A new polymorphism in the *ret* protooncogene (RET)

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Source and Description: Ret G is a 3.3 kb HindIII/BamHI genomic DNA fragment from the tyrosine kinase domain of the *ret* protooncogene (1).

Polymorphism: StyI digestion of genomic DNA and hybridization with the probe detects a two allele polymorphism comprising fragments of either 2.3 kb (A1) or 1.4 kb and 0.9 kb (A2). Constant bands of 0.35 kb and 0.25 kb are also observed.

Frequency: Allele frequencies estimated from 50 unrelated individuals
A1: 0.16
A2: 0.84

Not Polymorphic For: AvaI, AvaII, BamHI, BanI, BanII, BclI, BglII, BstEII, DdeI, DraI, EcoRI, EcoRV, HindIII, HinfI, KpnI, MspI, PstI, PvuII, RsaI, SphI, SstI, TaqI, XbaI, XhoI and XmnI.

Chromosomal Localization: The *ret* protooncogene has been mapped by in situ hybridization and somatic cell hybrid panel to 10q11.2 (2, 3).

Mendelian Inheritance: The StyI polymorphism shows mendelian segregation in 11 families with MEN2A.

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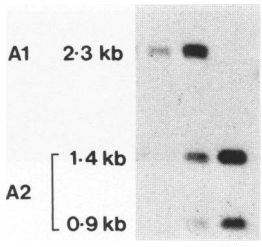

New TaqI polymorphism in the RRM1 gene

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Source/Description: The RFLP is detected by two probes, pE2.8 and pE1.8, which have been described elsewhere (1, 2).

Polymorphism: TaqI identifies a two-allele RFLP with fragments of 5162 bp (allele B1), and 3399 bp and 1763 bp (allele B2). The 1763 bp fragment of allele 2 is not detected by pE1.8. Exact sizes of all fragments are known from the sequence of this region of the RRM1 gene. No constant bands are identified.

Frequency: Estimated from 16 unrelated individuals.
Allele B1: 0.66
Allele B2: 0.34
Frequency of heterozygosity: 0.44.

Chromosomal Localization: RRM1 has been previously assigned to 11p15.4-p15.5 (3).

Mendelian Inheritance: Mendelian inheritance was observed in five two generation families (a total of 15 individuals).

Probe Availability: Both probes are available through ATCC, or from the authors.

Other Comments: 1) The polymorphism giving rise to this TaqI RFLP is located at nucleotide 1037 in the human RRM1 cDNA, as previously described (4). 2) Both pE1.8 and pE2.8 contain repeated sequences, and these must be saturated using sheared total human placental DNA prior to filter hybridization in order to reduce background. 3) A 6417 bp product of partial digestion may be detected by both pE1.8 and pE2.8.

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