SUPPLEMENTARY FIGURES AND TABLES

Figure S1

Repeat graph generated from a human WGS sequence library. We tested the RepeatNet algorithm using a fosmid end-sequence library (WIBR2). We retrieved the fosmid end sequences that contained the overrepresented k-mers shown in this figure and checked their repeat content using RepeatMasker. We found that the largest cluster (red) denotes the alpha-satellite repeats in the human genome, confirming the use of our RepeatNet algorithm. The components in the repeat graph are annotated by the repeat sequence they represent. The clusters from the largest to the smallest denote alpha-satellite (red), satellite II and III (green), LINE and SINE (yellow), homopolymer repeats (blue), and low complexity (orange).

Figure S2

Example of FISH results of CFA-specific fosmid clones. RepeatNet graph is reported in **(C)** showing four different repeat clusters. **(A)** FISH with the clone G630P8139H12_BI1-1903P24 corresponding to green cluster; **(B)** FISH with the clone G630P816490E11_BI1-411I22 corresponding to blue cluster; **(D)** FISH using the clone G630P84226G11_BI1-1356M22 corresponding to red cluster; and **(E)** FISH with the clone G630P88303G10_BI1-3749N20 corresponding to yellow cluster.

Figure S3

Amplification results obtained using primers designed on the specific consensus sequences of species-specific genomic DNA **(Table 2)**. 1, 2log ladder; 2, ECAcons70; 4, ECAcons71; 6 ECAcons421+424; 8, ECA3cons221; 10, ECA4cons450; 12 ECA5cons451; 14, CFAcons244+246; 16, DNOcons173; 18, LAFcons842+936; 20, MDOcons528 and 22, OANcons144. 3, 5, 7, 9, 11, 13, 15, 17, 19, 21 empty wells.

Figure S4

FISH results using PCR products as probes obtained for each consensus sequences. **(A)** FISH results with ECAcons70 on ECA metaphases; **(B)** FISH with LAFcons842+936 on LAF metaphases; **(C)** FISH with DNOcons173 on DNO metaphases; **(D)** FISH with MDOcons528 on MDO metaphases; and **(E)** FISH with OANcons144.1+144.2 on OAN metaphases.

Figure S5

Cohybridization results using species-specific amplification products (green) and ChIP (red) DNA in horse **(A)**, elephant **(B)**, and opossum **(C)**. In yellow, overlapping signals between immunoprecipitated DNA and PCR probes.

Table S1

Sequences extracted by PHRA and TFR (see text for details); FISH and ICHC results obtained on the six studied mammals. In brackets the positive chromosomes out of the full karyotype are reported.

Table S2

RepeatMasker analysis on the consensus sequences.

Table S3

FISH results with specific CFA centromeric fosmids (in parentheses the number of chromosomes according to (Breen et al. 1999)).

Table S4

ICHC results.