

1. Supplemental Tables

TABLE A. ISOCHORE FAMILIES IN THE HUMAN GENOME ^(a)					
	Amount %	Maxima GC	Minima GC	“Fixed” GC Ranges	“Extended” GC Ranges ^(b)
L1	19	35.5		33-37	→37.6
			37		
L2	36	38.7		37-41	36.4-42
			41		
H1	31	43.0		41-46	39.6-46.9
	86		46		
H2	11	48.5		46-53	45-54
			53		
H3	3	55.0		53-59	52→
	14				

(a) Modified from ref. 1. Values in bold are total amounts of L1+L2+H1 and H2+H3 families and correspond to the genome desert and the genome core, respectively.

(b) “Extended” ranges eliminate very small, local GC spikes (positive or negative) and avoid the oversegmentation linked to “fixed” ranges (Bernardi, in preparation).

TABLE B. STRUCTURAL AND FUNCTIONAL PROPERTIES OF THE GENOME CORE VS. THE GENOME DESERT (a)

GC level	+	(2)	Housekeeping genes	+	(2)
LINE density	-	(3)	Developmental genes	-	(19,20)
SINE density	+	(4)	tRNA genes	+	(21)
Gene density	+	(5,6)	Reverse bands	+	(22-24)
Chromatin	Open	(7,8)	Nuclear location	Central	(7,8,25)
Gene expression	+	(9-11)	Translocations	+	(26)
Supercoiling	-	(12)	Fragile sites	+	(27,28)
GC-rich trinucleotides	+	(13,14)	Proviral integration	+	(2,29)
CpG, mC, CpG islands	+	(15,16)	Insertions/deletions	+	(30)
Isochore size	-	(17)	Recombination	+	(31)
GC heterogeneity	+	(17)	Point mutations	+	(32)
Intron, UTR size	-	(18)	Replication	Early	(33-36)

(a) Modified from ref. 1. In general, the properties of the genome core are just opposite to those of the genome desert. +/- signs indicate positive/negative differences of the properties of the genome core compared to those of the genome desert.

TABLE C. ISOCHOIRES & INTERPHASE CHROMATIN^(a)

ISOCHOIRES	
Genome desert¹ (L1, L2, H1 families) gene-poor, LINES closed chromatin late replicating 86% of the genome	Genome core² (H2, H3 families) gene-rich, SINES open chromatin early replicating CpG islands, HK genes ^(a) (av. size 0.9Mb)
COMPARTMENTS⁽³⁷⁾	
B: closed chromatin	A: open chromatin
DOMAINS AND BORDERS/BOUNDARIES	
Domains: LADs, lamina-associated domains ⁽³⁸⁾ gene-poor, H3K27me3	Borders: CTCF, promoters, CpG islands gene-rich, H3K4me2
cLADs , constitutive LADs, GC-poor ⁽³⁹⁾	ciLADs , constitutive inter-LADs, GC-rich
Topological domains⁽²¹⁾ 91% of the genome (av. size 0.88Mb) Topologically associating domains TADs ⁽⁴⁰⁾	Boundaries + “unorganized chromatin” (av. size 0.56 Mb) 9% of the genome tRNAs, SINES, TSS ^(b) Housekeeping genes
Physical domains^{(c) (41,42)} repressive marks	Boundaries active marks
CHROMATIN STATES⁽⁴³⁾	
Large-scale repressed Repeat-associated	Promoter-associated Transcription-associated Active intergenic
CHROMATIN TYPES^{(c) (44)}	
Blue/Green: Heterochromatin Polycomb/H3K27me3, HPI/H3K9me2 Black: repressive chromatin all late replicating	Red, Yellow: active chromatin H3K4me2, H3K79me3 both early replicating
SUB-COMPARTMENTS⁽⁴⁵⁾	
B1, H3K27me3; facultative heterochromatin; replication → middle S phase B2, B3, replication → end S phase	A1, A2, gene-rich, high expression H3K36me3, H3K79me2 H3K27ac, H3K4me1 both early-replicating
CHROMATIN⁽⁴⁶⁾	
Heterochromatin gene-poor, LINES	Euchromatin gene-rich, SINES

(a) Modified from ref. 1; properties in red are shared or comparable between genome desert/genome core and the corresponding chromatin compartments, sub-compartments,

etc. (b) Abbreviations: HK, housekeeping; TSS, transcription start sites. (c) *Drosophila*. Other data concern mammalian cells.

References to Supplemental Tables S1-S3

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