

# Dinucleotide repeat polymorphisms at the D5S107, D5S108, D5S111, D5S117 and D5S118 loci

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**Source/Description:** Human genomic DNA fragments were cloned into m13 and selected by hybridization to poly(dC-dA)·poly(dG-dT). Sequencing of the clones provided the information necessary for polymerase chain reaction primer synthesis.

Locus	Clone Designation	Clone Length	Predicted Length of Amplified Fragment	Primer Sequences
D5S107	Mfd27	194 bp	145 bp	GATCCACTTTAACCACAAATAC (CA strand) GGCATCAACTTGAACAGCAT (GT strand)
D5S108	Mfd34	183 bp	88 bp	GGTTCTTTTTTCTAGTCTTC (CA strand) TCATATAGCCTTTTGTTC (GT strand)
D5S111	Mfd40	259 bp	169 bp	GGCATCATTTAGAAGGAAAT (CA strand) ACATTTGTTTCAGACCAAG (GT strand)
D5S117	Mfd48	323 bp	151 bp	TGCTCCTGCTGAGAAATAG (CA strand) TAATATCCAACCACAAAGGT (GT strand)
D5S118	Mfd63	305 bp	89 bp	CAAAACCAAAAACCAAGGC (CA strand) CAATCTGTGACAGTTTCTCA (GT strand)

**Frequency:** Mfd27: Estimated from 120 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.78.

Allele (bp)	Frequency	Allele (bp)	Frequency
155	0.01	143	0.10
153	0.07	141	0.04
151	0.12	139	0.02
149	0.31	135	0.01
147	0.25	133	0.07

Mfd34: Estimated from 122 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.45.

Allele (bp)	Frequency	Allele (bp)	Frequency
93	0.01	87	0.02
91	0.34	83	0.04
89	0.59		

Mfd40: Estimated from 102 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.51

Allele (bp)	Frequency	Allele (bp)	Frequency
171	0.59	167	0.22
169	0.20		

Mfd48: Estimated from 112 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.62.

Allele (bp)	Frequency	Allele (bp)	Frequency
163	0.05	155	0.05
161	0.01	153	0.33
159	0.08	151	0.02
157	0.45	147	0.01

Mfd63: Estimated from 122 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.48.

Allele (bp)	Frequency	Allele (bp)	Frequency
92	0.02	84	0.02
90	0.08	82	0.01
88	0.05	80	0.04
86	0.70	78	0.08

**Chromosomal Localization:** The five markers were assigned to 5 using DNA templates isolated from panels of somatic cell hybrids.

**Mendelian Inheritance:** Co-dominant segregation of Mfd27, Mfd34, Mfd40, Mfd48, and Mfd63 was observed in 15–18 two or three 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 for Mfd27, Mfd34, and Mfd40, and the sizes of the most intense bands for Mfd48 and Mfd63. The dinucleotide repeat sequence in Mfd27 was of the form (CA)<sub>9</sub>AA(CA)<sub>19</sub>(GA)<sub>7</sub>, in Mfd34 (AC)<sub>4</sub>AT(AC)<sub>15</sub>, in Mfd40 (CA)<sub>13</sub>C(CA)<sub>6</sub>T(AC)<sub>5</sub>, in Mfd48 (AC)<sub>17</sub>, and in Mfd63 (CA)<sub>20</sub>C. Sequences of all five clones have been submitted to GenBank.

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

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