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# An Integrated Map of Human Chromosome 13 Allowing Regional Localization of Genetic Markers

**Key Words**
Chromosome 13
Integrated map
EST
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**Abstract**
37 CA repeats, 5 STSs, 9 ESTs, and 4 genes were mapped to 19 different intervals of chromosome 13 determined by the cytogenetic breakpoints of 19 different cell lines with interstitial deletions or translocations involving various parts of chromosome 13. A framework genetic linkage map was constructed from 25 of these microsatellite markers, to which 26 markers from other genetic maps were added. Thus, an integrated map of chromosome 13 resulted. Since the microsatellite markers included in this study derive from different genetic maps, an approximate regional localization can now be assigned in principle to any genetic marker on chromosome 13.

## Introduction

Chromosome 13 contains 3.6% of the human haploid genome, i.e. 114 Mb DNA. It has a genetic length of 130 cM [1]. According to the genome database (GDB version 5.4, November 1994), 56 genes have been mapped to this acrocentric chromosome. Among these are the genes responsible for retinoblastoma, RB1 [2]; Wilson's disease, ATP7B [3, 4]; chronic B cell leukaemia, BCLL [5–7]; Duchenne-like muscular dystrophy, DLMD [8]; Hirschsprung's disease, HSCR2 [9]; a nonsyndromic form of recessively inherited childhood deafness, NSRD1 [10]; and a locus for familial breast cancer, BCRA2 [11]. In addition, 68 ESTs and 755 other anonymous DNA segments have been assigned to chromosome 13.

Relatively few of these loci have been regionally assigned. Six deletion hybrid maps have been presented, ordering a total of 171 markers in maximally 11 different intervals [12–16]. Genotypes have been generated for a total of 120 microsatellite and 59 restriction fragment length polymorphism (RFLP) markers. Linkage maps have been built from these data, but none of these genetic maps provide detailed cytogenetic locations for the microsatellite loci [17–25].

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In the present study, a first integrated map of chromosome 13 is presented, based upon the breakpoints of nineteen cell lines with interstitial deletions or translocations involving various parts of chromosome 13. Fifteen of the cell lines have been provisionally described in the HGM11 report [26]. Three cell lines, ICA, ICC, and ICD were generated by irradiating monochromosomal hybrid GF7 [27] with a low dosage of X rays [28]. The other cell lines have been derived from individuals with a rearranged chromosome 13 by fusion of cells from that individual with a rodent cell line and selection of a hybrid clone containing the der(13), but not the complete homologue of chromosome 13. In contrast to the three cell lines mentioned earlier, these rodent cell lines always contain other human chromosomes in addition to the der(13).

37 CA repeats, 5 STSs, 9 expressed sequence tags (ESTs), and 4 genes were mapped to 19 different intervals determined by the cytogenetic breakpoints in the cell lines. A framework genetic linkage map was constructed from 25 of these microsatellite markers, to which 26 markers from other genetic maps were added. Thus, an integrated map of chromosome 13 resulted, allowing an approximate regional localization of any genetic marker on chromosome 13.

## Materials and Methods

*Cell Lines*

The hybrid cell lines used were GF7 containing human chromosome 13 only [27], ICA containing 13pter-13q14.1 [28], ICC containing 13pter-13q14.1 [Buys, unpubl. data], ICD containing 13pter-13q14.3 [28], WC-H38B3B6 containing 13pter-q13::13q21.1-qter [29], WC-H12D12 containing 13pter-q14::13q22-qter [29], NM-87-26XT containing 13q12-q14::13q22-qter [30], PKII-90-P5b (= PK88-25) containing 13pter-q12::13q21.2-qter [30], BARF7 containing 13pter-q22::13q34-qter [12], KSF39 containing 13pter-q14.1 [12], PPF22 containing 13pter-q14::13q31-qter [12], KBF11 containing 13pter-q12::13q14-qter [12], E8 containing 13q14.1-qter [17], D1 containing 13pter-q14.1 [17], RHF 407 containing 13q14.3-13qter [6], RHF 2324 containing 13pter-13q14.3 [6], GS89a containing 13pter-q14::13q32-qter [16], X13-C9 containing 13pter-q13, CF25 containing 13q12-13qter [31], and CF27 containing 13pter-q14.1::13q22-qter [32]. The cell lines were grown in RPMI 1640 medium supplemented with 10% fetal bovine serum. After treatment of the cells with SDS and proteinase K, DNA was isolated by phenol extraction according to standard procedures.

