Supplementary Figure 1   Annotated sequence of the chimpanzee MSY. The background colors represent four different sequence classes: X-degenerate (yellow), ampliconic (blue), non-X-degenerate, single-copy (gray), and heterochromatic (pink stripes). Gaps are shown in white. All sequence features and BACs are drawn to scale.   a. Colored blocks within the ampliconic sequence represent amplicons or repeat units. Nearly identical amplicons are represented by the same color; different colors represent different species of amplicons. Palindromes P6, P7, and P8 are located within the X-degenerate sequence and are shown in blue. b. Arrows show orientation of amplicons and palindrome arms. c. The positions of all intact and actively transcribed genes in chimpanzee are shown. Plus (+) strand above, minus (-) strand below. d. The positions of all pseudogenes (Supplementary Table 3) are shown. e. Plot of intrachromosomal similarity. Using a 100 kb sliding window and 1 kb steps, each window of MSY sequence was compared to all other MSY sequences after repeat masking, and the highest sequence similarity (expressed as percent identity) for each window along the length of the MSY is plotted. All values >80% are shown. f. Plot of similarity to human Y chromosome. Same as in (e) but chimpanzee MSY sequence was compared to human MSY sequence.   g. G+C content (%) calculated in a 100 kb sliding window with 1 kb steps. h. Alu, LINE, and endogenous retrovirus (ERV) densities, expressed as percentage of nucleotides, calculated in a 200 kb sliding window with 1 kb steps. i. BAC and fosmid clones mapped to the chimpanzee MSY. Each bar represents the size and position of one BAC clone, labeled with the library identifier. Clones with no prefix are from the CHORI-251 BAC library. Clones with the prefix "P" are from the RPCI-43 BAC library. Clones with the prefix "C" are from the CHORI-1251 fosmid library. Red bars represent finished clones whose sequences were deposited in GenBank. Green bars represent clones that were mapped to the Y using STS content mapping. In some cases, the end sequences of these clones are known, so their positions on the Y were determined precisely. Grey shading at one or both ends of a clone indicates that the end was not sequenced, so its position was approximated by STS content.