Figure S1. Sequencing of large-scale gorilla chromosome rearrangements. (A) Sequence characterization of a gorilla inversion on chromosome 7(Egozcue and Chiarelli 1967; Miller et al. 1974). A schematic of the inversion (*top panel* ideogram) is refined by paired-end BES and confirmed by FISH (*bottom right panel*). A gorilla BAC clone (CH277-325N15) corresponding to the long-arm breakpoint is completely sequenced (AC242656.3). Miropeats analysis(Parsons 1995) compares two regions on human chromosome 7 (*middle panel*; blue and orange) to the gorilla sequence. (Repeat elements, LINE, SINEs, LTRs, SDs, and genes are annotated based on the human genome.) ClustalW alignment (*bottom left panel*) defines the precise breakpoint in an SD-rich territory.

Figure S2. Sequencing of large-scale gorilla chromosome rearrangements. (A) Sequence characterization of a gorilla inversion on chromosome 8(Egozcue and Chiarelli 1967; Miller et al. 1974). A schematic of the inversion (*top panel* ideogram) is refined by paired-end BES and confirmed by FISH (*bottom right panel*). A gorilla BAC clone (CH277-481C13) corresponding to the long-arm breakpoint is completely sequenced (AC242627.3). Miropeats analysis(Parsons 1995) compares two regions on human chromosome 8 (*middle panel*; blue and orange) to the gorilla sequence. (Repeat elements, LINE, SINEs, LTRs, SDs, and genes are annotated based on the human genome.) ClustalW alignment (*bottom left panel*) pinpoints a L1P3 (LINE) element (red) at the precise breakpoint.

Figure S3. Sequencing of large-scale gorilla chromosome rearrangements. (A) Sequence characterization of a gorilla inversion on chromosome 10(Egozcue and Chiarelli 1967; Miller et al. 1974). A schematic of the inversion (*top panel* ideogram) is refined by paired-end BES and confirmed by FISH (*bottom right panel*). A gorilla BAC clone (CH277-103D21) corresponding to the long-arm breakpoint is completely sequenced (AC241522.2). Miropeats analysis(Parsons 1995) compares two regions on human chromosome 10 (*middle panel*; blue and orange) to the gorilla sequence. (Repeat elements, LINE, SINEs, LTRs, SDs, and genes are annotated based on the human genome.) ClustalW alignment (*bottom left panel*) pinpoints L1m4 (LINE) (red) *AluSc* elements (blue) at the precise breakpoint.

Figure S4. Sequencing of large-scale gorilla chromosome rearrangements. (A) Sequence characterization of a gorilla pericentric inversion on chromosome 18(Egozcue and Chiarelli 1967; Miller et al. 1974). A schematic of the inversion (*top panel* ideogram) is refined by paired-end BES and confirmed by FISH (*bottom right panel*). A gorilla BAC clone (CH277-492f03) corresponding to the long-arm breakpoint is completely sequenced (AC243003.2). Miropeats analysis(Parsons 1995) compares two regions on human chromosome 18 (*middle panel*; blue and orange) to the gorilla sequence. (Repeat elements, LINE, SINEs, LTRs, SDs, and genes are annotated based on the human genome.) ClustalW alignment (*bottom left panel*) pinpoints an *AluSq* element (blue) at the precise breakpoint.

Figure S5. Schematic representation of breakpoint inversions in gorilla genome. Each inverted chromosome has been reported in the human (*left panel*) and gorilla (*right panel*) configuration, and repetitive elements flanking the breakpoints have been drawn by arrows defining the orientation of the found elements. Genomic locations of the breakpoints have been reported by vertical blue bars.

Figure S6. Example of deletion in gorilla genome. Deletion detected by read depth of coverage and array (A) and BAC end mapping (BEM) (B) in gorilla genome (green bar presents the supposed deleted region). FISH experiments show the heterozygous state of this deletion (C).

Figure S7. *Alu* new insertion in gorilla genome. Ten PCR validation sites for Kwan gorilla genome of the novel *Alu* integration sites (G, gorilla, ~450 bp) compared to human (H, human, ~150 bp). Marker 100 bp (by Biolabs) is displayed in the left lane.