*Polymerase Chain Reactions*

Reactions were carried out on a thermocycler with 96-well microtiter plates in 20-μl vol of 'Supertaq reaction buffer' (Sphearo Q HT Biotechnology, Leiden, The Netherlands) with final concentrations of 10 m*M* Tris-HCl, pH 9.0; 50 m*M* KCl; 1.5 m*M* $Mg^{2+}$; 0.1% Triton X-100; 0.01% gelatin; 0.2 m*M* dATP, dGTP, and dTTP; 0.02 m*M* dCTP; 0.025 μl [$^{32}$P]dCTP; 0.125 u Taq polymerase (Supertaq, Sphearo Q HT Biotechnology, Leiden, The Netherlands); 100 ng of each primer, and 100–300 ng template DNA. Thermal cycling was carried out for 30 cycles, consisting of denaturation at 93°C for 45 s (first step 3 min), annealing at 5–10°C below $T_d$ for 1 min, and extension at 72°C for 1 min, followed by a final extension step for 3 min. Products were size-separated on 4–6% polyacrylamide gels and analyzed after exposure to an X-ray-sensitive film.

*Map Construction*

The genetic map was constructed using the expert system MultiMap [24], based on CRI-MAP [33]. It was run on a DEC5000/25 workstation under Ultrix 4.3, with a CLISP interpreter. Sex differences in recombination were calculated using the program sexdif_d, written and made publicly available by J.E. Blaschak and A. Chakravarti.

For the genetic map we used the most informative loci from table 1. In addition, the following markers were included: D13S115, D13S122 D13S125 [20]; D13S138, D13S141 [21]; D13S154, D13S159, D13S172, D13S173, D13S176, D13S219 [18]; D13S232, D13S260, D13S263, D13S267, D13S274, D13S283, D13S285, D13S289, D13S291 [22]; D13Z1 [34]; COL4A1 [36]; D13S107, D13S234, D13S235 [23, 37]; sLDA-1 [38]. Forty CEPH families were used in the genetic analysis: 1331, 1332, 1347, 1362, 1413, 1416, 884, 102, 13291, 13292, 13293, 13294, 1333, 1334, 1340, 1341, 1344, 1345, 1346, 1349, 1350, 1375, 1377, 1408, 1418, 1420, 1421, 1423, 1424, 66, 12, 23, 21, 2, 17, 37, 35, 28, 45, 104.

