

## Dinucleotide repeat polymorphism at the D18S34 locus

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*Source/Description:* A human genomic *AluI* fragment was cloned into mp10 and selected by hybridization to poly(dC-dA)·poly(dG-dT). The cloned fragment was designated Mfd26. Sequencing of Mfd26 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was 223 bp, and the predicted length of the amplified fragment was 115 bp.

*Primer sequences:* CAGAAAATTCTCTCTGGCTA (CA strand); CTCATGTTCTGGCAAGAAT (GT strand).

*Frequency:* Estimated from 108 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.78.

Allele (bp)	Frequency	Allele (bp)	Frequency
119	0.01	109	0.20
117	0.03	107	0.06
115	0.07	105	0.11
113	0.28	103	0.01
111	0.22		

*Chromosomal Localization:* Assigned to chromosome 18 using DNA templates isolated from panels of somatic cell hybrids.

*Mendelian Inheritance:* Co-dominant segregation was observed in 15 two generation families.

*Other Comments:* Conditions for the amplification reactions were as described in the reference except that samples were processed through 27 temperature cycles consisting of 1 min at 94°, 2 min at 55° and 2 min at 72°. Sizes of the alleles were determined by comparison to mp8 DNA sequencing ladders and were the averages of the sizes of the GT-strand and CA-strand bands. The dinucleotide repeat sequence in Mfd26 was of the form (AC)<sub>28</sub>A. The sequence of Mfd26 has been submitted to GenBank.

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*Reference:* Weber, J.L. and May, P.E. (1989) *Am. J. Hum. Genet.* **44**, 388–396.

## Dinucleotide repeat polymorphism at the D3S240 locus

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*Source/Description:* A human genomic *AluI* fragment was cloned into mp10 and selected by hybridization to poly(dC-dA)·poly(dG-dT). The cloned fragment was designated Mfd30. Sequencing of Mfd30 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was 221 bp, and the predicted length of the amplified fragment was 92 bp.

*Primer sequences:* CCATGTCCCATATCTCTACA (CA strand); TGAAATCACTGATGACAATG (GT strand).

*Frequency:* Estimated from 122 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.30.

Allele (bp)	Frequency	Allele (bp)	Frequency
99	0.01	91	0.02
97	0.08	89	0.01
95	0.01	87	0.82
93	0.01	83	0.04

*Chromosomal Localization:* Assigned to chromosome 3 using DNA templates isolated from panels of somatic cell hybrids.

*Mendelian Inheritance:* Co-dominant segregation was observed in 15 two generation families.

*Other Comments:* Conditions for the amplification reactions were as described in the reference except that samples were processed through 27 temperature cycles consisting of 1 min at 94°, 2 min at 55° and 2 min at 72°. Sizes of the alleles were determined by comparison to mp8 DNA sequencing ladders and were the averages of the sizes of the GT-strand and CA-strand bands. The dinucleotide repeat sequence in Mfd30 was of the form (AC)<sub>18</sub>A. The sequence of Mfd30 has been submitted to GenBank.

*Acknowledgements:* This work was supported by the Marshfield Clinic and NIH grant GM41773.

*Reference:* Weber, J.L. and May, P.E. (1989) *Am. J. Hum. Genet.* **44**, 388–396.

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