Phage 8-9 defines a cluster of site polymorphisms on chromosome 16q22-q24 [HGM9 no. D16S20]

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SOURCE AND DESCRIPTION OF CLONE: Phage 8-9 was isolated from a genomic library of a mouse x human somatic cell hybrid (CF-52) containing an 11q-16q translocation as the only human chromosome. A 17 kb partial Sau 3A fragment was cloned in the BamHI site of EMBL3.

POLYMORPHISMS: Sac I identifies constant bands at 4.1, 2.3 and 1.3 kb and two 2-allele RFLPs with A1=10, A2=7.4 +2.6 kb and B1=2.9, B2=1.9+1.0 kb. Bgl II identifies a constant band of 8 kb and a 3-allele RFLP with C1>20, C2=14 and C3=8.5 +5.2 kb. Pvu II identifies 8 constant bands <3.5 kb and a 2-allele RFLP with D1= 6.5, D2=5.8+0.7 kb.

FREQUENCIES: Studied at least 34 European Caucasians. A1=.43, A2=.57; B1=.26, B2=.74; C1=.03, C2=.71, C3=.29; D1=.32, D2=.68.

CHROMOSOMAL LOCALIZATION: 16q22-q24, by in situ hybridization. Localized approx. 7 cM distal to CTRB on CEPH linkage map of chromosome 16.

MENDELIAN INHERITANCE: Codominant inheritance has been shown at each of the four loci in at least 2 informative families with a total of at least 13 children.

PROBE AVAILABILITY: Will be available from ATCC.

OTHER COMMENTS: The probe must be prehybridized with excess human DNA to compete out hybridization of repeated sequences. Of 36 unrelated individuals typed at loci A, B and D, 31 (86%) were heterozygous at one or more of the 3 loci. D16S20 is also polymorphic with Pst I, Bgl I, Taq I, Msp I, BstNI, Asp 700, Bcl I and Hae III, but not with EcoR I, Hind III, BamH I, Rsa I, Xba I, Apa I or Dra I. For 428 bp screened, the average heterozygosity per bp was .0072.

REFERENCES: 1.)CL Maslen, C Jones, T Glaser, RE Magenis, R Sheehy, J Kellogg and M Litt(1988)Genomics 2:66-75. 2.)GM Lathrop, M Leppert, Y Nakamura, P O'Connell, M Litt, C Maslen, P Cartwright, J-M Lalouel and R White. (1988) Cytogenet Cell Genet, in press.

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