

Dinculeotide repeat polymorphisms at the D16S164, D16S168 and D16S186 loci at 16q21-q22.1

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Source/Description: The probes 16−15 (D16S164), 16−42 (D16S168) and 16−101 (D16S186) were positive when hybridized with poly(dC-dA).poly(dG-dT). Fragments from Sau3A1 digests (16PHAC- 15 and 16PHAC-42) or HaeIII digests (16PHAC-101) were subcloned into BamHI cut M13mp18 or SmaI cut M13mp19. Positive clones were selected for sequencing.

D16S164 Locus: Clone designation 16PHAC-15, predicted length 169 bp. The dinucleotide repeat was of the form $(GT)_{11}AT(GT)_4(GA)_9$.

Primer Sequences:
forward: 5′ CCT GTC TAA AAT ACC AAG AAG AAT CCA GG 3′
reverse 5′ GAC ATG TTA CCT TGC TTT AGG 3′

Allele Frequency: Estimated from 152 chromosomes of unrelated Caucasians. Heterozygosity = 0.38

Allele (bp)	Frequency	Allele (bp)	Frequency
A1 (179)	0.01	A4 (171)	0.04
A2 (177)	0.18	A5 (169)	0.75
A3 (173)	0.03		

D16S168 Locus: Clone designation 16PHAC-42, predicted length 143 bp. The dinucleotide repeat was of the form $(AC)_5AT(AC)_{10}$.

Primer Sequences:
forward 5′ CTA ACA AAC ACC TGA TGC TTG CAC C 3′
reverse 5′ TTA GGC AAC TGT GCA AAG AAG AGC C 3′

Allele Frequency: Estimated from 110 chromosomes of unrelated Caucasians. Heterozygosity = 0.16

Allele (bp)	Frequency	Allele (bp)	Frequency
A1 (145)	0.10	A2 (143)	0.90

D16S186 Locus: Clone designation 16PHAC-101, predicted length 132 bp. The dinucleotide repeat was of the form $(GT)_{13}$.

Primer Sequences:
forward 5′ GTT GGA GTC AAA CAA AGA GGA GAG C 3′
reverse 5′ AGG GTT ACA ATG CTA ACC AGT GGT G 3′

Allele Frequency: Estimated from 224 chromosomes of unrelated Caucasians. Heterozygosity = 0.57

Allele (bp)	Frequency	Allele (bp)	Frequency
A1 (178)	0.01	A6 (156)	0.01
A2 (174)	0.08	A7 (136)	0.01
A3 (170)	0.01	A8 (134)	0.01
A4 (168)	0.01	A9 (132)	0.58
A5 (160)	0.10	A10 (130)	0.21

Chromosomal Localisation: The D16S164 and D16S186 loci map to the proximal part of 16q2.1 proximal to FRA16B (1).

Mendelian Inheritance: Autosomal co-dominant inheritance was observed in 24 CEPH families for D16S164, 2 CEPH families for D16S168 and 35 CEPH families for D16S186. Visualisation of D16S186 alleles A1−A6 required longer exposure than alleles A7−A10.

PCR Conditions: Conditions for the PCR amplification were: 10 cycles of 1 minute at 94°C, 1.5 minutes at 60°C and 1.5 minutes at 72°C, then 25 cycles of 1 minute at 94°C, 1.5 minutes at 55°C and 1.5 minutes at 72°C. The final elongation cycle was 10 minutes at 72°C.

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Reference: 1) Chen,L.Z., Harris,P.C., Apostolou,S., Baker,E., Holman,K., Lane,S.A., Nancarrow,J.K., Whitmore,S.A., Stallings,R.L., Hildebrand,C.E., Richards,R.I., Sutherland,G.R. and Callen,D.F. (1991) *Genomics* **10**, 308−312.

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