

Microbiology

The polymorphic subtelomeric regions of *Plasmodium falciparum*

chromosomes contain arrays of repetitive sequence elements

(malaria/recombination/genome organization)

a random clone isolated from the Malaysian CAMP strain

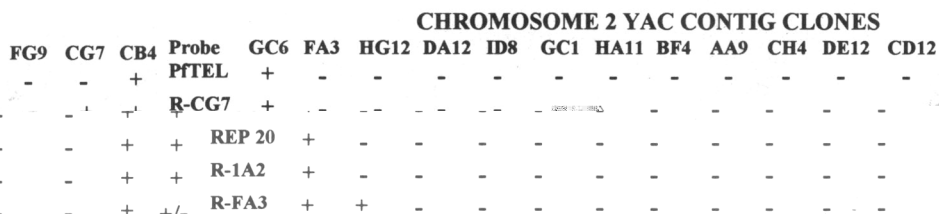
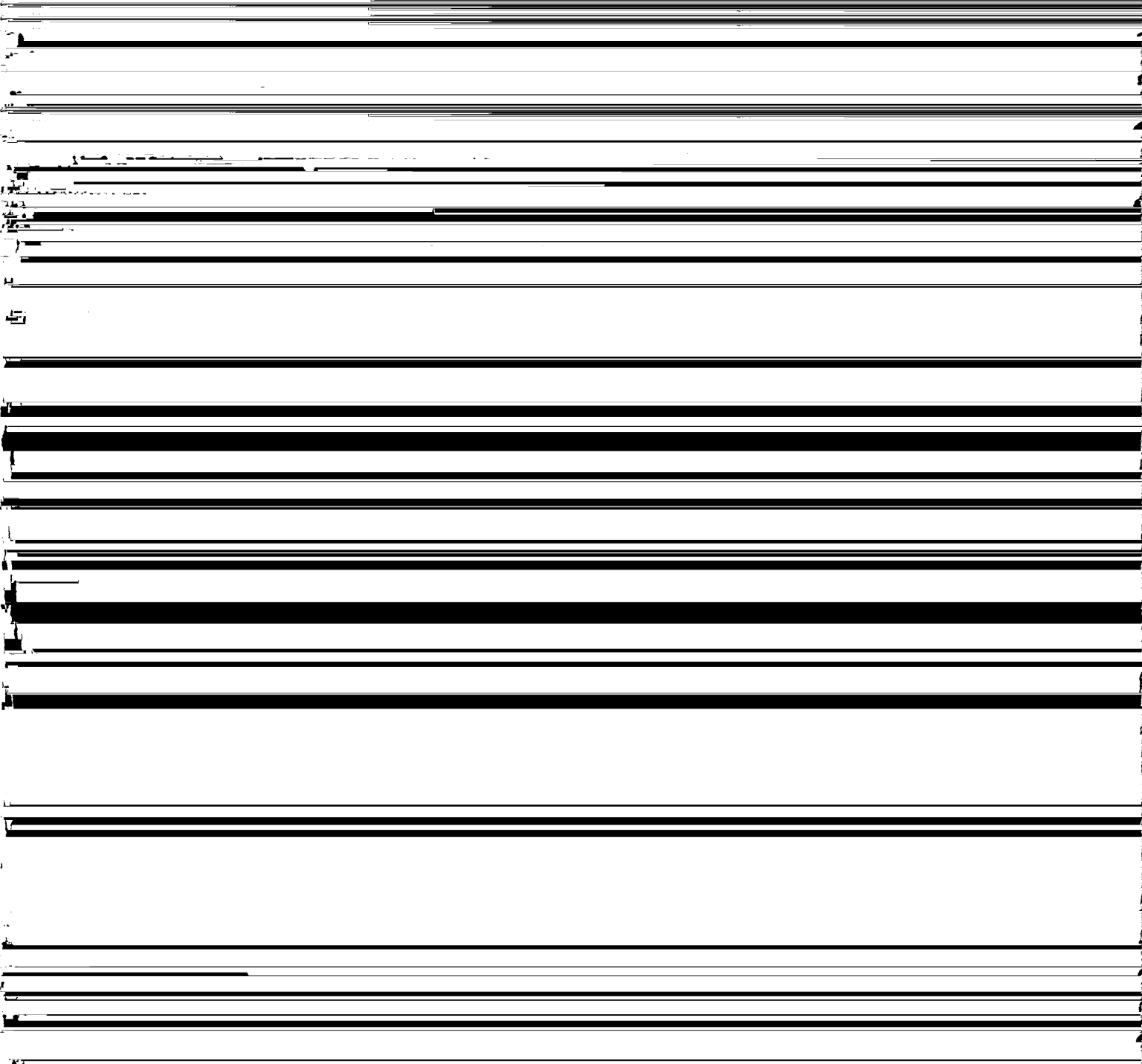