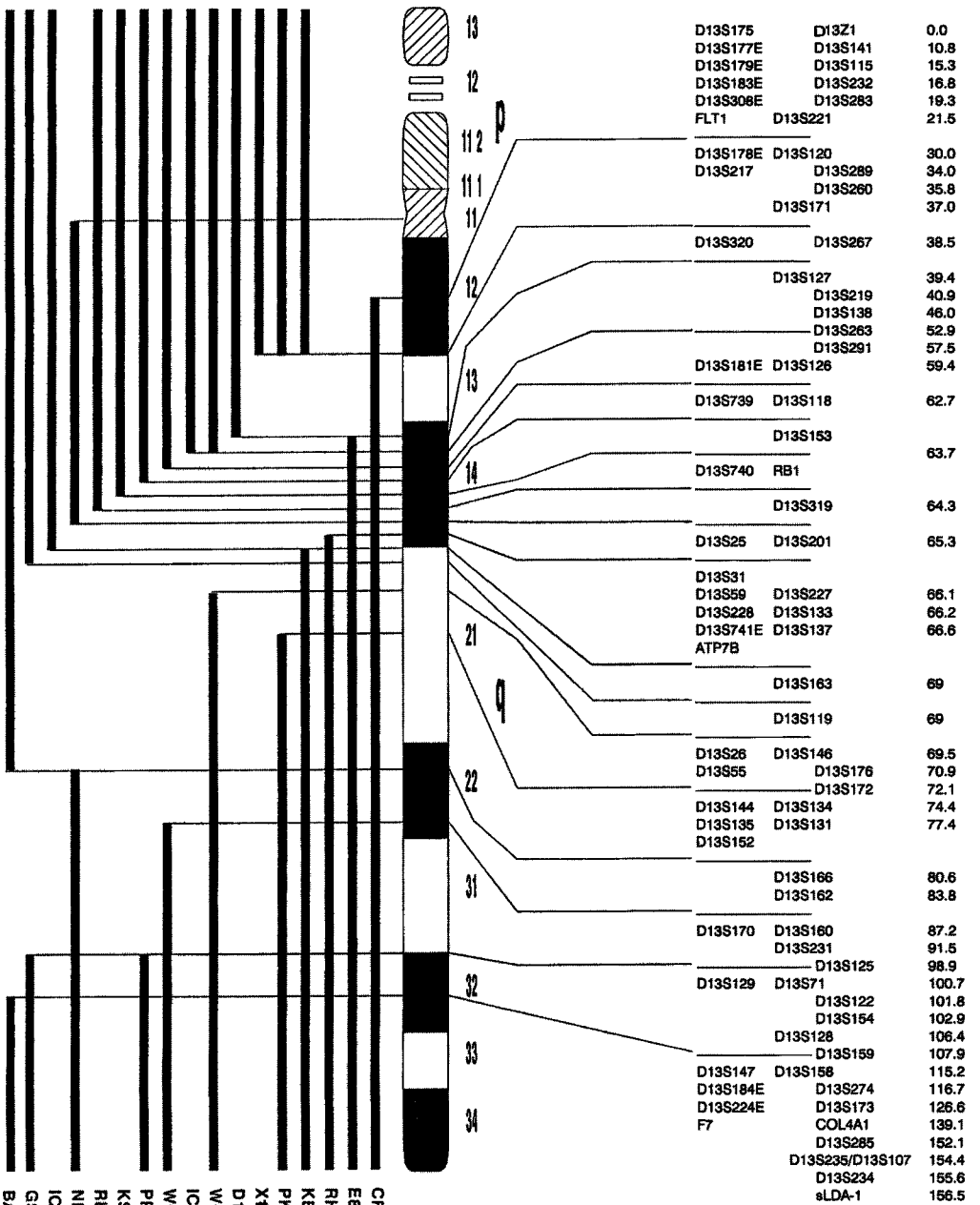
**Table 1.** Chromosome 13 loci used as STS in the deletion hybrid map

| Locus | Amplified sequence | Reference No. | Locus | Amplified sequence | Reference No. |
|---|---|---|---|---|---|
| ATP7B | STS | 3 | D13S163 | $(CA)_n$* | 18 |
| D13S25 | STS | 45 | D13S166 | $(CA)_n$* | 18 |
| D13S26 | STS | 16 | D13S170 | $(CA)_n$ | 18 |
| D13S31 | STS | 41 | D13S171 | $(CA)_n$* | 18 |
| D13S55 | STS | 16 | D13S175 | $(CA)_n$ | 18 |
| D13S59 | STS | 41 | D13S177E | EST | 48 |
| D13S71 | $(CA)_n$* | 46 | D13S178E | EST | 48 |
| D13S118 | $(CA)_n$* | 20 | D13S179E | EST | 48 |
| D13S119 | $(CA)_n$* | 20 | D13S181E | EST | 48 |
| D13S120 | $(CA)_n$* | 20 | D13S183E | EST | 48 |
| D13S126 | $(CA)_n$* | 20 | D13S184E | EST | 48 |
| D13S127 | $(CA)_n$* | 20 | D13S224E | EST | 48 |
| D13S128 | $(CA)_n$* | 21 | D13S201 | $(CA)_n$* | 39 |
| D13S129 | $(CA)_n$ | 21 | D13S217 | $(CA)_n$ | 18 |
| D13S131 | $(CA)_n$* | 21 | D13S221 | $(CA)_n$* | 18 |
| D13S133 | $(CA)_n$* | 21 | D13S227 | $(CA)_n$* | 45 |
| D13S134 | $(CA)_n$* | 21 | D13S228 | $(CA)_n$ | 45 |
| D13S137 | $(CA)_n$* | 21 | D13S231 | $(CA)_n$* | 49 |
| D13S135 | $(CA)_n$ | 21 | D13S308E | $(CAT)_n$ | 50 |
| D13S144 | $(CA)_n$ | 20 | D13S319 | $(CA)_n$* | 16 |
| D13S146 | $(CA)_n$* | 47 | D13S320 | $(CA)_n$ | 16 |
| D13S147 | $(CA)_n$ | 47 | D13S739 | $(CA)_n$ | this study |
| D13S152 | $(CA)_n$ | 18 | D13S740 | $(CA)_n$ | this study |
| D13S153 | $(CA)_n$* | 18 | D13S741E | EST | this study |
| D13S158 | $(CA)_n$* | 18 | FLT1 | $(CA)_n$ | 51 |
| D13S160 | $(CA)_n$* | 18 | F7 | VNTR | 52 |
| D13S162 | $(CA)_n$* | 18 | RB1 | RFLP* | 53 |

