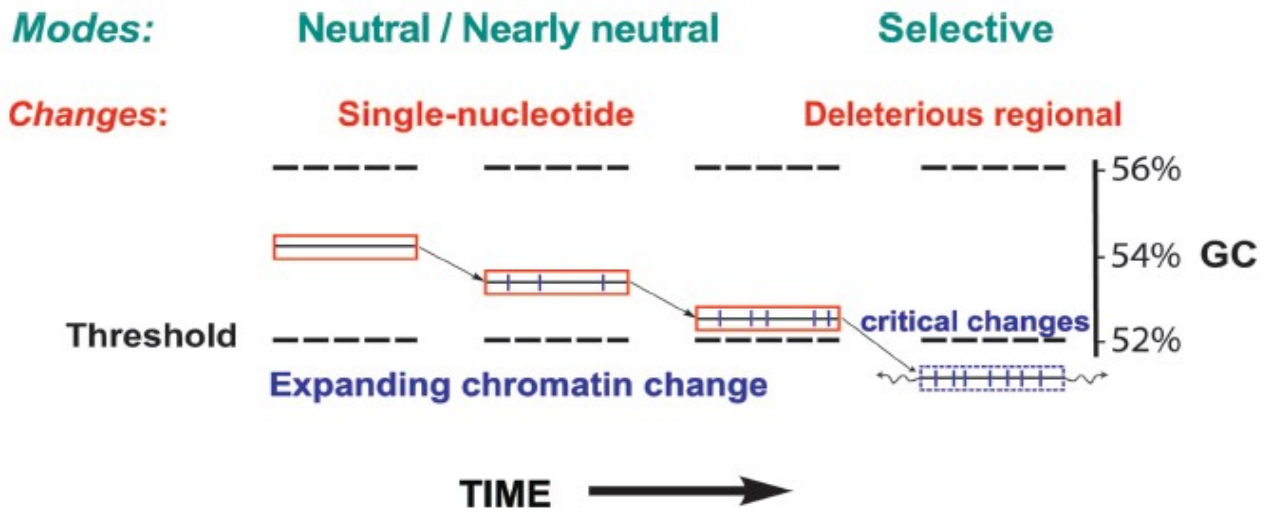
Gene distribution



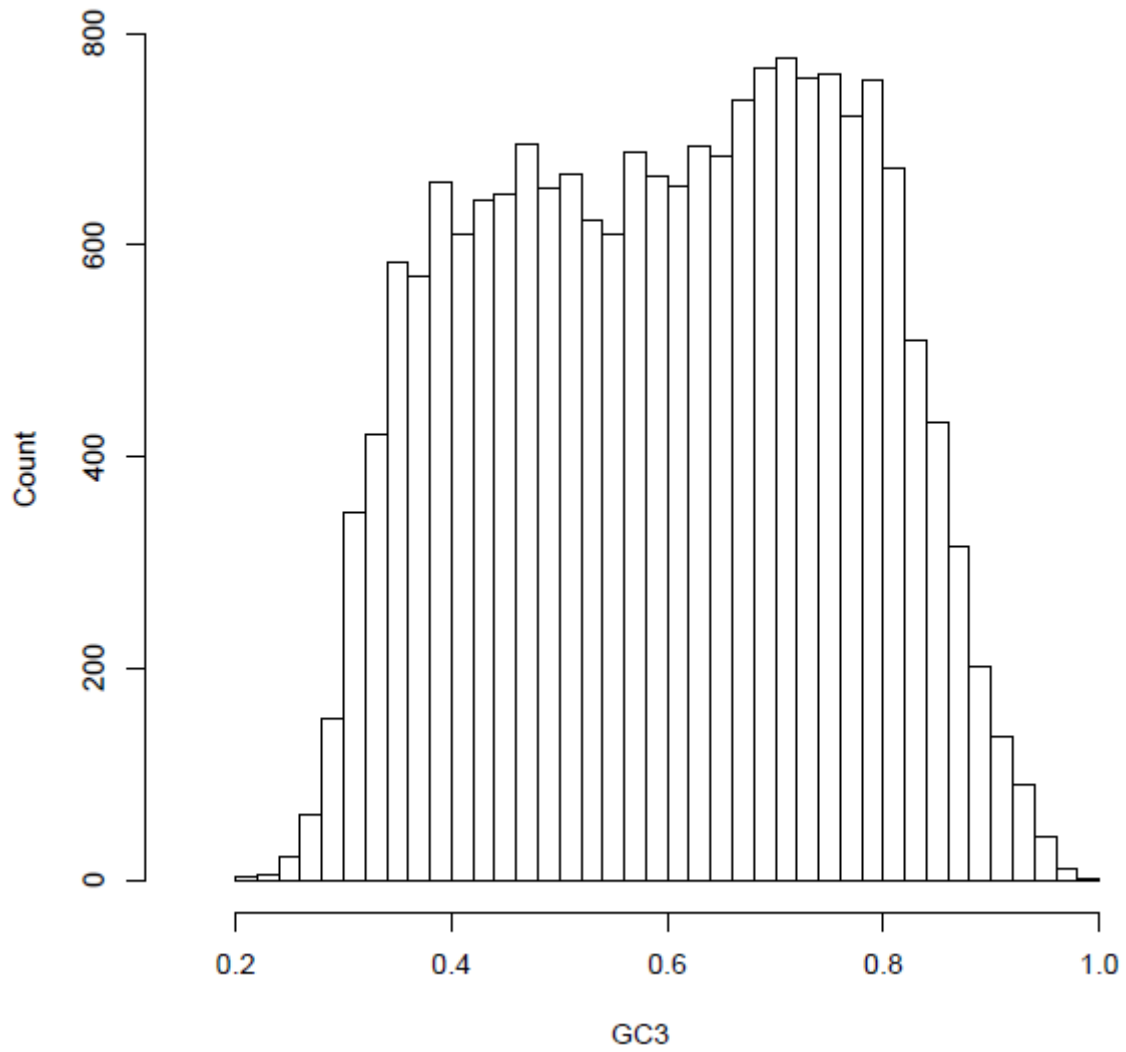
Increasing GC →

Correlations of gene spaces with structures and functions

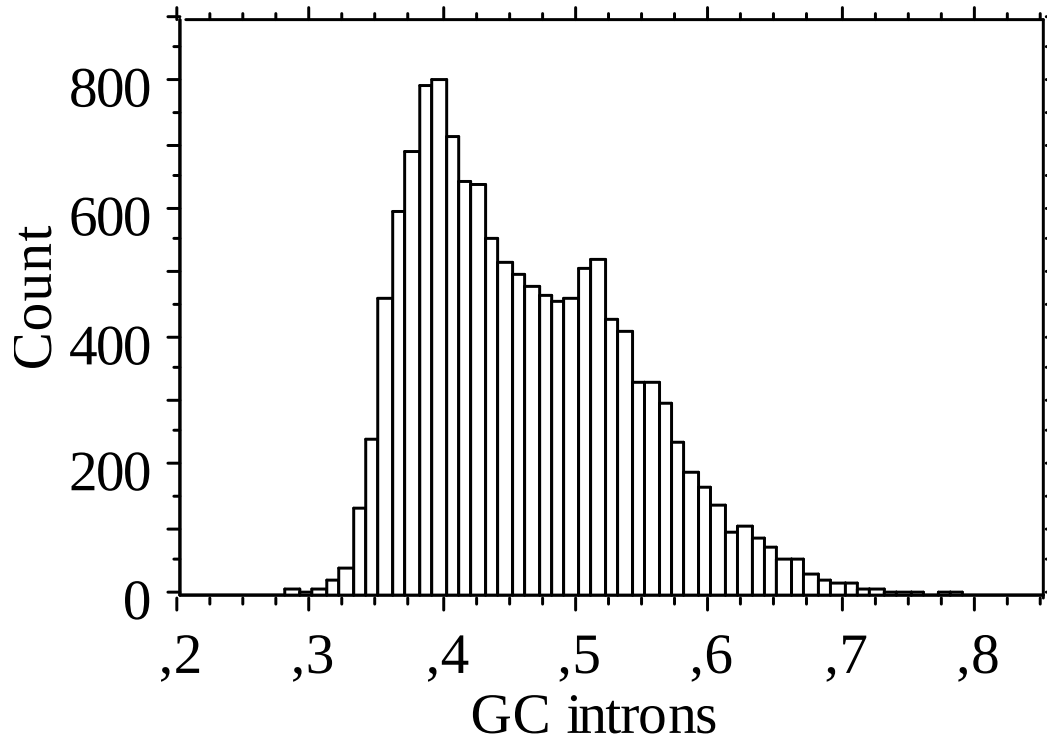
Intron, UTR size	Large	Small
Chromatin structure	Closed	Open
GC heterogeneity	Low	High
SINEs	Low	High
LINES	High	Low
Gene expression	Low	High
Replication timing	Late	Early
Recombination	Low	High