FIG. 2. Southern analysis of PFG-separated parasite chromosomes identifies repetitive DNA elements. Parasite chromosomal DNA



ysis were carried out to localize the repetitive DNA elements thereby preventing the silencing of transcriptional activity

on the chromosome 2 telomere and subtelomere YAC clones. (21–24). While the effect of *P. falciparum* subtelomeric

GC6, CB4, and CG7, and on two additional, random telomere sequences on either chromosome maintenance or transcrip-

YAC clones, 1A3 and 2H1 (Fig. 3). The 60-kb telomere YAC tional activity remains unclear, we propose a model whereby

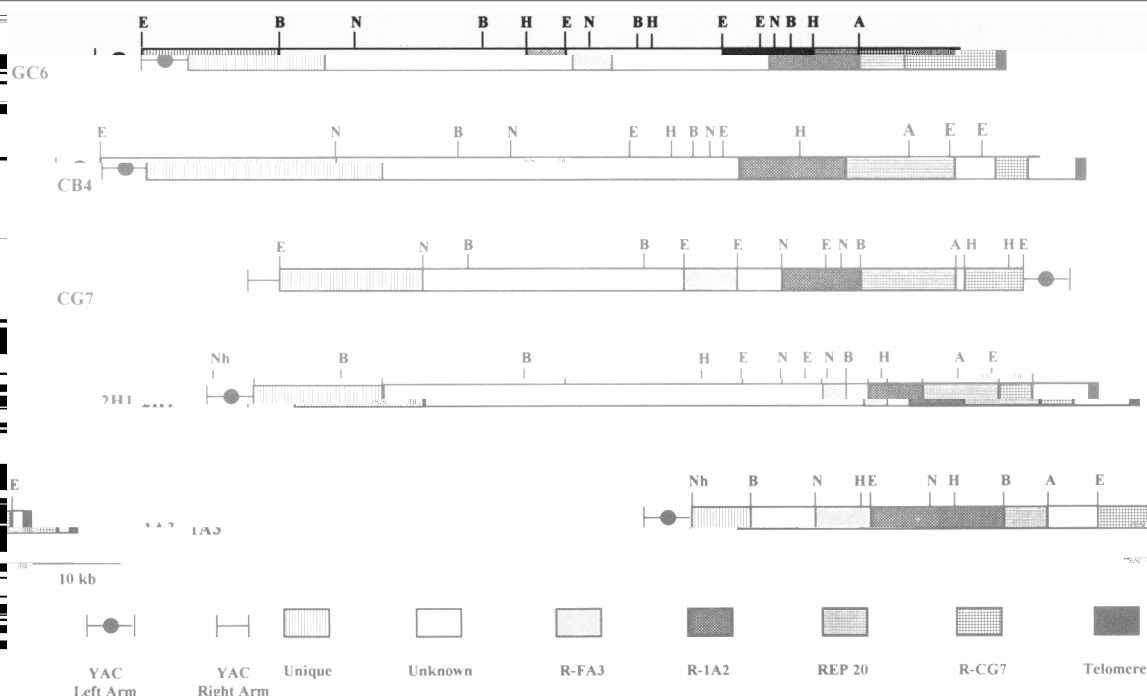


FIG. 5. (A) Map of chromosome 2 subtelomeric region. The left end of chromosome 2

contains $\approx 60\text{--}80$ kb of repetitive DNA se-

These sequences display a conserved order between all chromosome ends examined. Transcription units flanking the KAHRP locus [the poly(A)⁺ transcribed *K3A* and *GLARP* and the poly(A)⁻ transcribed *KA*⁻] are indi-

cated (5). The approximate size range of the

zation of *P. falciparum* chromosome 2. The chromosomal polymorphisms are restricted to

within 100 kb at either end of the chromosome.

The polymorphic ends are composed of con-

served arrays of repetitive DNA sequences