Asterisks indicate the most informative loci used for the genetic map. VNTR = Variable number of tandem repeat.

By a previously described approach [17, 37], two new markers were developed, D13S739, amplified by primers mgg11X: 5′-TGCTTCCTATGGCTGCCAG-3′, and mgg11Z: 5′-CTGTCCGTGGAAGTTAT-GAG-3′, and D13S740, amplified by primers mgg9X: 5′-GGGATAACAAAGAATGGAGG-3′, and mgg9Z: 5′-GCTTAACTGTCTCTGATTCG-3′. D13S741E, amplified by primers mgg16X: 5′-CAAGTGCTAC-CATACGGACA-3′, and mgg16Y: 5′-GCTGACTCA-TATGGCCTTAG-3′, is part of cDNA clone LGA3, identified when screening a liver cDNA library [40] with YAC 10H9.

**Fig. 1.** An integrated map of chromosome 13. The bars on the left schematically represent the breakpoints of the der(13) of the cell lines. Of the three columns of loci, the first two were physically mapped on the deletion hybrid panel to 1 of the 19 intervals, the last two were genetically ordered. The numerals represent the sex-average cumulative genetic distance from the centromeric region to the telomeric region in Kosambi cM. The KSF39 breakpoint is a genetic anchor for RB1, as the der(13) of this cell line has a break interrupting the RB1 gene [11]. The RB1 haplotype used in the genetic map [23] falls in intervals 7 and 8. D13S153 is also an RB1 intragenic marker.


13
12
11 2
11 1
11
12
13
14
21
22
31
32
33
34
p
q
D13S175 D13Z1 0.0
D13S177E D13S141 10.8
D13S179E D13S115 15.3
D13S183E D13S232 16.8
D13S308E D13S283 19.3
FLT1 D13S221 21.5
D13S178E D13S120 30.0
D13S217 D13S289 34.0
D13S260 35.8
D13S171 37.0
D13S320 D13S267 38.5
D13S127 39.4
D13S219 40.9
D13S138 46.0
D13S263 52.9
D13S291 57.5
D13S181E D13S126 59.4
D13S739 D13S118 62.7
D13S153 63.7
D13S740 RB1
D13S319 64.3
D13S25 D13S201 65.3
D13S31
D13S59 D13S227 66.1
D13S228 D13S133 66.2
D13S741E D13S137 66.6
ATP7B
D13S163 69
D13S119 69
D13S26 D13S146 69.5
D13S55 D13S176 70.9
D13S172 72.1
D13S144 D13S134 74.4
D13S135 D13S131 77.4
D13S152
D13S166 80.6
D13S162 83.8
D13S170 D13S160 87.2
D13S231 91.5
D13S125 98.9
D13S129 D13S71 100.7
D13S122 101.8
D13S154 102.9
D13S128 106.4
D13S159 107.9
D13S147 D13S158 115.2
D13S184E D13S274 116.7
D13S224E D13S173 126.6
F7 COL4A1 139.1
D13S285 152.1
D13S235/D13S107 154.4
D13S234 155.6
sLDA-1 156.5
BARF7
GS89a
ICD
NM-87-26-XT
RHF 2324
KSF39
PPF22
WC-H12D12 +CF27
ICA + ICC
WC-H38B386
D1
X13-C9
PKII-90-P5b
KBF11
RHF 407
E8
CF25