GC3 of CDS (All Chromosomes) n=19,046

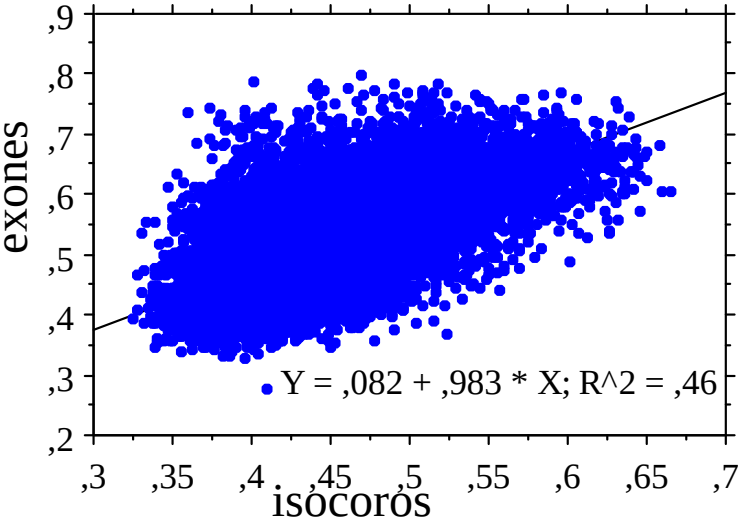


Contenido en GC de los intrones humanos

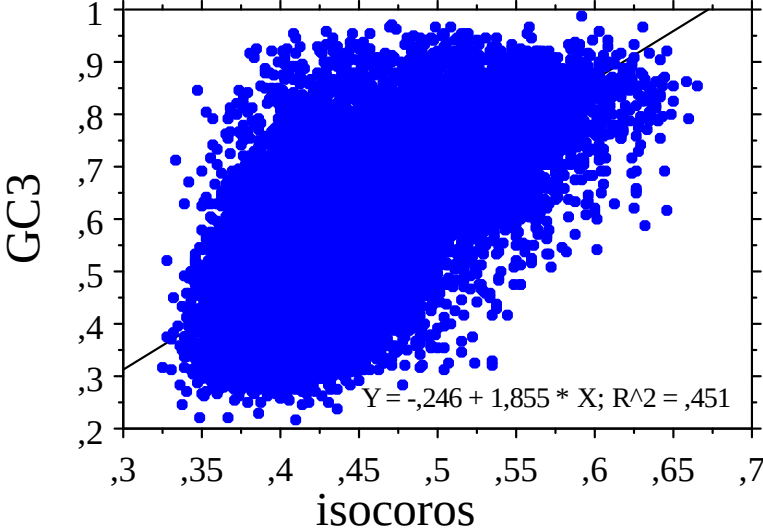


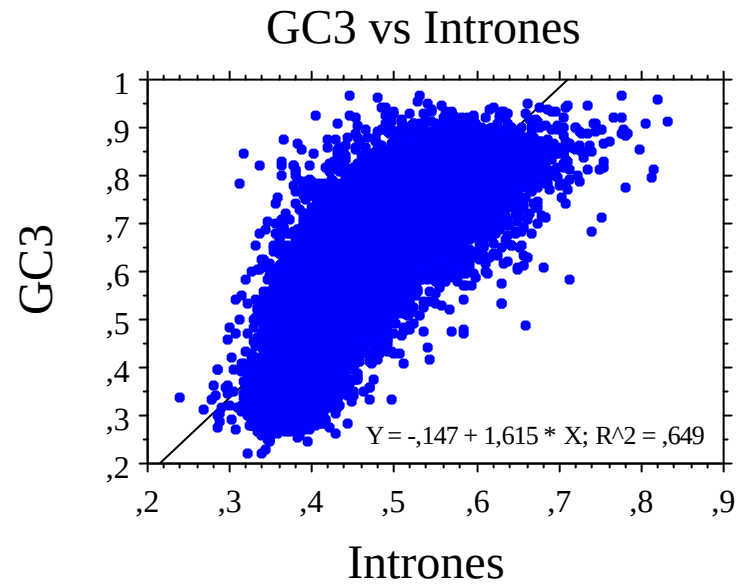
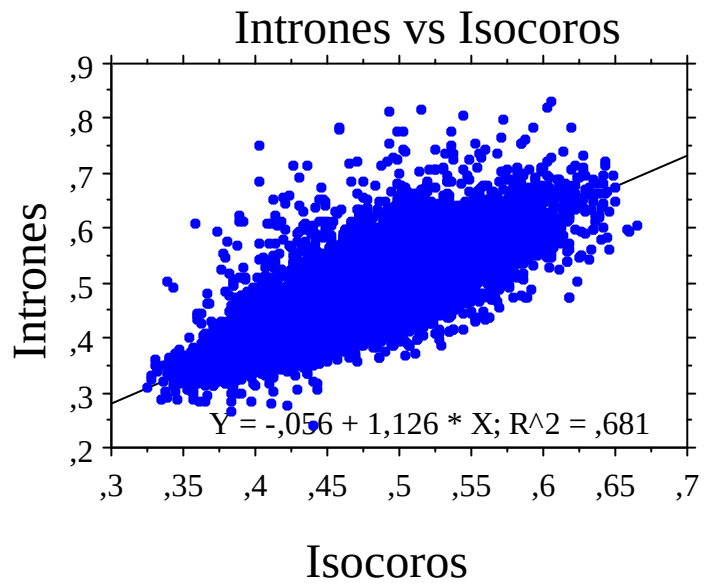
CORRELACIONES COMPOSICIONALES

GC exones vs Isocoros

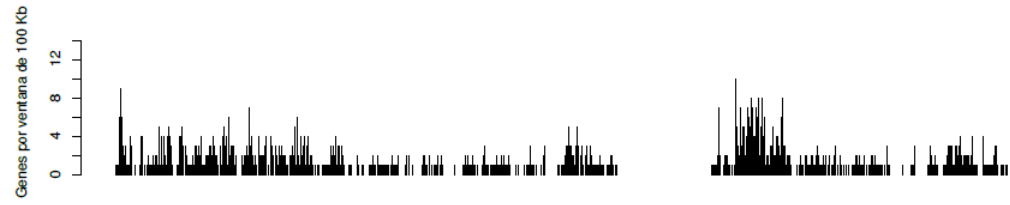
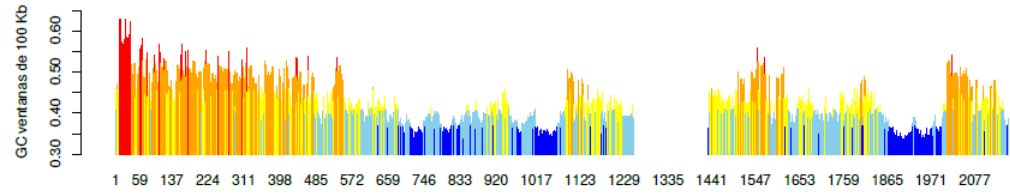


GC3 vs Isocoros

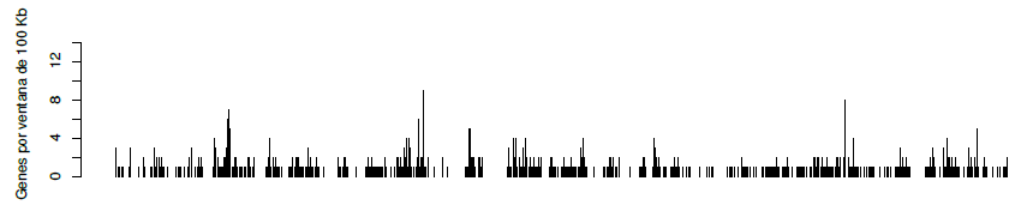
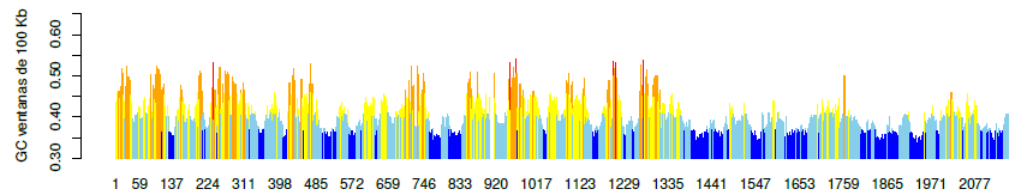




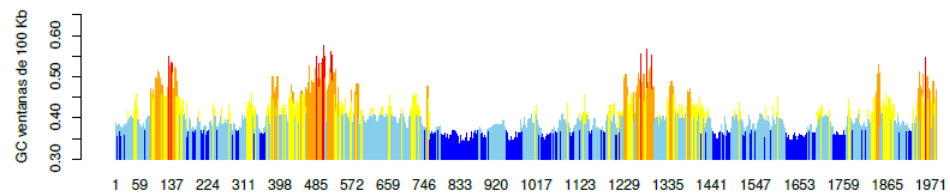
Chr 1



Chr 2

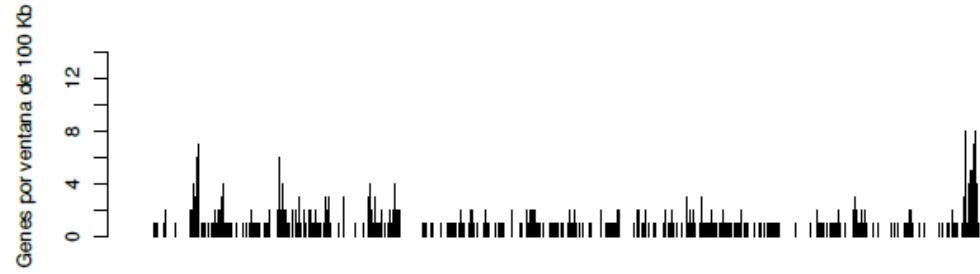
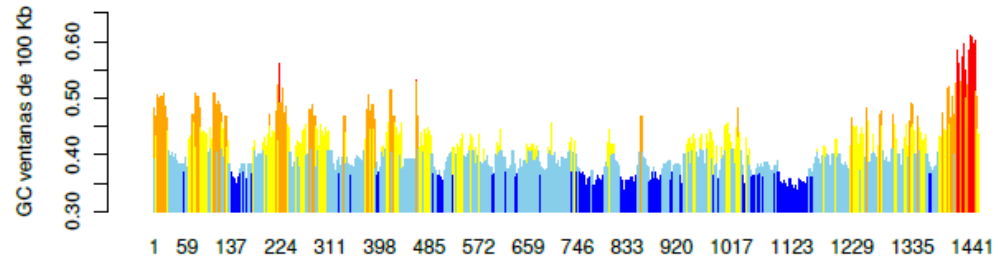


