*Bgl*II restriction fragment length polymorphism at the gene locus coding for the leukocyte surface antigen *CD37*

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Source/Description: The cDNA coding for the leukocyte surface antigen CD37 was isolated using a COS cell expression system as described (1). A 1.1 kilobase (kb) *CD37* cDNA insert which was cut out with *Xba*I from a pCDM8 vector was used in this study.

Polymorphism: The 1.1 kb cDNA probe identified a two-allele *Bgl*II polymorphism with fragment sizes 5.1 (A2) and 4.8 kb (A1). A 3.0 kb invariant fragment was detected in all the samples studied.

Frequency: 31 unrelated Caucasians were studied. Overall frequencies: A1 allele = 0.58; A2 allele = 0.42
Observed heterozygosity = 0.71
Calculated heterozygosity = 0.49

Chromosomal Localization: The *CD37* gene has been mapped by Southern hybridization to 19p13−q13.4 (2).

Mendelian Inheritance: Codominant segregation was observed in one Caucasian family.

Probe Availability: Contact Dr Brian Seed (1).

Acknowledgements: This study was funded by the Academy of Finland and the Oskar Öflund Foundation. We would like to thank Dr Brian Seed for the *CD37* cDNA and Dr Brendan Classon for his help.

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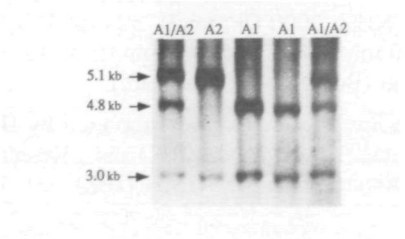

Figure 1. A two allele *Bgl*II polymorphism with 4.8 kb (A1) and 5.1 kb (A2) alleles and 3.0 kb constant fragment was detected in a Caucasian family with the *CD37* cDNA probe.

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A *Ban*II RFLP in the ZNF34 zinc finger gene on chromosome 8

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Source/Description: Kox 32 is a 1.4 kb cDNA fragment of the ZNF34 zinc finger gene cloned into the *Eco*RI site of the Bluescript plasmid vector (1).

Polymorphism: Kox 32 identifies a two-allele restriction fragment length polymorphism as revealed by Southern blot hybridization of *Ban*II digested DNA (Fig. 1). Allele A1 is 4.5 kb, allele A2 is 6.0 kb.

Frequency: Estimated from 44 chromosomes of Caucasian origin:

A1	4.5 kb	0.59
A2	6.0 kb	0.41

Observed heterozygosity = 0.48

Not Polymorphic For: Unknown.

Chromosomal Location: ZNF34 was mapped to 8q24, proximal to MYC (1). As MYC is located in 8q24.12−q24.13 (2) and both genes are intact in two patients with Langer-Giedion syndrome and a deletion of 8q22.3−q24.11 and 8q23.3−q24.12, respectively (La Pillo *et al.*, unpublished results), ZNF34 is located in 8q24.12−q24.13.

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

Other Comments: As ZNF34 maps outside of the Langer- Giedion syndrome chromosome region, it can be excluded from being involved in this disorder. However, the ZNF34 *Ban*II RFLP reported here may be useful for linkage studies in families with other diseases that have been mapped to 8q24.1.

Acknowledgements: This work was supported in part by the Deutsche Forschungsgemeinschaft. We thank Prof. E.Passarge for continuous support.

References: 1) Huebner,K., Druck,T. *et al.* (1991) *Am. J. Hum. Genet.* **48**, 726−740. 2) Takahashi,E., Hori,T. *et al.* (1991) *Cytogenet. Cell Genet.* **57**, 109−111.

Figure 1. Genomic DNA samples from ten unrelated individuals were digested with *Ban*II and analyzed by Southern blot hybridization with Kox 32. Fragment sizes were estimated from *Hind*III digested lambda DNA.

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