## Results and Discussion

*Definition of Intervals*

The markers used to construct the EUROGEM map of chromosome 13 [23] were tested by radioactive polymerase chain reaction for their possible presence in one or more of the 19 hybrid cell lines. Thus, 13 intervals could be distinguished. To increase the resolution of the map, a further number of markers were tested, including those described previously [17]. All markers were tested at least in duplicate. Included were 37 CA repeats from different genetic maps 5 STS markers, generated from probes that detect RFLP, 4 genes and 9 EST markers (see table 1). Out of 30 potential intervals that can be inferred from the chromosome 13 breakpoints in the 19 cell lines, these 54 loci define 19 different intervals (see fig. 1, first and second row of loci). For all cell lines the cytogenetic breakpoints of chromosome 13 are known (for references see Materials and Methods). All breakpoints and deletions described, except the distal deletion of cell line KBF11 and the proximal breakpoint of cell line NM-87-26-XT, have been used in constructing the intervals. Some breakpoints, however, were indistinguishable from each other. When the intervals were portrayed alongside chromosome 13, no ambiguities appeared, neither with respect to groups of loci per interval, nor with respect to the locations of a few probes that have been well-assigned previously, including D13Z1 at the centromeric region [34], RB1 at 13q14.2-q14.3 [35], D13S31 at the junction of bands 13q14.3-21.1 [41], D13S71 at proximal 13q32 [42], D13S158 at 13q33 [43], and COL4A1 [36], D13S107, D13S234, and D13S235 at 13q34 [23, 37].

The 19 intervals divide 98 Mb of the long arm of chromosome 13, but are not evenly distributed, as 8 out of 19 intervals identified are in band 13q14.

*The Genetic Map*

A genetic linkage map was constructed along the deletion hybrid breakpoint map. Using the MultiMap program [24], an initial linkage map was constructed with the most informative microsatellite markers ordered by the breakpoints of the cell lines. This initial map consisted of 25 ordered loci (second row in fig. 1). It was subsequently used as a framework map for the incorporation of a further 26 highly informative markers taken from different genetic maps. Genotypes were generated as described [23], downloaded from public databases, or obtained from the authors. All orders determined genetically are supported by at least 1,000:1 odds. Markers that increased any interval with more than 10% of its original genetic length were not incorporated. The final result was a map consisting of 50 distinct loci, mostly ordered genetically. In interval 11 the order D13S227-D13S133-D13S137 has been determined, however, by mapping to a YAC contig (Kooy, unpubl. data, confirming results obtained previously with a different YAC contig [44]). The genetic map spans 156.5 cM (fig. 1). It is the first chromosome 13 map to approach the genetic endpoint of the long arm by including sLDA-1, a marker isolated from a telomeric YAC [38]. The average female to male recombination ratio is 0.169. An excess male over female ratio is observed in the (peri-)centromeric region, the telomeric region, and in the intervals between the markers D13S171-D13S118, D13S146-D13S176, and D13S154-D13S128.

By comparing markers from genetic maps of human chromosome 13, with our integrated map (fig. 1), and genetic marker can now in principle be assigned to a specific cytogenetic region. A direct application of the map can be found, e.g. in the selection of YACs to characterize by fluorescence in situ hybridization abnormalities of chromosome

13, preliminarily identified by conventional chromosome analysis. YACs to be used for a more detailed characterization should contain either an STS which is on the map or one which is not on the map but flanked by two others that are included in the map.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## References


1 Morton NE: Parameters of the human genome. Proc Natl Acad Sci USA 1991;88:7474–7476.

2 Friend SH, Bernards R, Rogelj S, Weinberg RA, Rapaport JM, Albert DM, Dryja TP: A human DNA segment with properties of the gene that predisposes the retinoblastoma and osteosarcoma. Nature 1986; 323:643–646.

3 Bull PC, Thomas GR, Rommens JM, Forbes JR, Cox DW: The Wilson disease gene is a putative copper transporting P-type ATPase similar to the Menkes gene. Nature Genet 1993;5:327–337.

4 Tanzi RE, Petrukhin K, Chernov I, Pellequer JL, Wasco W, Ross B, Romano DM, Parano E, Pavone L, Brzustowicz LM, Devoto M, Peppercorn J, Bush AI, Sternlieb I, Pirastu M, Gusella JF, Evgrafov O, Penchaszadeh GK, Honig B, Edelman IS, Soares MB, Scheinberg IH, Gilliam TC: The Wilson disease gene is a copper transporting ATPase with homology to the Menkes disease gene. Nature Genet 1993;5:344–350.

