Two HinfI RFLPs detected by p α 10RP8 at D10Z1

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Source and Description: A 0.95 kb fragment cloned into the PstI and SmaI sites of PUC9. This clone recognizes repetitive, alpha satellite sequences (1).

Polymorphisms: HinfI recognizes two dominant polymorphisms. The F polymorphism is defined by the presence or absence of a 570 bp band. The G polymorphism is defined by the presence or absence of a 280 bp band. There are four constant bands at 1050 bp, 630 bp, 137 bp and 126 bp.

Frequency: Estimated from 52 unrelated individuals.

F+G+ haplotype: 0.5

F+G- haplotype: not seen

F-G+ haplotype: 0.02

F-G- haplotype: 0.48

Chromosomal Location: Localized to the centromere of chromosome 10 by *in situ* hybridization (1) and by linkage using the A and B alleles detected in PstI digests, to chromosome 10 pericentromeric markers (2). The lod score between the HinfI and the PstI RFLPs was 3.30 at $\theta = 0$.

Mendelian Inheritance: Dominant inheritance of both the F+ and G+ alleles occurred in several MEN2A families. Several instances of familial inheritance of the F-G+ haplotype were observed confirming the independence of the F and G polymorphic systems.

Probe Availability: Contact Dr. H.Willard, Department of Genetics, Stanford University School of Medicine, Stanford, CA 94305, USA

Other Comments: The F and G polymorphisms are in strong linkage disequilibrium with each other. High stringency hybridization and washing conditions are necessary due to the repetitive nature of the probe. See references 1 and 2.

Acknowledgements: We thank Dr. H.Willard for providing p α 10rp8. This study was supported by the Medical Research Council of Canada and an MRC studentship to N.L.C.

References: (1) Devilee,P. *et al.* (1988) *Genomics* 3, 1-7; (2) Wu,J. *et al.* (1990) *Hum. Genet.* in press.

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