Chr 3

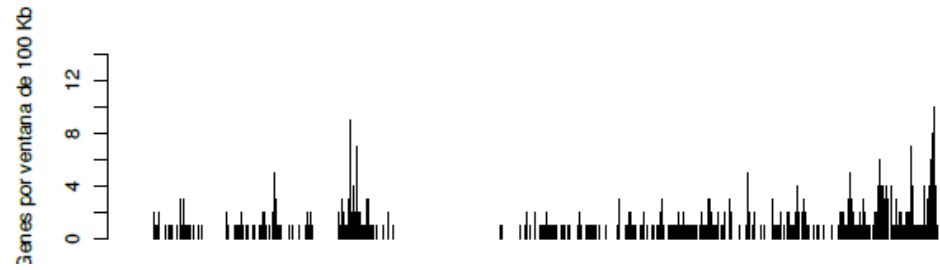
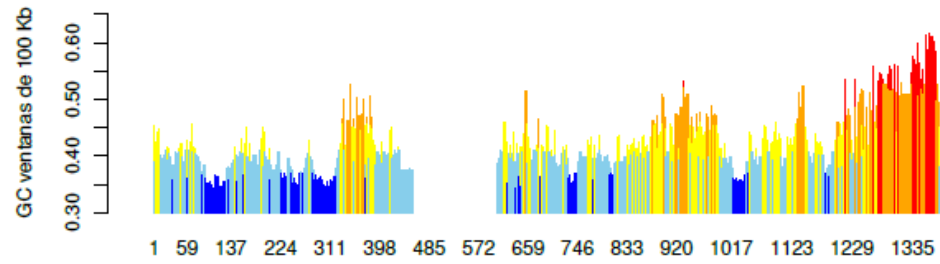


0 Kb

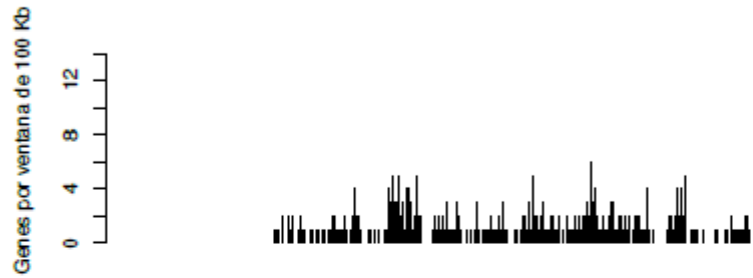
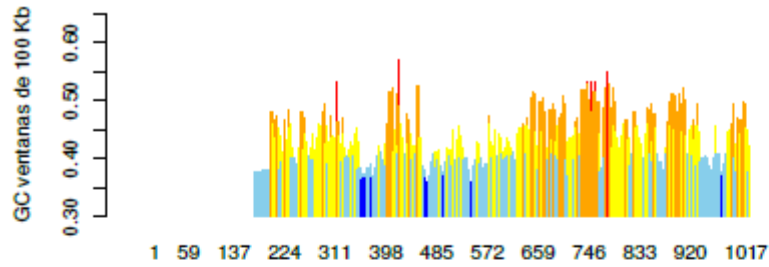
Chr 8



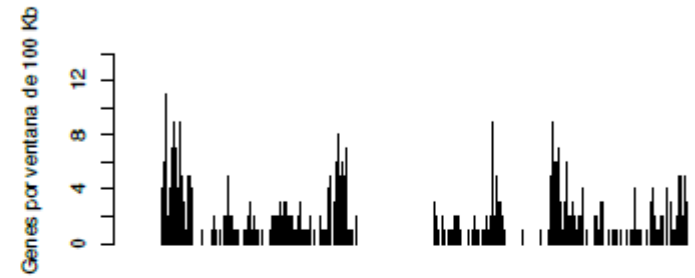
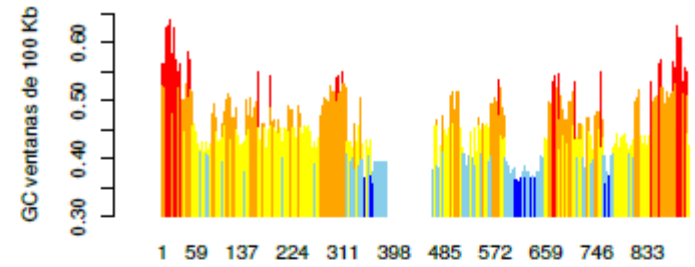
Chr 9



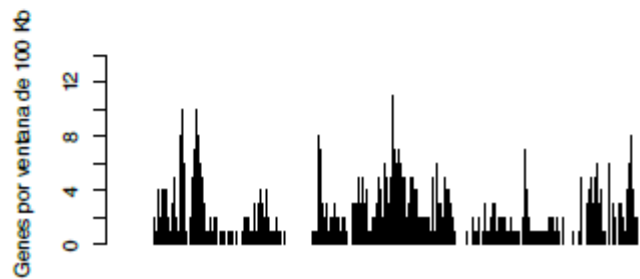
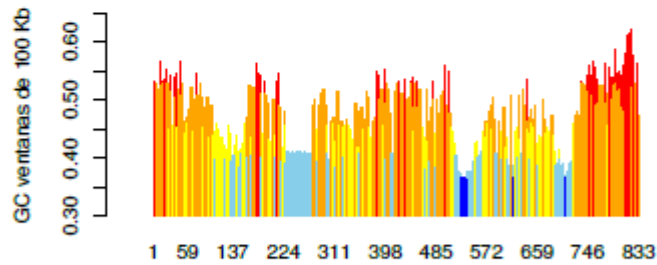
Chr 15



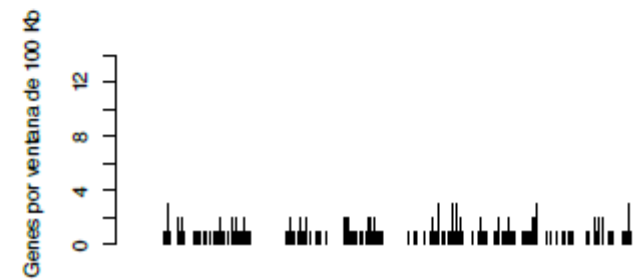
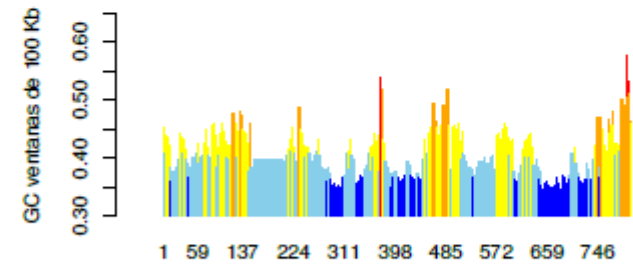
Chr 16