5 Brown AG, Ross FM, Dunne EM, Steel CM, Weir-Thompson EM: Evidence for a new tumour suppressor locus (DBM) in human B-cell neoplasia telomeric to the retinoblastoma gene. Nature Genet 1993; 3:67–72.

6 Hawthorn LA, Chapman R, Oscier D, Cowell JK: The consistent 13q14 translocation breakpoint seen in chronic B-cell leukaemia (BCLL) involved a deletion of the D13S25 locus which lies distal to the retinoblastoma predisposition gene. Oncogene 1993;8:1415–1419.

7 Liu Y, Szekely L, Grandér D, Söderhäll S, Juliusson G, Gahrton G, Linder S, Einhorn S: Chronic lymphocytic leukemia cells with allelic deletions at 13q14 commonly have one intact RB1 gene: Evidence for a role of an adjacent locus. Proc Natl Acad Sci USA 1993;90:8697–8701.

8 Ben Othmane K, Ben Hamida M, Pericak-Vance MA, Ben Hamida C, Blel S, Carter SC, Bowcock AM, Petruhkin K, Gilliam TC, Roses AD, Hentati F, Vance JM: Linkage of Tunesian autosomal recessive Duchenne-like muscular dystrophy to the pericentromeric region of chromosome 13q. Nature Genet 1992;2: 315–317.

9 Puffenberger EG, Hosoda K, Washington SS, Nakao K, de Witt D, Yanagisawa M, Chakravarti A: A missense mutation of the endothelin-B receptor gene in multigenic Hirschsprung's disease. Cell 1994;79: 1257–1266.

10 Guilford P, Ben Arab S, Blanchard S, Levilliers J, Weissenbach J, Belkahia A, Petit C: A non-syndromic form of neurosensory, recessive deafness maps to the pericentromeric region of chromosome 13q. Nature Genet 1993;6:24–28.

11 Wooster R, Neuhausen SL, Mangion J, Quirk Y, Ford D, Collins N, Nguyen K, Seal S, Tran T, Averill D, Fields P, Marshall G, Narod S, Lenoir GM, Lynch H, Feunteun J, Deville P, Cornelisse CJ, Menko FH, Daly PA, Ormiston W, McManus R, Pyle C, Lewis CM, Cannon-Albright LA, Peto J, Ponder BAJ, Skolnick MH, Easton DF, Goldgar DE, Stratton MR: Localization of a breast cancer susceptibility gene, BCRA2, to chromosome 13q12-13. Science 1994;265:2088–2090.

12 Cowell JK, Mitchel CD: A somatic cell hybrid mapping panel for regional assignment of human chromosome 13 DNA sequences. Cytogenet Cell Genet 1989;52:1–6.

13 Houwen RHJ, Paulter SE, Barwell JA, Arden K, Buchanan JA, James CD, Cavenee WK, Buys CHCM, Cowell JK, Cox DW: Isolation and regional localization of twenty-five anonymous DNA probes on a chromosome 13 hybrid panel. Cytogenet Cell Genet 1991;57:97.

14 Washington SS, Bowcock AM, Gerken S, Matsunami N, Lesh D, Osborne-Lawrence SL, Cowell J, Ledbetter DH, White RL, Chakravarti A: A somatic cell hybrid map of human chromosome 13. Genomics 1993;18:486–495.

15 Michalski AJ, Cowell JK: Assignment of four sequence-tagged sites to three subregions of 13q12 using a somatic cell hybrid mapping panel. Genomics 1993;18:141–143.

