Figure S1: Annotated sequence of SHR/Akr rat Y.

Background colors represent sequence classes: pseudoautosomal (green); ancestral single-copy (yellow); X-transposed (red) ampliconic (blue); other (gray); heterochromatic (pink stripes). Gaps shown in white. All sequence features and BACs drawn to scale. Positions of all actively transcribed (a) intact protein-coding genes; (b) non-coding transcripts; and (c) pseudogenes. Plus (+) strand above, minus (-) strand below. (d) G+C content (%) calculated in a 100-kb sliding window with 1-kb steps. (e) SINE (red), LINE (green), ERV (blue), and Satellite (black) repeat densities, calculated in a 200-kb sliding window with 1-kb steps. (f) Sequenced BACs and WGS contigs. Each bar represents the size and position of a sequence within the assembly. Sequences with no prefix, RNAEX library; prefix “E”, RNECO library; prefix “Link” WGS contigs supported by nanopore reads. Dark green, sequences in the tiling path; dark grey bars, other finished BAC clones; light grey, unfinished BAC clones.