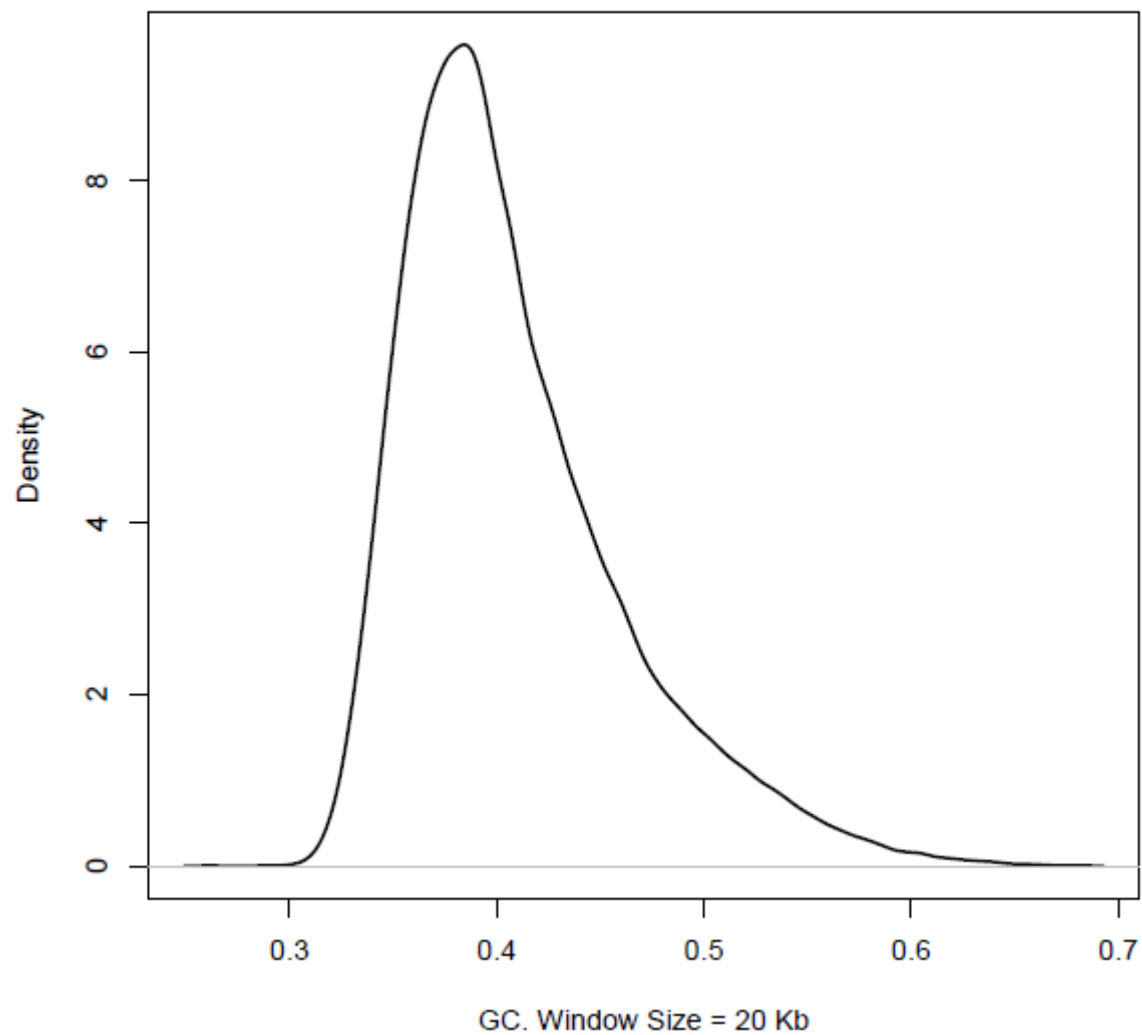
Chr 17



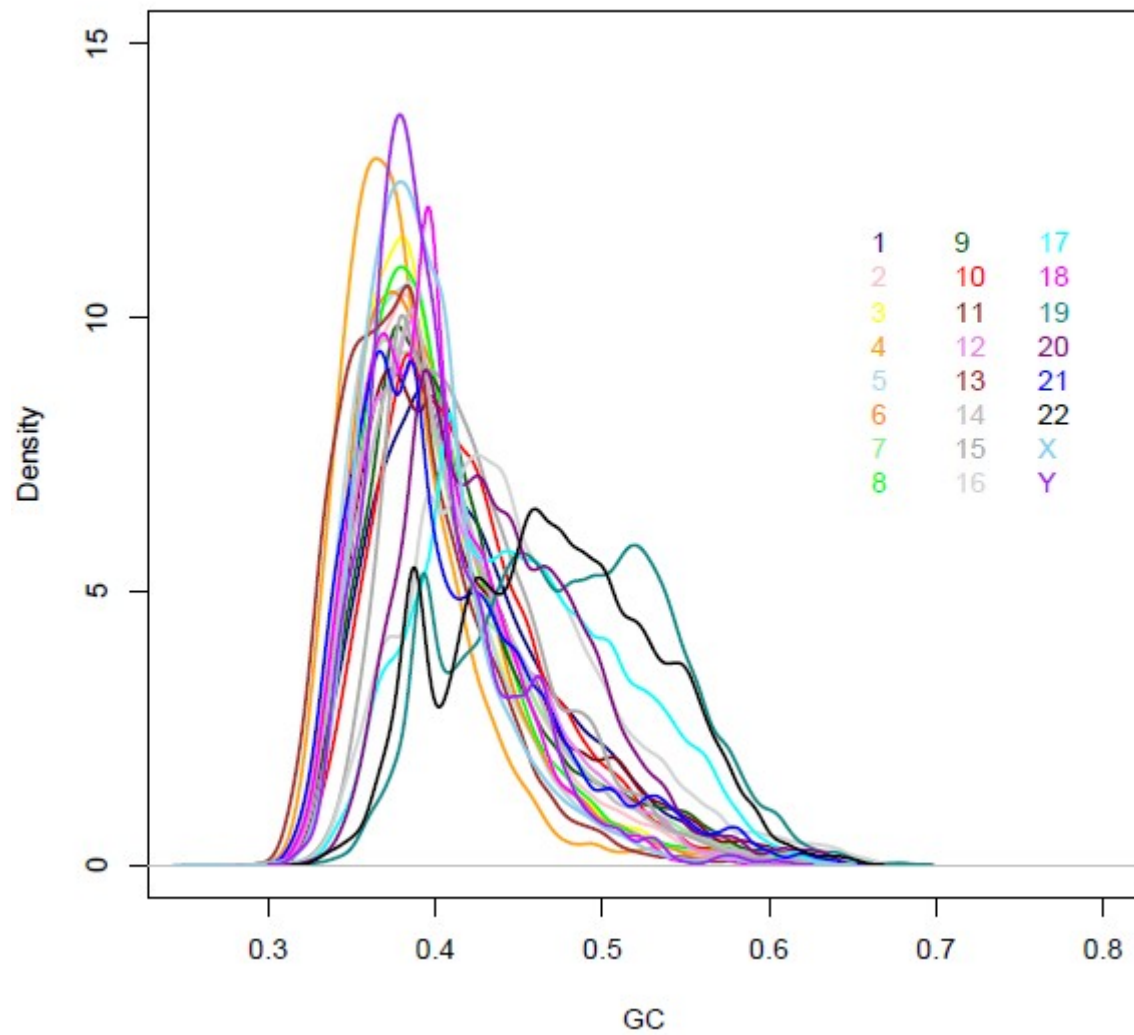
Chr 18



Human Genome: GC distribution

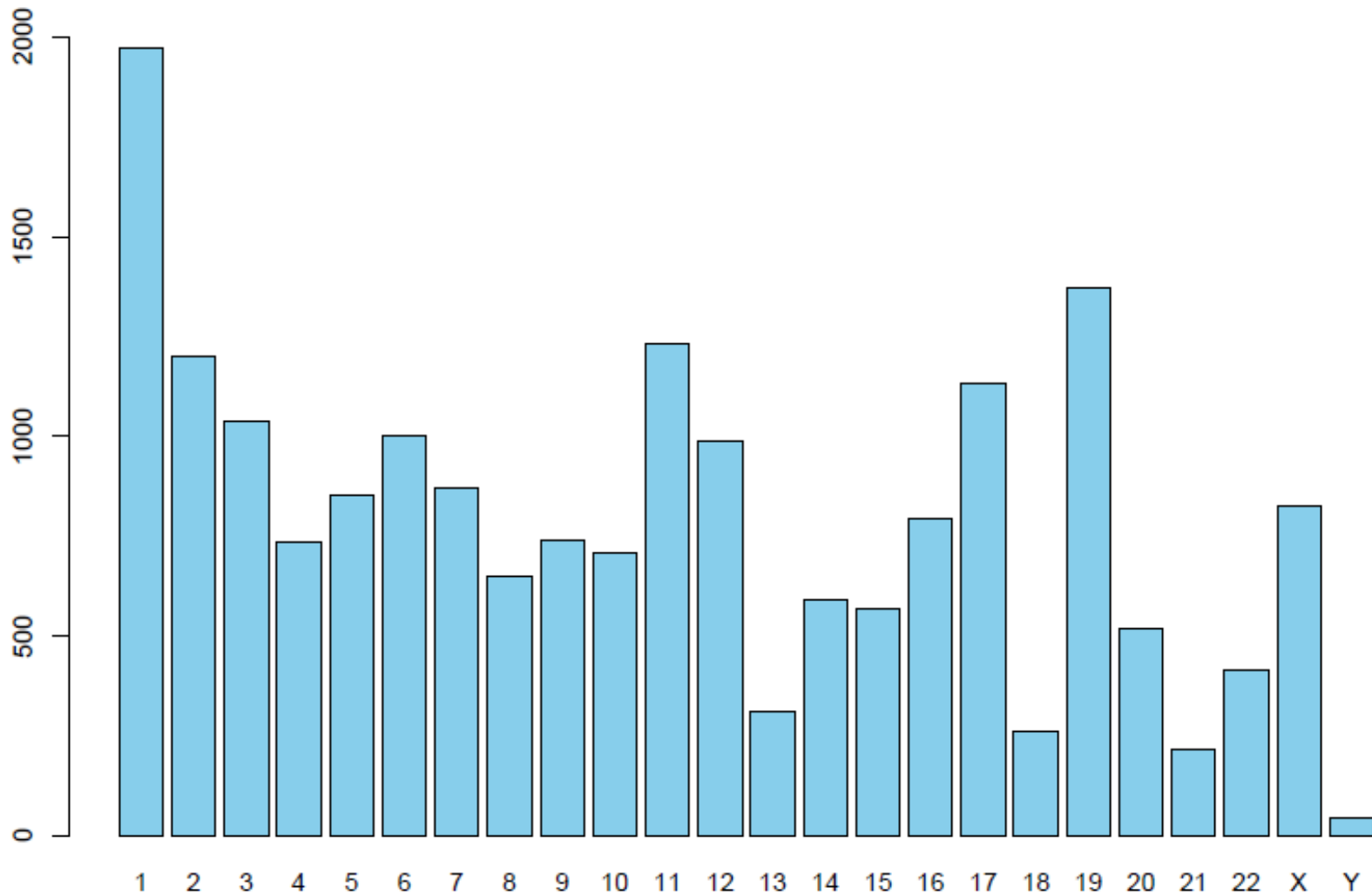


All Chromosomes

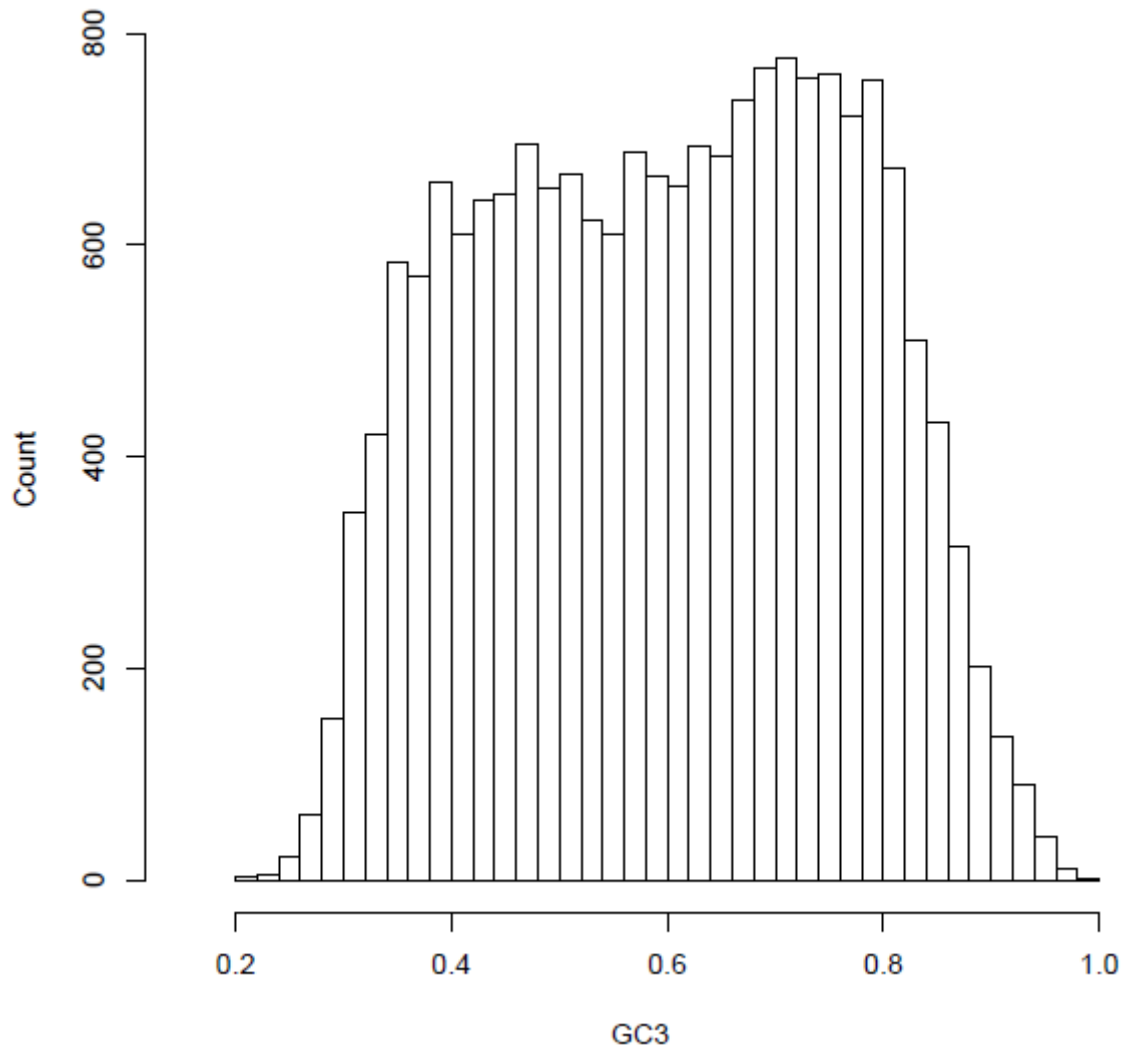


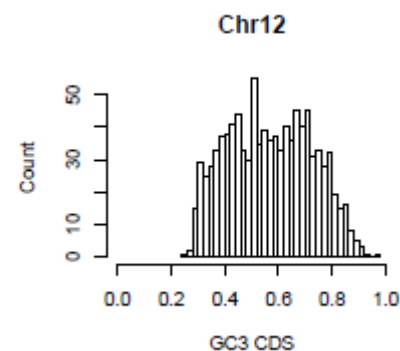
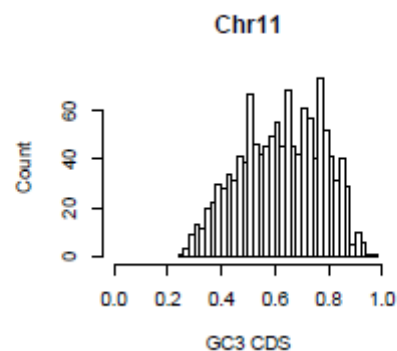
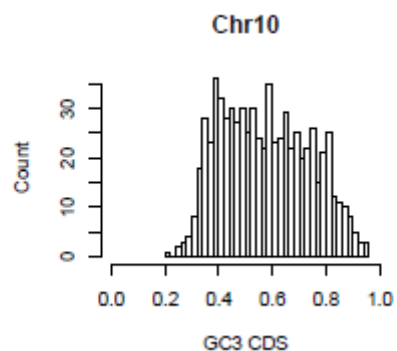