16 Warburton D, Yu M-T, Tantravahi U, Lee C, Cayanis E, Russo J, Fisher SG: Regional localization of 32 *Not*I-*Hind*III fragments from a human chromosome 13 library by a somatic cell hybrid panel and in situ hybridization. Genomics 1993;16: 355–360.
17 Kooy RF, Verlind E, Houwen RHJ, Shapiro DN, Hawthorn LA, Cowell JK, Scheffer H, Buys CHCM: A deletion hybrid breakpoint map of the chromosomal region 13q14-q21, which includes the Wilson disease locus (WND), orders 19 genetic markers in 10 intervals. Eur J Hum Genet 1994;2:59–65.
18 Weissenbach J, Gyapay G, Dib C, Vignal A, Morissette J, Millasseau P, Vaysseix G, Lathrop M: A second generation linkage map of the human genome. Nature 1992;359: 794–801.
19 Bowcock AM, Gerken SC, Barnes RI, Shiang R, Wang Jabs E, Warren AC, Antonarakis S, Retief AE, Vergnaud G, Leppert M, Lalouel J-M, White RL, Cavalli-Sforza LL: The CEPH consortium linkage map of human chromosome 13. Genomics 1993;16:486–496.
20 Bowcock A, Osborne-Lawrence S, Barnes R, Chakravarti A, Washington S, Dunn C: Microsatellite polymorphism linkage map of human chromosome 13q. Genomics 1993; 15:376–486.
21 Petruhkin KE, Speer MC, Cayanis E, De Fátima Bonaldo M, Tantravi U, Soares MB, Fisher SG, Warburton D, Gillian TC, Ott J: A microsatellite genetic linkage map of human chromosome 13. Genomics 1993;15:76–85.
22 Gyapay G, Morissette J, Vignal A, Dib C, Fizames C, Millasseau P, Marc S, Bernardi G, Lathrop M, Weissenbach J: The 1993–94 Généthon human genetic linkage map. Nature Genet 1994;7:246–339.
23 Kooy RF, Wijngaard A, Verlind E, Vergnaud G, Scheffer H, Buys CHCM: The EUROGEM map of human chromosome 13. Eur J Hum Genet 1994;2:228–229.
24 Matise TC, Perlin M, Chakravarti A: Automated construction of genetic linkage maps using an expert system (MultiMap): A human genome linkage map. Nature Genet 1994;6: 385–390.
25 Buetow KH, Weber JL, Ludwigsen S, Schepbier-Heddema T, Duyk GM, Sheffield VC, Wang Z, Murray JC: Integrated human genome-wide maps constructed using the CEPH reference panel. Nature Genet 1994; 6:391–393.
26 Bowcock AM, Taggart RT: Report of the committee on the genetic constitution of chromosome 13, Human Gene Mapping 11. Cytogenet Cell Genet 1991;58:580–605.
27 Scheffer H, van der Lelie D, Aanstoot GH, Goor N, Nienhaus AJ, van der Hout AH, Pearson PL, Buys CHCM: A straightfoward approach to isolate DNA sequences with potential linkage to the retinoblastoma locus. Hum Genet 1986;74:249–255.
28 Buys CHCM, Scheffer H, Pearson PL, Aanstoot GH, Goor N, Niehaus AJ: Construction and application of a hybrid cell panel for regional localization of chromosome 13-specific DNA probes. Cytogenet Cell Genet 1985;40:597.
29 Griffin CA, Emanuel BS, Hansen JR, Cavenee WK, Myers JC: Human collagen genes encoding basement membrane 1(IV) and 2(IV) chains map to the distal long arm of chromosome 13. Proc Natl Acad Sci USA 1987;84:512–516.
30 Warburton D, Gerken S, Yu M-T, Jackson C, Handelin B, Housman D: Monochromosomal rodent-human hybrids from microcell fusion of human lymphoblastoid cells containing an inserted dominant selectable marker. Genomics 1990;6:358–366.
31 Mohandas T, Sparkes RS, Shapiro LJ: Genetic evidence for the inactivation of a human autosomal locus attached to an inactive X chromosome. Am J Hum Genet 1982;34: 811–817.
32 Sparkes RS, Kalina RE, Pagon RA, Salk DJ, Disteche CM: Separation of retinoblastoma and esterase D loci in a patient with sporadic retinoblastoma and del(13)(q14.1q22.3). Hum Genet 1984;68:258–259.
33 Lander ES, Green P: Construction of multi-locus genetic linkage maps in humans. Proc Natl Acad Sci USA 1987;84:2363–2367.
34 Warren AC, Bowcock AM, Farrer LA, Antonarakis SE: An alpha satellite DNA polymorphism specific for the centromeric region of chromosome 13. Genomics 1990;7:110–114.
35 Bowcock AM, Farrer LA, Hebert JM, Bale AE, Cavalli-Sforza L: Contiguous linkage map of chromosome 13q with 39 distinct loci separated on average by 5.1 centimorgans. Genomics 1991;11:517–529.
36 Bowcock AM, Farrer LA, Herbert JM, Bale AE, Cavalli-Sforza L: High recombination rate between two physically close human basement membrane collagen genes at the distal end of chromosome 13q. Proc Natl Acad Sci USA 1988;85:2701–2705.
37 Vergnaud G, Mariat D, Apiou F, Aurias A, Lathrop M, Lauthier V: The use of synthetic tandem repeats to isolate new VNTR loci: Cloning of a human hypermutable sequence. Genomics 1991;11:135–144.
38 Vocero-Akabani A, Sanjurjo H, Fair K, Helms C, Donis-Keller H: Progress in the characterization of a human genomic YAC library selected on the basis of homology to $T_2AG_3$. Am J Hum Genet 1994; 55(suppl):1198.
39 Kooy RF, Verlind E, Wijngaard A, Shapiro DN, Scheffer H, Buys CHCM: A highly informative dinucleotide repeat polymorphism at D13S201, between RB1 and WND. Hum Genet, in press.
40 van den Hoff MJB, Geerts WJC, Das AT, Moorman AFM, Lamers WH: cDNA sequence of the long mRNA for human glutamine synthase. Biochim Biophys Acta 1991; 1090:249–251.
41 Kooy RF, Van der Veen AY, Verlind E, Houwen RHJ, Scheffer H, Buys CHCM: Physical localisation of the chromosomal marker D13S31 places the Wilson disease locus at the junction of bands q14.3 and q21.1 of chromosome 13. Hum Genet 1993;91:504–506.
42 Spielvogel H, Hennies H-C, Claussen U, Washington SS, Chakravarti A, Reis A: Band-specific localization of microsatellite at D13S71 by microdissection and enzymatic amplification. Am J Hum Genet 1992;50: 1031–1037.

