An anonymous human single copy genomic clone, D11S29 (L7) at 11q23, identifies a moderately frequent RFLP

L.Warnich, M.J.Kotze, A.E.Retief, E.Dietzsch, M.F.Fox, G.M.Kotze, D.L.Nicholson, E.Retief and C.J.J.Oosthuizen

MRC Cytogenetic Research Unit, University of Stellenbosch, Faculty of Medicine, P.O. Box 63, Tygerberg, 7505, South Africa

SOURCE AND DESCRIPTION OF CLONE: A 10.22 kb Bam HI fragment subcloned into pBR322 from a 11.67 kb human insert of a phage clone isolated from a human genomic library (vector λ L47.1).

POLYMORPHISM: Taq I (T/CGA) (BRL Ltd) identifies a simple two allele polymorphism with a band at either 13.9 kb (A1) or 10.9 kb (A2) (Figure).

FREQUENCY: Studied 23 Caucasians, 13.9 kb allele (A1) 0.24 10.9 kb allele (A2) 0.76

NOT POLYMORPHIC FOR: Eco RI, Msp I, Hind III, Pst I, Bam HI with DNA from a panel of 12 unrelated Caucasians.

CHROMOSOMAL LOCALISATION: The probe was localised to 11q22 - qter using a panel of somatic cell hybrids (Fox & Retief, in press) and localised to band 11q23 by means of <u>in-situ</u> hybri=dization.

MENDELIAN INHERITANCE: Co-dominant segregation shown in 4 informative families (20 individuals).

PROBE AVAILABILITY: Available for collaborators.

OTHER COMMENTS: No problems on RFLP analysis under normal conditions. Almost no background at stringency of 0.1xSSC.

REFERENCE: Fox MF and Retief AE, "Aspects of human chromo= some segregation in somatic cell hybrids: establishment of a hybrid mapping panel" SAJ Science (in press).

ACKNOWLEDGEMENTS: This work was supported by the Medical Re= search Council, Cape Provincial Administration and the Stichting Stellenburg.