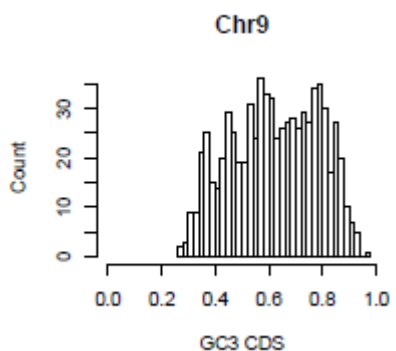
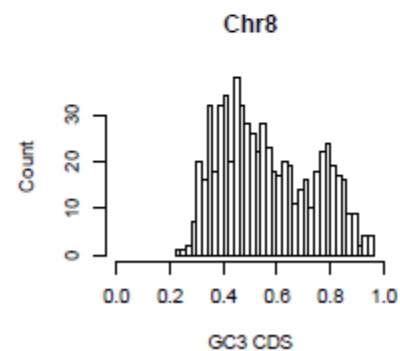
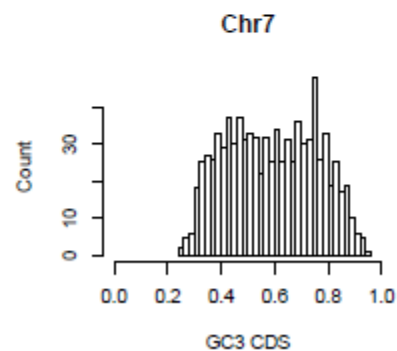
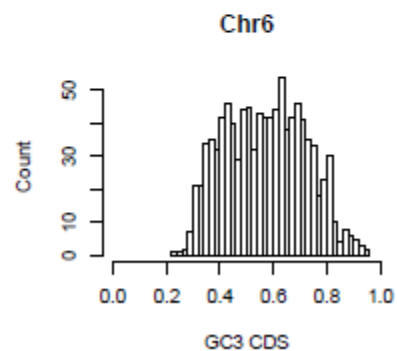
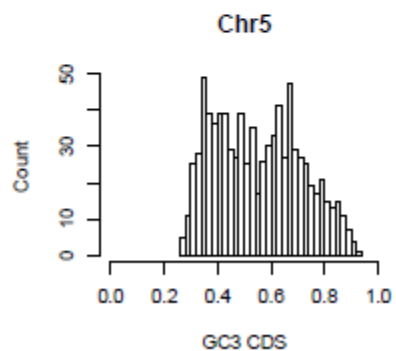
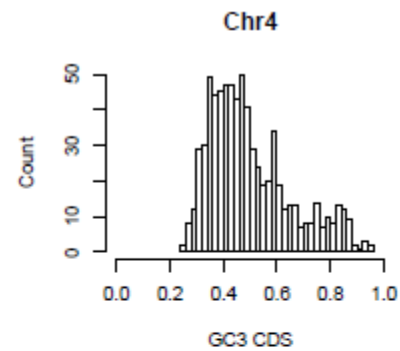
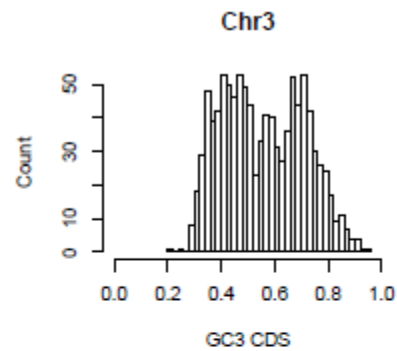
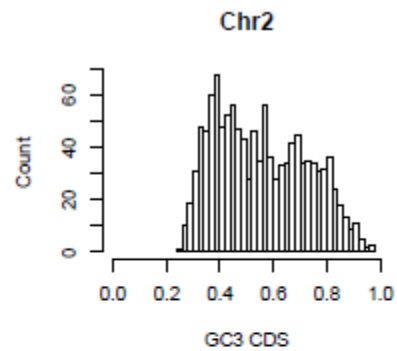
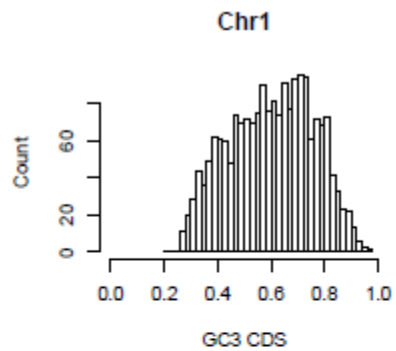
Genes por cromosoma