43 Sames S, Clarkson SG, Blaschak J, Chakravarti A, Morris MA, Scherly D, Antonarakis SE: Dinucleotide repeat polymorphism within ERCC5 gene. Hum Molec Genet 1994;3: 214.
44 White A, Tomfohrde J, Stewart E, Barnes R, Le Paslier D, Weissenbach J, Cavalli-Sforza L, Farrer L, Bowcock A: A 4.5 megabase yeast artificial chromosome contig from human chromosome 13q14.3 ordering 9 polymorphic microsatellites (22 sequence tagged sites) tightly linked to the Wilson disease locus. Proc Natl Acad Sci USA 1993;90: 10105–10109.
45 Stuart EA, White A, Tomfohrde J, Osborne-Lawrence S, Prestridge L, Bonne-Tamir B, Scheinberg IH, St George-Hyslop P, Giagheddu M, Kim J-W, Seo JK, Lo WH-Y, Ivanova-Smolenskaya IA, Limborska SA, Cavalli-Sforza LL, Farrer LA, Bowcock AM: Polymorphic microsatellite and Wilson disease. Am J Hum Genet 1993;53:864–873.
46 Weber JL, Kwitek AE, May PE: Dinucleotide repeat polymorphism at the D13S71 locus. Nucleic Acids Res 1990;18:4638.
47 Hennies H-C, Reis A: Three dinucleotide microsatellite polymorphism on human chromosome 13. Hum Molec Genet 1993;2:87.
48 Adams MD, Dubnick M, Kerlage AR, Moreno AR, Kelley JM, Utterback TR, Nagle JW, Fields C, Venter JC: Sequence identification of 2375 human brain genes. Nature 1992;355:632–634.
49 Saksova L, Hennies H-C, Reis A: Dinucleotide repeat polymorphism at the locus D13S231. Hum Molec Genet 1993;2:1082.
50 Haddad LA, Pena SDJ: CAT repeat polymorphism in a human expressed sequence tag (EST00444) (D13S308). Hum Molec Genet 1993;2:1748.
51 Polymeropoulos MH, Rath DS, Xiao H, Merril CR: Dinucleotide repeat polymorphism at the human fms-related tyrosine kinase gene (FLT1). Nucleic Acids Res 1991;19: 2803.
52 Marchetti G, Gemmati D, Patracchini P, Pinotti M, Bernardi F: PCR detection of a repeat polymorphism within the F7 gene. Nucleic Acids Res 1991;19:4570.
53 Vaughn GL, Toguchida J, McGee TL, Dryja TP: PCR detection of the Tth111I RFLP at the RB locus. Nucleic Acids Res 1990;18:4965.