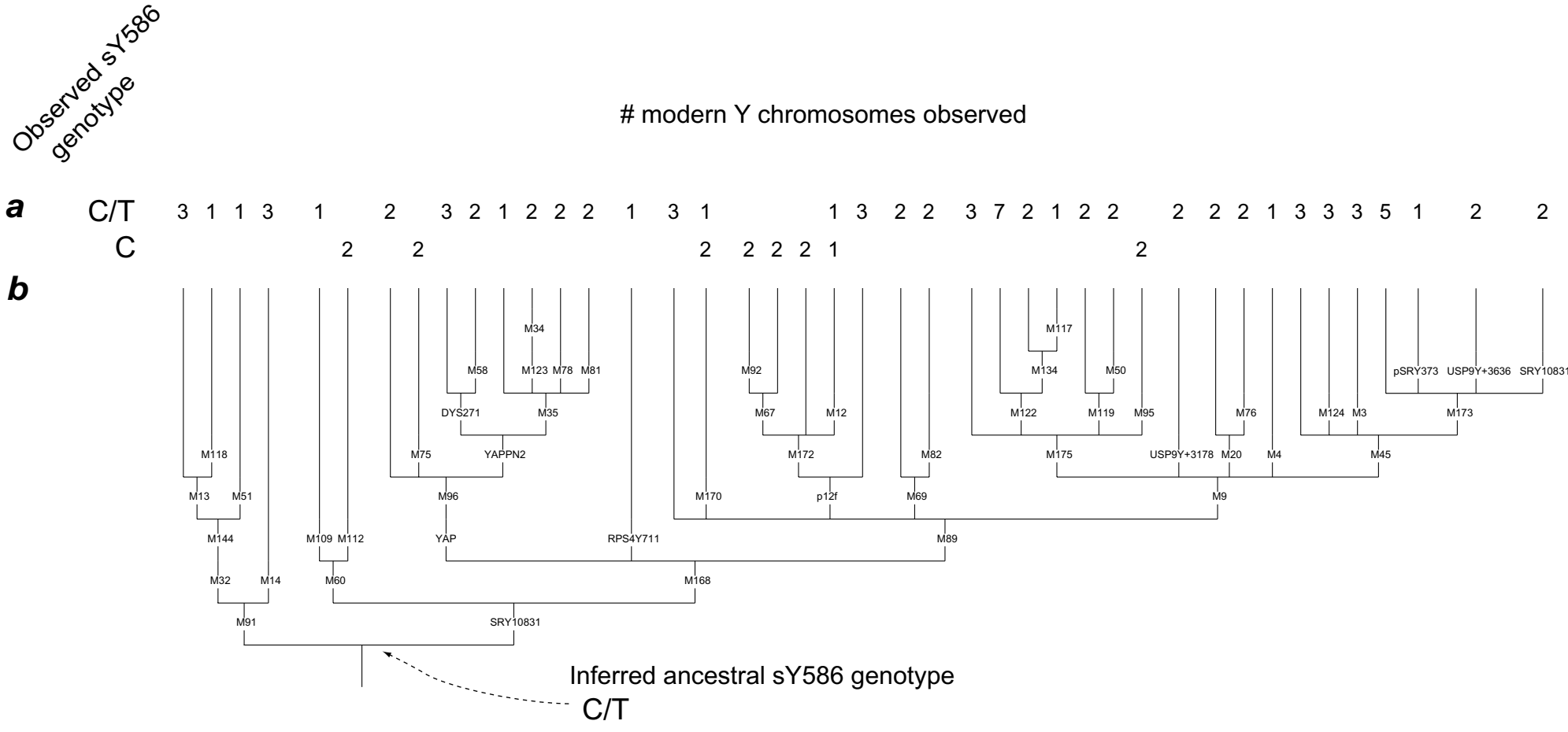
Rozen *et al*. Abundant gene conversion between arms of palindromes in human and ape Y chromosomes. *Nature* **423**, 873-876 (2003)

Supplementary Figure 3. Distribution of sY586 genotypes (see Discussion, below) across the genealogical tree of the human MSY. ***a***, The number of Y chromosomes with each sY586 genotype observed at each terminal branch of the tree. ***b***, MSY genealogical tree and haplotypes as in Supplementary Figure 1. The common ancestor of all extant human Y chromosomes is inferred to have had the C/T genotype.



Discussion. sY586 is an STS that amplifies a site of sequence variation that occurs in the arms of palindromes P1 and P2 (four copies total; Saxena et. al, 2000; Kuroda-Kawaguchi et al., 2001). In the MSY reference sequence and in clones from a second Y chromosome, 3 copies of sY586 have C at the variant site, while one copy has a T, resulting in a C/T genotype. One might expect that homogenization from a C/T genotype to a T genotype (T at all 4 copies of sY586) would be rare, because production of this genotype from a chromosome with C at 3 copies of sY586 and a T at one copy would require 3 gene-conversion events. Conversely, change to a C genotype (C at all 4 copies) would require only a single gene conversion, and might be frequent. The distribution of sY586 genotypes shown here displays the expected pattern: the C/T genotype occurs in most haplotypes, the C genotype also occurs in several haplotypes, while the T genotype has not been observed.

Saxena, R. *et al*. Four *DAZ* genes in two clusters found in *AZFc* region of human Y chromosome. *Genomics* **67**, 256-267 (2000)

Kuroda-Kawaguchi *et al*. The *AZFc* region of the Y chromosome features massive palindromes and uniform recurrent deletions in infertile men. *Nature Genetics* **29**, 279-286 (2001)