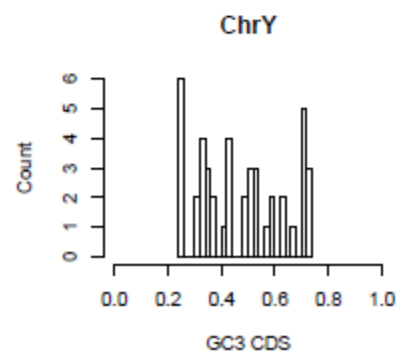
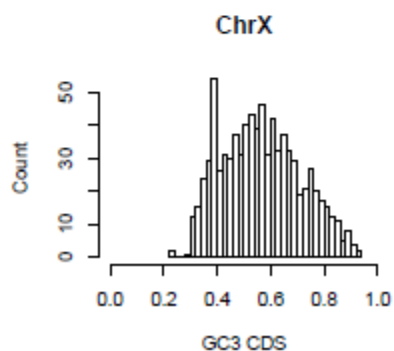
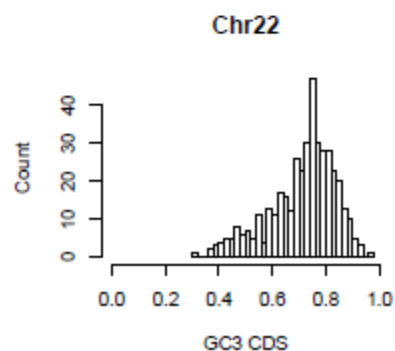
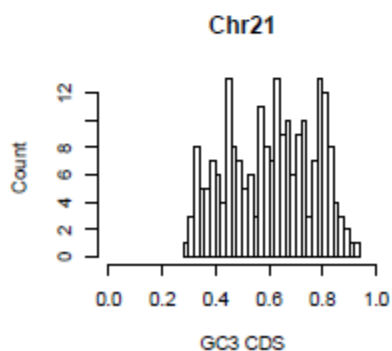
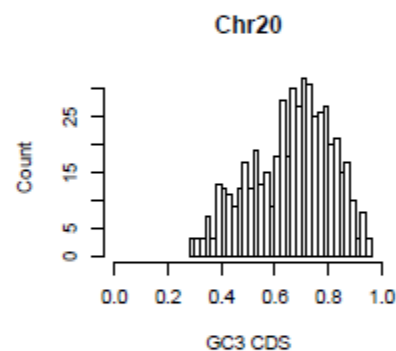
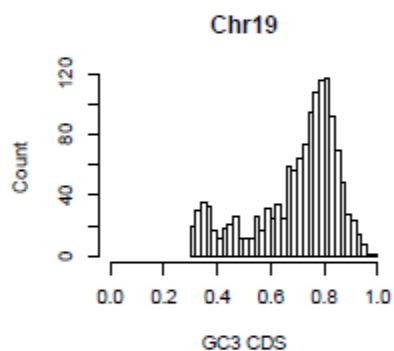
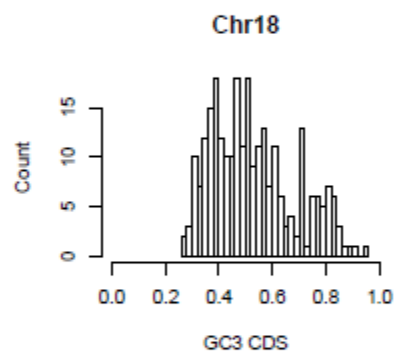
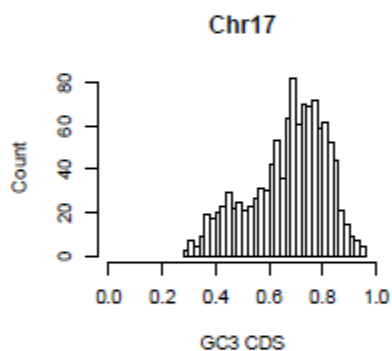
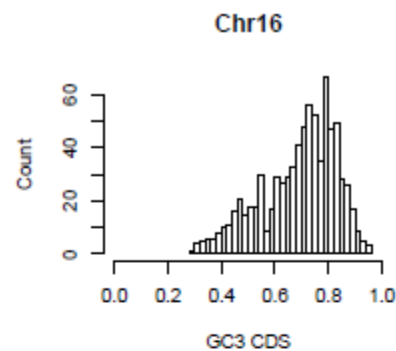
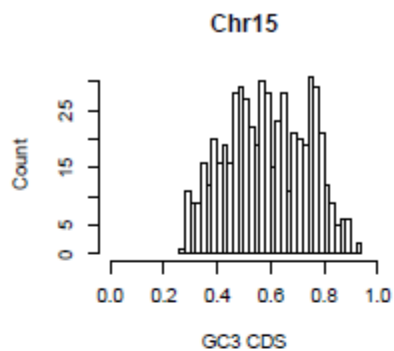
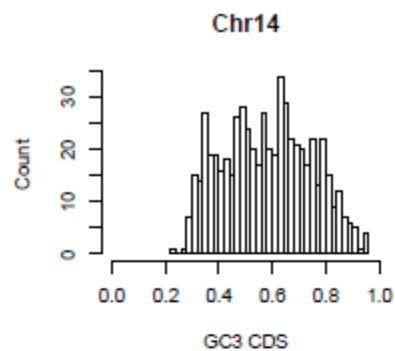
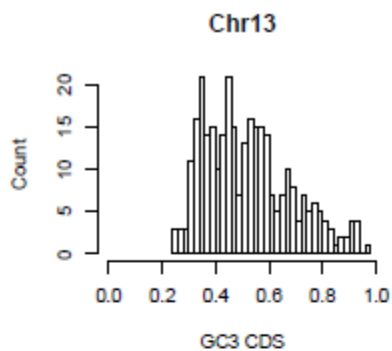
Genes per Chromosome, n=19,046



