Isolation and mapping of a polymorphic DNA sequence pYNH37.3 on chromosome 17p [D17S28]

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SOURCE/DESCRIPTION: A 1.6 kb MspI fragment from the cosmid YNH37 identified with the HBV-2 oligonucleotide (1) was subcloned into AccI site of pUC18.

POLYMORPHISM: TaqI identifies a 5 allele VNTR polymorphism with bands between 2.0 kb and 4.0 kb. MspI and RsaI also detect the same polymorphism.

HETEROZYGOSITY: 78% heterozygosity was observed in 104 unrelated Caucasians.

NOT POLYMORPHIC FOR: not detected.

CHROMOSOMAL LOCALIZATION: This probe has been assigned to chromosome 17p by multifactor linkage analysis (2) to loci (D17S1, MYH2, D17Z1) known to span this region.

MENDELIAN INHERITANCE: Co-dominant segregation of the pYNH37.3 VNTR was observed demonstrated in 52 three generation families.

PROBE AVAILABILITY: Available from the ATCC. Or contact Y.N..

OTHER COMMENTS: RFLPs were observed under normal hybridization stringency.

REFERENCES:

1. Y. Nakamura et al., Science 235: 1616-1622 (1987)
2. G.M. Lathrop et al., Am. J. Hum. Genet. 37:482-498 (1985)
3. S. Naylor et al., Cytognet. Cell Genet. 40:242-267 (1985)
4. Y. Nakamura et al., abstract sumbitted to the Human Gene Mapping Workshop 9