Nhe I and Hinc II polymorphisms in the human laminin B1 chain gene on 7q22

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SOURCE AND DESCRIPTION OF CLONES: pHL-40 and pHL-42 are overlapping cDNA clones that code for 4.2 kb of the 3' end of the 5.5 kb mRNA (1).

POLYMORPHISM: Nhe I detects a two allele polymorphism with fragments of 4.3 kb or 4.0 kb and an invariant band of 10.0 kb.

Hinc II detects a two allele polymorphism with fragments of 6.6 kb or 5.5 kb and 1.1 kb and invariant bands of 7.8 kb, 4.0 kb, 3.3 kb, 2.3 kb and 0.6 kb.

FREQUENCY: Studied in 60 chromosomes of unrelated Finnish individuals

(i) Nhe I:	4.3 kb allele	0.68
	4.0 kb allele	0.32
(ii) Hinc II:	6.6 kb allele	0.45
	5.5/1.1 kb allele	0.55

NOT POLYMORPHIC FOR: Bam HI, Eco RI, Hae III, Hind III, Hinf I, Msp I, Pst I, Rsa I or Taq I in 20 unrelated Finnish individuals.

CHROMOSOMAL LOCALIZATION: Chromosome 7q22 by somatic cell and *in situ* hybridization (1).

MENDELIAN INHERITANCE: Codominant inheritance of the Nhe I RFLP in one family and of the Hinc II RFLP in five families.

PROBE AVAILABILITY: Contact Karl Tryggvason

OTHER COMMENTS: The Hinc II polymorphism was recently described in 53 unrelated Caucasians with frequency of a 7 kb allele 0.37 and that of a 5.8/1.2 allele 0.63 (2).

REFERENCES: (1) Pikkarainen *et al.*, J. Biol. Chem. 262, 10454-10462, 1987
(2) Ardinger *et al.*, Nucleic Acids Res. 16, 8742, 1988.

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