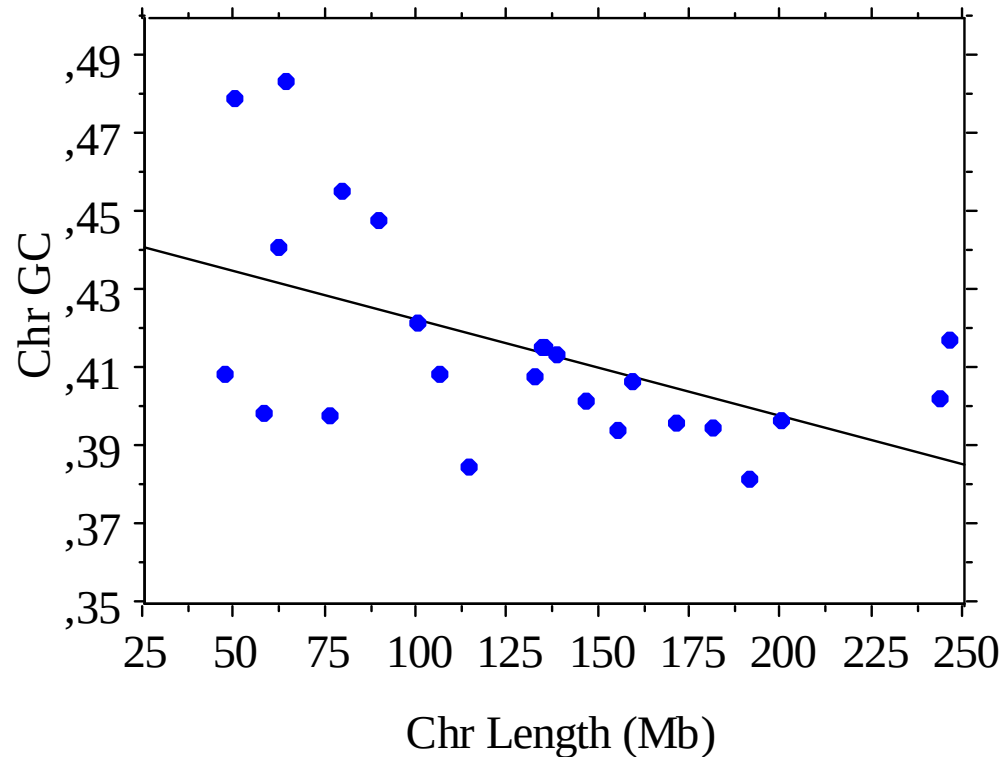
GC3 of CDS (All Chromosomes) n=19,046







Correlación entre el contenido en GC de los cromosomas y la respectiva longitud

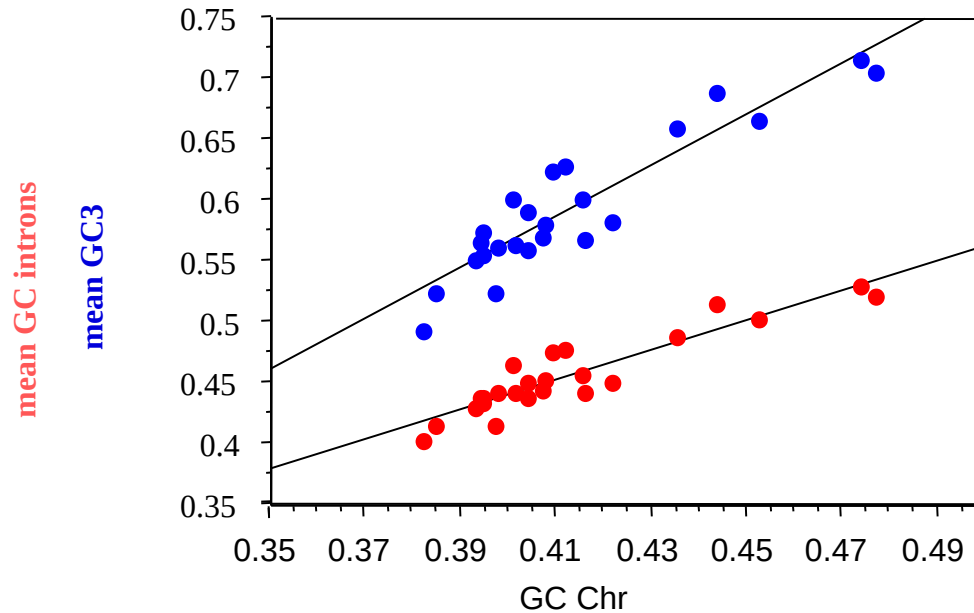


$$Y = ,447 - 2,462E-4 * X; R^2 = ,277; P = 0,008$$

Correlaciones entre el GC de cada cromosoma y la media de GC3 y de los intrones

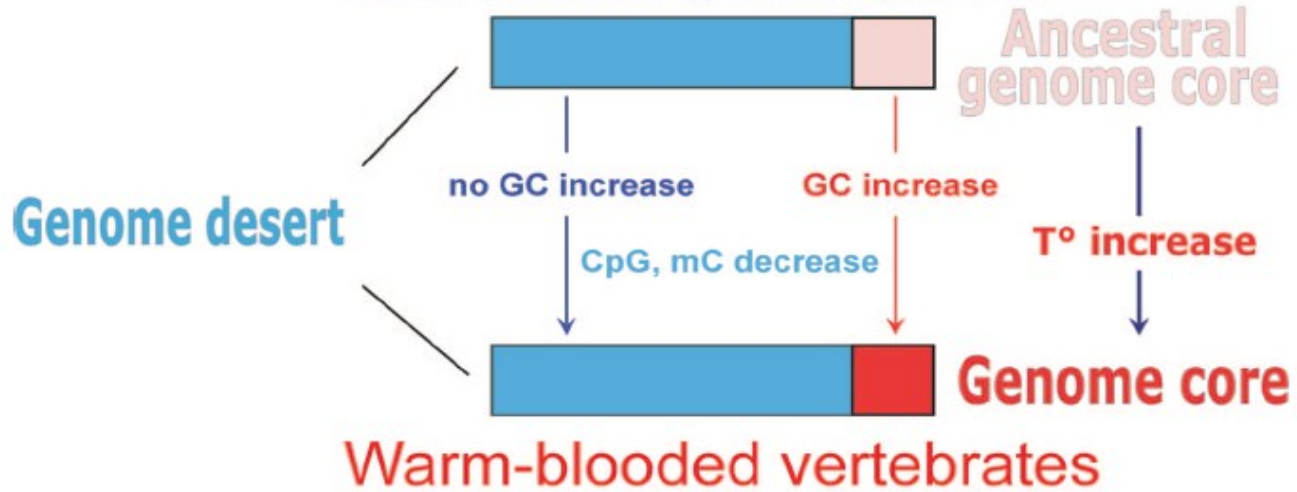
$$Y = -0.272 + 2.099 * X; R^2 = 0.849$$

$$Y = -0.049 + 1.224 * X; R^2 = 0.852$$

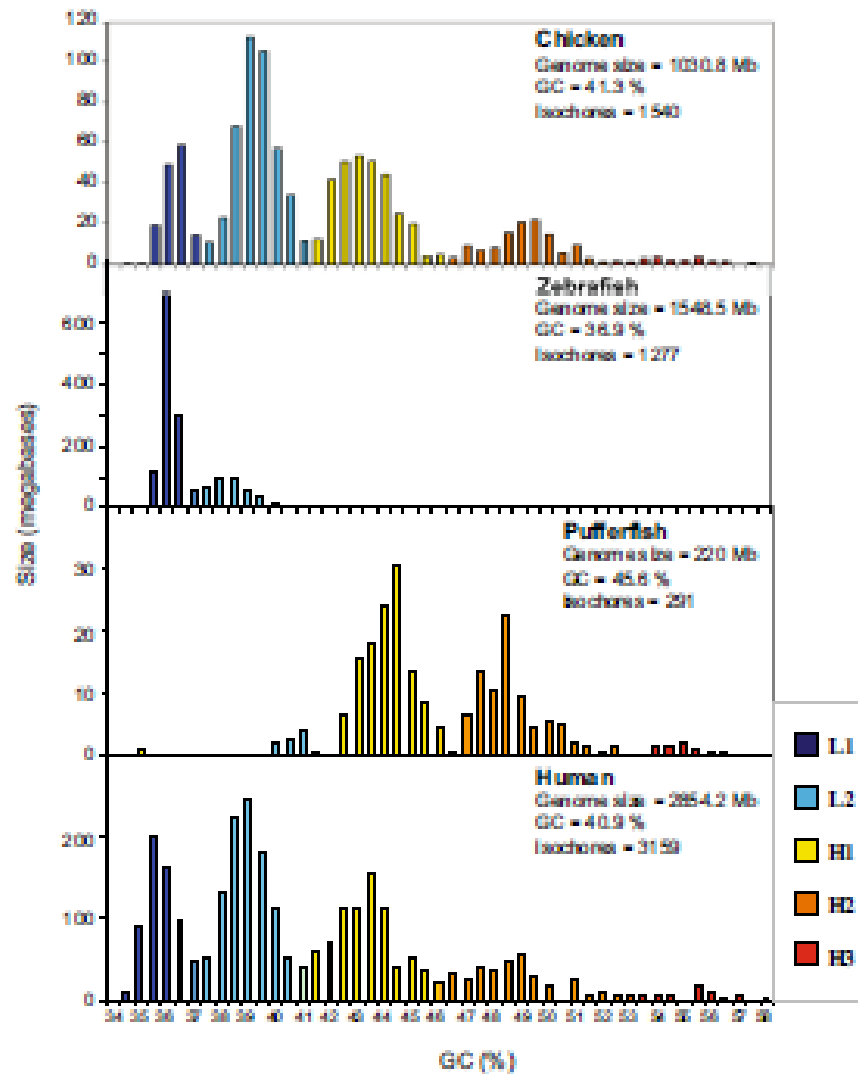


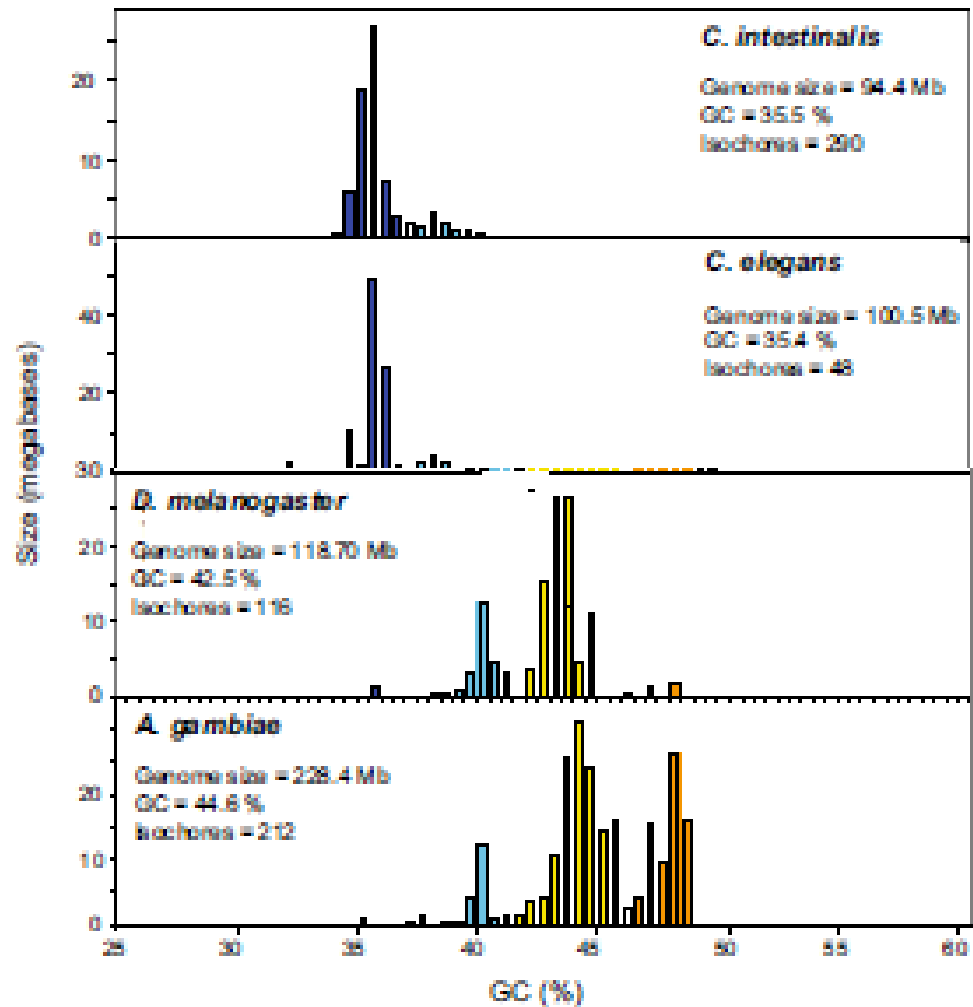
Transitional mode

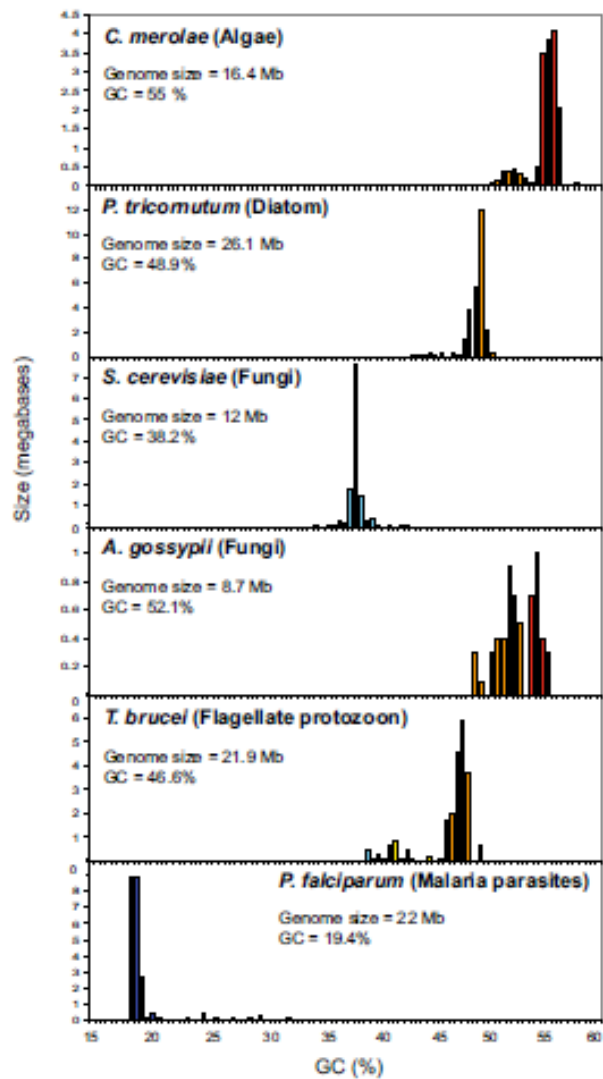
Cold-blooded vertebrates



Conservative mode

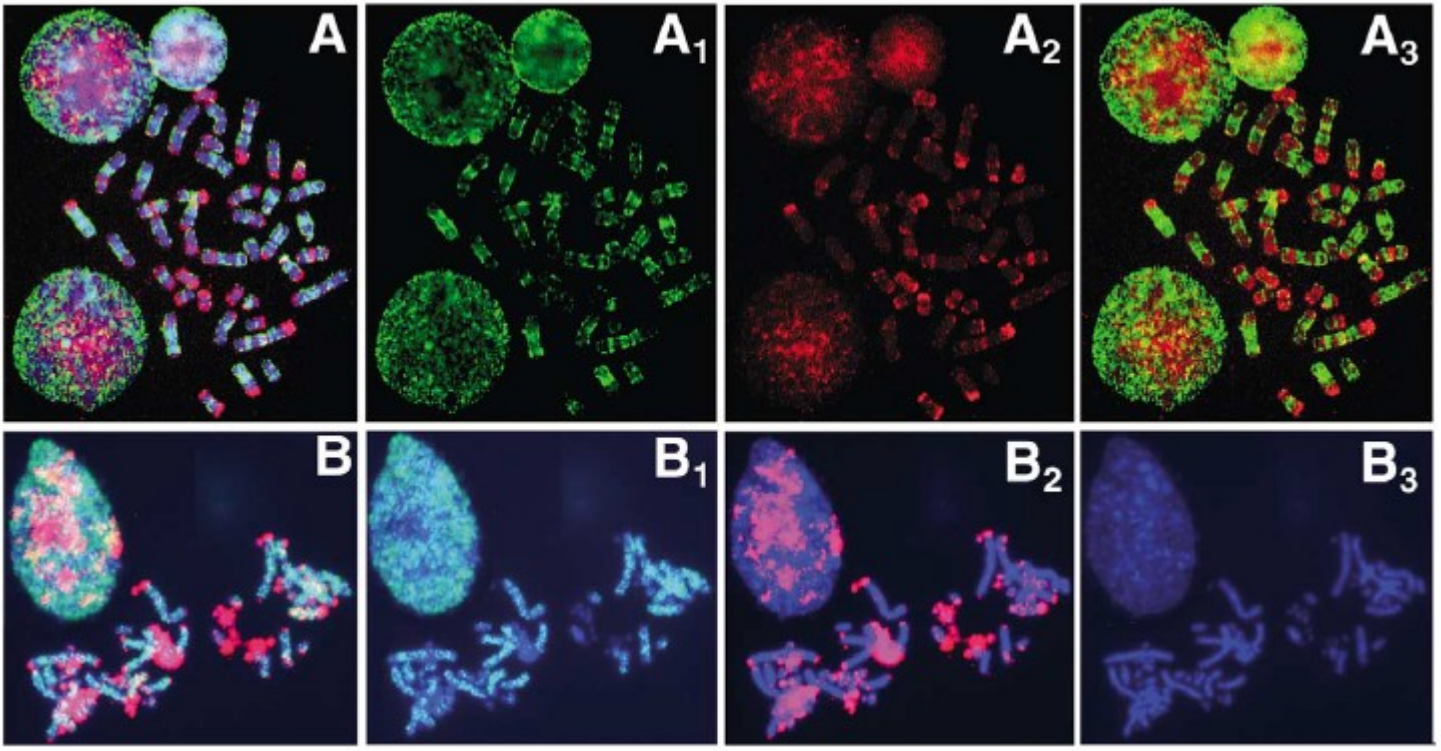




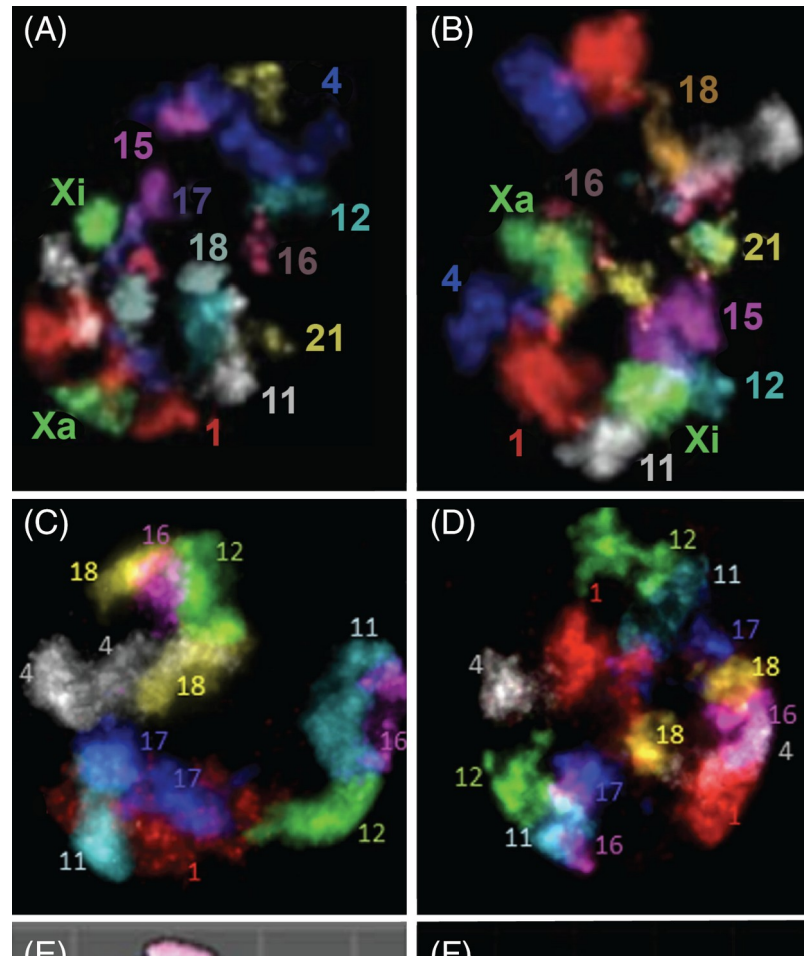


Genoma Eucariota: estructura 3-D

El genoma de los mamíferos es un objeto de una dimensión (1-D) «metido» en un núcleo que es 400.000 veces más corto que el eje más largo de todo el ADN. Esta **restricción espacial** necesita una compactación jerárquica del genoma 1-D hasta la cromatina 3-D dentro del núcleo.



Territorios cromosómicos en humano (FISH)



Origen isocoros

- a) Teoría seleccionista: aumento de GC como adaptación a la mayor temperatura de mamíferos y aves.
- b) Teoría neutralista: biased gene conversion

Origen isocoros

Importante: el sesgo mutacional de los mamíferos, en todos los isocoros, es hacia AT... entonces???

Además, como vimos, tienen distintas propiedades funcionales y estructurales los isocoros ricos y pobres en GC... ¿Actúa la selección natural?